ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880277	14427	36583	531	177

Description

6500733279 rne:hi0413 ribonuclease e:rnase e (gtcfc:7.1:10.9) (ec:3.1.4.-) (keggfc:4.4) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0413 HI0413 Haemophilus influenzae 727 -11537137 124412 ribonuclease e (cl:ribonuclease e) (ec:3.1.4.-) (db:pir1.dat) E64066 E64066 Haemophilus influenzae 727 -11537137 7500953296 hi0413 ribonuclease e rne (db:genpept-bct1) (de:haemophilus influenzae rd section 39 of 163 of the complete genome.) (nt:similar to sp:p21513 gb:x67470 gb:l23942 gb:m62747) (le:7169) (re:10024) (di:direct) U32724 U32724 g1573386 Haemophilus influenzae Rd 71421 -11537137 5000694375 (de:(hi0413) (pn:rnase e:ribonuclease e:rne) (gn:rne) (gtcfc:7.1) (ec:3.1.4.-) (rne_haein) (keggfc:4.4) (tigrfc:11.1) (db:gtc-haemophilus influenzae)) HI0413 HI0413 Haemophilus influenzae 727 10066104

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880280	14428	36584	1182	393

Description

6500733280 lpxb:hi1060 lipid a disaccharide synthetase:lipid-a-disaccharide synthase (gtcfc:7.1:11.2) (ec:2.4.1.182) (keggfc:4.4) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1060 HI1060 Haemophilus influenzae 727 -11537138 82458 lpxb:hi1060 (ec:2.4.1.182) (de:lipid-a-disaccharide synthase,) (db:swissprot) LPXB_HAEIN P45011 HAEMOPHILUS INFLUENZAE 727 -11537138 7500885145 hi1060 lipid-a-disaccharide synthetase lpxb (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to gb:m19334 sp:p10441 pid:1208953) (le:7344) (re:8516) (di:complement) U32786 U32786 g1574611 Haemophilus influenzae Rd 71421 -11537138 5000694378 (de:(hi1060) (pn:lipid-a-disaccharide synthase:lipid a disaccharide synthetase:lpxb) (gn:lpxb) (gtcfc:7.1) (ec:2.4.1.182) (lpxb_haein) (keggfc:4.4) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI1060 HI1060 Haemophilus influenzae 727 10126707

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880284	14429	36585	1353	450

Description

6500733281 lpxa:hi1061 udp-n-acetylglucosamine acetyltransferase:acyl-acyl-carrier-protein udp-n-acetylglucosamine o-acyltransferase (gtcfc:7.1:11.2) (ec:2.3.1.129) (keggfc:4.4) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1061 HI1061 Haemophilus influenzae 727 -11537139 82453 lpxa:hi1061 (ec:2.3.1.129) (de:(ec 2.3.1.129) (udp-n-acetylglucosamine acyltransferase)) (db:swissprot) LPXA_HAEIN P43887 HAEMOPHILUS INFLUENZAE 727 -11537139 138020 acyl-acyl-carrier-protein --udp-n-acetylglucosamine o-acyltransferase,) (cl:udp-n-acetylglucosamine acyltransferase) (ec:2.3.1.129) (db:pir2.dat) F64180 F64180 Haemophilus influenzae 727 -11537139 7500885143 hi1061 udp-n-acetylglucosamine acetyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to gb:m19334 sp:p10440 pid:1208952) (le:8583) (re:9371) (di:complement) U32786 U32786 g1574612 Haemophilus influenzae Rd 71421 -11537139 5000694379 (de:(hi1061) (pn:acyl-:udp-n-acetylglucosamine acetyltransferase:lpxa) (gn:lpxa) (gtcfc:7.1) (ec:2.3.1.129) (lpxa_haein) (keggfc:4.4) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI1061 HI1061 Haemophilus influenzae 727 10024675

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880302	14430	36586	273	90

Description

5000694380 mura:murz:hi1081 murz:udp-n-acetylglucosamine 1-carboxyvinyltransferase:enoylpyruvate transferase:udp-n-acetylglucosamine enolpyruvyl transferase:ept (gtcfc:7.1:11.4) (ec:2.5.1.7) (keggfc:4.4) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1081 HI1081 Haemophilus influenzae 727 -11537140 84697 mura:murz:hi1081 (ec:2.5.1.7) (de:transferase) (ept)) (db:swissprot) MURA_HAEIN P45025 HAEMOPHILUS INFLUENZAE 727 -11537140 167245 udp-n-acetylglucosamine 1-carboxyvinyltransferase (cl:udp-n-acetylglucosamine 1-carboxyvinyltransferase murz) (ec:2.5.1.7) (db:pir2.dat) A64182 A64182 Haemophilus influenzae 727 -11537140 7500886092 hi1081 udp-n-acetylglucosamine (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to gb:m92358 sp:p28909 pid:146902) (le:5547) (re:6821) (di:complement) U32788 U32788 g1574635 Haemophilus influenzae Rd 71421 -11537140 6500733282 mura:murz murz:udp-n-acetylglucosamine 1-carboxyvinyltransferase:enoylpyruvate transferase:udp-n-acetylglucosamine enolpyruvyl transferase:ept (gtcfc:7.1:11.4) (ec:2.5.1.7) (keggfc:4.4) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1081 HI1081 Haemophilus influenzae 727 -11537140

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880303	14431	36587	411	136

Description

6500733283 ispb:hi0881 sp:p19641:octaprenyl-diphosphate synthase:octaprenyl pyrophosphate synthetase (gtcfc:7.1:9.12:11.3:14.1) (ec:2.5.1.-) (keggfc:7.2:9.13) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0881 HI0881 Haemophilus influenzae 727 -11537141 79995 ispb:hi0881 (ec:2.5.1.-) (de:synthetase)) (db:swissprot) ISPB_HAEIN P44916 HAEMOPHILUS INFLUENZAE 727 -11537141 166551 hypothetical protein hi0881 (cl:prenyl transferase a) (db:pir2.dat) I64160 I64160 Haemophilus influenzae 727 -11537141 7500884299 hi0881 octaprenyl-diphosphate synthase ispb (db:genpept-bct1) (de:haemophilus influenzae rd section 85 of 163 of the complete genome.) (nt:similar to sp:p19641 gb:x68873 pid:388220) (le:137) (re:1126) (di:direct) U32770 U32770 g1573899 Haemophilus influenzae Rd 71421 -11537141 5000694391 (de:(hi0881) (pn:octaprenyl pyrophosphate synthetase:octaprenyl-diphosphate synthase:p19641) (gn:ispb) (gtcfc:7.2:9.12) (ec:2.5.1.-) (ispb_haein) (keggfc:7.2:9.13) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0881 HI0881 Haemophilus influenzae 727 10022245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880310	14432	36588	435	144

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880313	14433	36589	1062	353

Description

6500733284 malq:hi1356 4-alpha-glucanotransferase:amylomaltase:disproportionating enzyme:d-enzyme (gtcfc:7.2) (ec:2.4.1.25) (keggfc:7.1) (tigrfc:5.2) (db:gtc-haemophilus influenzae) HI1356 HI1356 Haemophilus influenzae 727 -11537142 82909 malq:hi1356 (ec:2.4.1.25) (de:(disproportionating enzyme) (d-enzyme)) (db:swissprot) MALQ_HAEIN P45176 HAEMOPHILUS INFLUENZAE 727 -11537142 165997 4-alpha-glucanotransferase homolog (db:pir2.dat) H64118 H64118 Haemophilus influenzae 727 -11537142 7500885275 hi1356 4-alpha-glucanotransferase malq (db:genpept-bct1) (de:haemophilus influenzae rd section 130 of 163 of the completegenome.) (nt:similar to gb:m32793 sp:p15977 pid:146715) (le:61) (re:2160) (di:direct) U32815 U32815 g1574819 Haemophilus influenzae Rd 71421 -11537142 5000694392 (de:(hi1356) (pn:4-alpha-glucanotransferase:disproportionating enzyme:d-enzyme:amylomaltase:malq) (gn:malq) (gtcfc:7.2) (ec:2.4.1.25) (malq_haein) (keggfc:11.1) (tigrfc:5.2) (db:gtc-haemophilus influenzae)) HI1356 HI1356 Haemophilus influenzae 727 10025129

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880316	14434	36590	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880319	14435	36591	264	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880328	14436	36592	261	86

Description

6500733285 glgb:hi1357 1:4-alpha-glucan branching enzyme:glycogen branching enzyme (gtcfc:7.2) (ec:2.4.1.18) (keggfc:7.1) (tigrfc:5.5) (db:gtc-haemophilus influenzae) HI1357 HI1357 Haemophilus influenzae 727 -11537143 73785 glgb:hi1357 (ec:2.4.1.18) (de:enzyme)) (db:swissprot) GLGB_HAEIN P45177 HAEMOPHILUS INFLUENZAE 727 -11537143 138081 1:4-alpha-glucan branching enzyme (cl:1,4-alpha-glucan branching enzyme) (ec:2.4.1.18) (db:pir2.dat) I64118 I64118 Haemophilus influenzae 727 -11537143 7500882400 hi1357 1:4-alpha-glucan branching enzyme glgb (db:genpept-bct1) (de:haemophilus influenzae rd section 130 of 163 of the completegenome.) (nt:similar to gb:m13751 sp:p07762 pid:146142) (le:2170) (re:4362) (di:direct) U32815 U32815 g1574820 Haemophilus influenzae Rd 71421 -11537143 5000694387 (de:(hi1357) (pn:glycogen branching enzyme:1,4-alpha-glucan branching enzyme:glgb) (gn:glgb) (gtcfc:7.2) (ec:2.4.1.18) (glgb_haein) (keggfc:7.1) (tigrfc:5.5) (db:gtc-haemophilus influenzae)) HI1357 HI1357 Haemophilus influenzae 727 10016317

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880337	14437	36593	1659	553

Description

6500733286 glgc:hi1359 adp-glucose synthetase:glucose-1-phosphate adenylyltransferase:adp-glucose synthase:adp-glucose pyrophosphorylase (gtcfc:7.2) (ec:2.7.7.27) (keggfc:7.1) (tigrfc:5.5) (db:gtc-haemophilus influenzae) HI1359 HI1359 Haemophilus influenzae 727 -11537144 73800 glgc:hi1359 (ec:2.7.7.27) (de:synthase) (adp-glucose pyrophosphorylase)) (db:swissprot) GLGC_HAEIN P43796 HAEMOPHILUS INFLUENZAE 727 -11537144 139277 glucose-1-phosphate adenylyltransferase (cl:glucose-1-phosphate adenylyltransferase) (ec:2.7.7.27) (db:pir2.dat) B64119 B64119 Haemophilus influenzae 727 -11537144 7500882403 hi1359 glucose-1-phosphate adenylyltransferase glgc (db:genpept-bct1) (de:haemophilus influenzae rd section 130 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1789837 percent ident:) (le:6427) (re:7761) (di:direct) U32815 U32815 g1574822 Haemophilus influenzae Rd 71421 -11537144 5000694388 (de:(hi1359) (pn:glucose-1-phosphate adenylyltransferase:adp-glucose synthase:adp-glucose pyrophosphorylase:adp-glucose synthetase:glgc) (gn:glgc) (gtcfc:7.2) (ec:2.7.7.27) (glgc_haein) (keggfc:7.1) (tigrfc:5.5) (db:gtc-haemophi) HI1359 HI1359 Haemophilus influenzae 727 10016332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880349	14438	36594	327	108

Description

6500733287 glga:hi1360 glycogen synthase:starch:bacterial glycogen synthase (gtcfc:7.2) (ec:2.4.1.21) (keggfc:7.1) (tigrfc:5.5) (db:gtc-haemophilus influenzae) HI1360 HI1360 Haemophilus influenzae 727 -11537145 73777 glga:hi1360 (ec:2.4.1.21) (de:synthase)) (db:swissprot) GLGA_HAEIN P45179 HAEMOPHILUS INFLUENZAE 727 -11537145 138105 adpglucose--starch bacterial glycogen glucosyltransferase (cl:starch synthase) (ec:2.4.1.21) (db:pir2.dat) C64119 C64119 Haemophilus influenzae 727 -11537145 7500882396 hi1360 glycogen synthase glga (db:genpept-bct1) (de:haemophilus influenzae rd section 130 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1789836 percent ident:) (le:7869) (re:9299) (di:direct) U32815 U32815 g1574823 Haemophilus influenzae Rd 71421 -11537145 5000694389 (de:(hi1360) (pn:starch:bacterial glycogen synthase:glycogen synthase:glga) (gn:glga) (gtcfc:7.2) (ec:2.4.1.21) (glga_haein) (keggfc:7.1) (tigrfc:5.5) (db:gtc-haemophilus influenzae)) HI1360 HI1360 Haemophilus influenzae 727 10016309

Tc542 U.S. PTO 09/417507 10/14/99

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880357	14439	36595	423	140

Description

6500733288 glgp:hi1361 alpha-glucan phosphorylase:glycogen phosphorylase (gtcfc:7.2) (ec:2.4.1.1) (keggfc:7.1) (tigrfc:5.5) (db:gtc-haemophilus influenzae) HI1361 HI1361 Haemophilus influenzae 727 -11537146 89699 glgp:hi1361 (ec:2.4.1.1) (de:glycogen phosphorylase,) (db:swissprot) PHSG_HAEIN P45180 HAEMOPHILUS INFLUENZAE 727 -11537146 138062 glycogen phosphorylase (cl:phosphorylase) (ec:2.4.1.1) (db:pir2.dat) D64119 D64119 Haemophilus influenzae 727 -11537146 7500888079 hi1361 glycogen phosphorylase glgp (db:genpept-bct1) (de:haemophilus influenzae rd section 130 of 163 of the completegenome.) (nt:similar to gb:j03966 sp:p13031 gb:m22368 gb:x16931) (le:9545) (re:12010) (di:direct) U32815 U32815 g1574824 Haemophilus influenzae Rd 71421 -11537146 5000694390 (de:(hi1361) (pn:glycogen phosphorylase:alpha-glucan phosphorylase:glgp) (gn:glgp) (gtcfc:7.2) (ec:2.4.1.1) (phsg_haein) (keggfc:7.1) (tigrfc:5.5) (db:gtc-haemophilus influenzae)) HI1361 HI1361 Haemophilus influenzae 727 10031821

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880366	14440	36596	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880374	14441	36597	669	222

Description

6500733289 pldb:hi0645 lysophospholipase l2:probable lysophospholipase l2:lecithinase b (gtcfc:8.4:13.10) (ec:3.1.1.5) (keggfc:8.4) (tigrfc:5.3) (db:gtc-haemophilus influenzae) HI0645 HI0645 Haemophilus influenzae 727 -11537147 89964 pldb:hi0645 (ec:3.1.1.5) (de:probable lysophospholipase l2, (lecithinase b)) (db:swissprot) PLDB_HAEIN P44800 HAEMOPHILUS INFLUENZAE 727 -11537147 166974 lysophospholipase l2 homolog (db:pir2.dat) A64084 A64084 Haemophilus influenzae 727 -11537147 7500888156 hi0645 lysophospholipase l2 pldb (db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the complete genome.) (nt:similar to pid:1449198 percent ident: 37.83;) (le:9642) (re:10583) (di:complement) U32747 U32747 g1573643 Haemophilus influenzae Rd 71421 -11537147 5000694404 (de:(hi0645) (pn:probable lysophospholipase l2:lecithinase b:lysophospholipase l2:pldb) (gn:pldb) (gtcfc:8.4) (ec:3.1.1.5) (pldb_haein) (keggfc:8.4) (tigrfc:5.3) (db:gtc-haemophilus influenzae)) HI0645 HI0645 Haemophilus influenzae 727 10032084

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880375	14442	36598	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880376	14443	36599	570	189

Description

6500733290 lgt:hi0904 prolipoprotein diacylglyceryl transferase (gtcfc:8.5:11.1) (ec:2.4.99.-) (keggfc:8.5) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0904 HI0904 Haemophilus influenzae 727 -11537148 82006 lgt:hi0904 (ec:2.4.99.-) (de:prolipoprotein diacylglyceryl transferase,) (db:swissprot) LGT_HAEIN P44930 HAEMOPHILUS INFLUENZAE 727 -11537148 167110 prolipoprotein diacylglyceryl transferase (cl:prolipoprotein diacylglyceryl transferase) (ec:2.4.99.-) (db:pir2.dat) F64101 F64101 Haemophilus influenzae 727 -11537148 7500884984 hi0904 prolipoprotein diacylglyceryl transferase lgt (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to sp:p37149 gb:u12289 pid:516036) (le:3285) (re:4091) (di:direct) U32772 U32772 g1573923 Haemophilus influenzae Rd 71421 -11537148 5000694405 (de:(hi0904) (pn:prolipoprotein diacylglyceryl transferase:lgt) (gn:lgt) (gtcfc:8.5) (ec:2.4.99.-) (lgt_haein) (keggfc:8.5) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0904 HI0904 Haemophilus influenzae 727 10024240

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880381	14444	36600	354	117

Description

6500733291 hemx:hi0603 putative uroporphyrin-iii c-methyltransferase:urogen iii methylase (gtcfc:9.10) (ec:2.1.1.107) (keggfc:9.10) (db:gtc-haemophilus influenzae) HI0603 HI0603 Haemophilus influenzae 727 -11537149 76770 hemx:hi0603 (ec:2.1.1.107) (de:iii methylase)) (db:swissprot) HEMX_HAEIN P44773 HAEMOPHILUS INFLUENZAE 727 -11537149 167260 uroporphyrin-iii c-methyltransferase homolog (db:pir2.dat) D64080 D64080 Haemophilus influenzae 727 -11537149 7500883203 hi0603 uroporphyrin-iii c-methyltransferase hemx (db:genpept-bct1) (de:haemophilus influenzae rd section 57 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p09127 gb:x12614 gb:x13406) (le:6790) (re:7482) (di:complement) U32742 U32742 g1573595 Haemophilus influenzae Rd 71421 -11537149 5000694406 (de:(hi0603) (pn:putative uroporphyrin-iii c-methyltransferase:urogen iii methylase) (gn:hemx) (gtcfc:9.10) (ec:2.1.1.107) (hemx_haein) (keggfc:9.10) (db:gtc-haemophilus influenzae)) HI0603 HI0603 Haemophilus influenzae 727 10019133

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880386	14445	36601	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880389	14446	36602	549	182

Description

5000694407 hemh:visa:hi1160 visa:ferrochelatase:protoheme ferro-lyase:heme synthetase (gtcfc:9.10) (ec:4.99.1.1) (keggfc:9.10) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI1160 HI1160 Haemophilus influenzae 727 -11537150 76780 hemh:visa:hi1160 (ec:4.99.1.1) (de:synthetase)) (db:swissprot) HEMZ_HAEIN P43868 HAEMOPHILUS INFLUENZAE 727 -11537150 142062 hemh:visa ferrochelatase::heme synthetase:protoheme ferro-lyase (cl:ferrochelatase) (ec:4.99.1.1) (db:pir2.dat) I64186 I64186 Haemophilus influenzae 727 -11537150 7500883208 hi1160 ferrochelatase hemh (db:genpept-bct1) (de:haemophilus influenzae rd section 111 of 163 of the completegenome.) (nt:similar to gb:d90259 sp:p23871 pid:285770 gb:u00096) (le:173) (re:1144) (di:complement) U32796 U32796 g1574087 Haemophilus influenzae Rd 71421 -11537150 6500733292 hemh:visa visa:ferrochelatase:protoheme ferro-lyase:heme synthetase (gtcfc:9.10) (ec:4.99.1.1) (keggfc:9.10) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI1160 HI1160 Haemophilus influenzae 727 -11537150

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880394	14447	36603	558	185

Description

6500733293 hxuc:hi0113 heme utilization protein:heme-hemopexin utilization protein c precursor (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI0113 HI0113 Haemophilus influenzae 727 -11537151 78310 hxuc:hi0113 (de:heme-hemopexin utilization protein c precursor) (db:swissprot) HXC1_HAEIN P44523 HAEMOPHILUS INFLUENZAE 727 -11537151 166181 outer membrane protein hxuc homolog (db:pir2.dat) B64049 B64049 Haemophilus influenzae 727 -11537151 7500883648 hi0113 hemin receptor hemr (db:genpept-bct1) (de:haemophilus influenzae rd section 11 of 163 of the complete genome.) (nt:similar to sp:q56989 pid:1407797 percent identity:) (le:8199) (re:10433) (di:direct) U32696 U32696 g1573065 Haemophilus influenzae Rd 71421 -11537151 5000694408 (de:(hi0113) (pn:heme-hemopexin utilization protein c precursor:heme utilization protein:hxuc) (gn:hxuc) (gtcfc:9.10) (ec:) (hxc1_haein) (keggfc:11.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae)) HI0113 HI0113 Haemophilus influenzae 727 10020649

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880403	14448	36604	615	205

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880404	14449	36605	417	138

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880422	14450	36606	1104	367

Description

GTC ORF with score 145 to: (sr:fruit fly) (db:genpept-inv) (de:drosophila melanogaster rga and atu genes, complete cds.) (nt:contains arg-ser and ser-arg dipeptides; c-terminal) (le:78:1474:2325) (re:1373:2260:2388) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880423	14451	36607	321	106

Description

6500733294 hxub:hi0263 heme-hemopexin utilization:heme-hemopexin utilization protein b (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI0263 HI0263 Haemophilus influenzae 727 -11537152 78273 hxub:hi0263 (de:heme-hemopexin utilization protein b precursor) (db:swissprot) HXB1_HAEIN P44601 HAEMOPHILUS INFLUENZAE 727 -11537152 166184 hxub outer membrane protein hxub (db:pir2.dat) D64058 D64058 Haemophilus influenzae 727 -11537152 7500883647 hi0263 heme-hemopexin utilization protein b hxub (db:genpept-bct1) (de:haemophilus influenzae rd section 27 of 163 of the complete genome.) (nt:similar to sp:p45356 pid:1573229 percent identity:) (le:5083) (re:6780) (di:direct) U32712 U32712 g1573229 Haemophilus influenzae Rd 71421 -11537152 5000694409 (de:(hi0263) (pn:heme-hemopexin utilization protein b:heme-hemopexin utilization:hxub) (gn:hxub) (gtcfc:9.10) (ec:) (hxb1_haein) (keggfc:11.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae)) HI0263 HI0263 Haemophilus influenzae 727 10020612

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880426	14452	36608	1371	457

Description

5000694410 oxygen-independent coproporphyrinogen iii oxidase:hemn:hypothetical protein (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI0463 HI0463 Haemophilus influenzae 727 -11537153 112361 hi0463 (de:hypothetical protein hi0463) (db:swissprot) YGGW_HAEIN P43899 HAEMOPHILUS INFLUENZAE 727 -11537153 167064 hypothetical protein hi0463 (cl:oxygen-independent coproporphyrinogen oxidase) (db:pir2.dat) B64070 B64070 Haemophilus influenzae 727 -11537153 7500924207 hi0463 oxygen-independent coproporphyrinogen iii (db:genpept-bct1) (de:haemophilus influenzae rd section 44 of 163 of the complete genome.) (nt:similar to pid:882484 sp:p52062 gb:u00096) (le:2654) (re:3805) (di:direct) U32729 U32729 g1573441 Haemophilus influenzae Rd 71421 -11537153 6500733295 oxygen-independent coproporphyrinogen iii oxidase:hemn:hypothetical protein (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI0463 HI0463 Haemophilus influenzae 727 -11537153

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880460	14453	36609	1179	393

Description

6500733296 hemy:hi0602 protoporphyrinogen oxidase:hemg homolog:protein homolog (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI0602 HI0602 Haemophilus influenzae 727 -11537154 76773 hemy:hi0602 (de:hemy protein homolog) (db:swissprot) HEMY_HAEIN P44772 HAEMOPHILUS INFLUENZAE 727 -11537154 167121 hemy protein homolog (db:pir2.dat) C64080 C64080 Haemophilus influenzae 727 -11537154 7500883205 hi0602 hemy protein hemy (db:genpept-bct1) (de:haemophilus influenzae rd section 57 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p09128 gb:x12614 pid:148201) (le:4972) (re:6258) (di:complement) U32742 U32742 g1573594 Haemophilus influenzae Rd 71421 -11537154 5000694411 (de:(hi0602) (pn:protein homolog:protoporphyrinogen oxidase:hemg homolog:hemy) (gn:hemy) (gtcfc:9.10) (ec:) (hemy_haein) (keggfc:11.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae)) HI0602 HI0602 Haemophilus influenzae 727 10019136

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880484	14454	36610	1962	653

Description

5000694412 protoporphyrinogen oxidase:hemk:hypothetical adenine-specific methylase hi1201 (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI1201 HI1201 Haemophilus influenzae 727 -11537155 111827 hi1201 (ec:2.1.1.72) (de:hypothetical adenine-specific methylase hi1201,) (db:swissprot) YFCB_HAEIN P45106 HAEMOPHILUS INFLUENZAE 727 -11537155 167122 protoporphyrinogen oxidase homolog (db:pir2.dat) F64189 F64189 Haemophilus influenzae 727 -11537155 7500923366 hi1201 adenine specific methylase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to sp:p39199 gb:u00096 pid:1788670 percent) (le:7242) (re:8186) (di:complement) U32799 U32799 g1574130 Haemophilus influenzae Rd 71421 -11537155 6500733297 protoporphyrinogen oxidase:hemk:hypothetical adenine-specific methylase hi1201 (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI1201 HI1201 Haemophilus influenzae 727 -11537155

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880509	14455	36611	348	115

Description

6500733298 hemk:hi1559 protoporphyrinogen oxidase:possible protoporphyrinogen oxidase (gtcfc:9.10) (ec:1.3.3.-) (keggfc:14.1) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI1559 HI1559 Haemophilus influenzae 727 -11537156 76736 hemk:hi1559 (de:hemk protein homolog) (db:swissprot) HEMK_HAEIN P45253 HAEMOPHILUS INFLUENZAE 727 -11537156 167123 hemk hemk protein::protoporphyrinogen oxidase (ec:1.3.3.-) (db:pir2.dat) H64129 H64129 Haemophilus influenzae 727 -11537156 7500883186 hi1559 hemk protein hemk (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:d28567 sp:p37186 pid:466533) (le:13851) (re:14729) (di:complement) U32830 U32830 g1574403 Haemophilus influenzae Rd 71421 -11537156 5000694413 (de:(hi1559) (pn:possible protoporphyrinogen oxidase:protoporphyrinogen oxidase:hemk) (gn:hemk) (gtcfc:9.10) (ec:1.3.3.-) (hemk_haein) (keggfc:11.1) (tigrfc:2.3) (db:gtc-haemophilus influenzae)) HI1559 HI1559 Haemophilus influenzae 727 10019099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880510	14456	36612	555	184

Description

5000694414 hemm protein:hemm:hemm protein homolog (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI1607 HI1607 Haemophilus influenzae 727 -11537157 76742 lolb:hemm:hi1607 (de:outer membrane lipoprotein lolb precursor) (db:swissprot) LOLB_HAEIN P45270 HAEMOPHILUS INFLUENZAE 727 -11537157 166855 hypothetical protein hi1607 (db:pir2.dat) I64172 I64172 Haemophilus influenzae 727 -11537157 7500883189 hi1607 hemm protein hemm (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:similar to gb:m77236 sp:p30752 pid:154281 percent) (le:6828) (re:7457) (di:direct) U32834 U32834 g1574449 Haemophilus influenzae Rd 71421 -11537157 6500733299 hemm protein:hemm:hemm protein homolog (gtcfc:9.10) (keggfc:14.2) (tigrfc:2.3) (db:gtc-haemophilus influenzae) HI1607 HI1607 Haemophilus influenzae 727 -11537157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880511	14457	36613	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880512	14458	36614	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880515	14459	36615	666	221

Description

6500733300 chln:hi0118 molybdopterin biosynthesis protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI0118 HI0118 Haemophilus influenzae 727 -11537158 4000708116 hi0118 (de:hypothetical protein hi0118) (db:swissprot) YGDL_HAEIN Q57097 HAEMOPHILUS INFLUENZAE 727 -11537158 167005 hypothetical protein hi0118 (db:pir2.dat) C64049 C64049 Haemophilus influenzae 727 -11537158 7500924090 hi0118 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the complete genome.) (nt:similar to gb:d21145 pid:471103 pid:882707) (le:1205) (re:1990) (di:direct) U32698 U32698 g1573073 Haemophilus influenzae Rd 71421 -11537158 5000694415 (de:(hi0118) (pn:molybdopterin biosynthesis protein:chln) (gn:chln) (gtcfc:9.11) (ec:) (keggfc:11.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae)) HI0118 HI0118 Haemophilus influenzae 727 10088253

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880516	14460	36616	399	132

Description

5000694416 moba:mob:hi0844 molybdopterin-guanine dinucleotide biosynthesis protein:mob:molybdopterin-guanine dinucleotide biosynthesis protein a:protein fa (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI0844 HI0844 Haemophilus influenzae 727 -11537159 83959 moba:mob:hi0844 (de:fa)) (db:swissprot) MOBA_HAEIN P44899 HAEMOPHILUS INFLUENZAE 727 -11537159 167008 molybdopterin-guanine dinucleotide biosynthesis protein a homolog (db:pir2.dat) A64098 A64098 Haemophilus influenzae 727 -11537159 7500885742 hi0844 molybdopterin-guanine dinucleotide biosynthesis (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32173 pid:304963 gb:u00096) (le:3394) (re:3972) (di:complement) U32766 U32766 g1573858 Haemophilus influenzae Rd 71421 -11537159 6500733301 moba:mob molybdopterin-guanine dinucleotide biosynthesis protein:mob:molybdopterin-guanine dinucleotide biosynthesis protein a:protein fa (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI0844 HI0844 Haemophilus influenzae 727 -11537159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880526	14461	36617	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880532	14462	36618	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880533	14463	36619	1998	665

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880545	14464	36620	708	235

Description

5000694417 molybdenum-pterin binding protein:mopi:probable molybdenum-pterin binding protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1370 HI1370 Haemophilus influenzae 727 -11537160 84022 hi1370 (de:probable molybdenum-pterin binding protein) (db:swissprot) MOP_HAEIN P45183 HAEMOPHILUS INFLUENZAE 727 -11537160 167002 molybdenum-pterin-binding protein (db:pir2.dat) I64119 I64119 Haemophilus influenzae 727 -11537160 7500885776 hi1370 molybdenum-pterin binding protein mopi (db:genpept-bct1) (de:haemophilus influenzae rd section 132 of 163 of the completegenome.) (nt:similar to gb:m17157 sp:p04952 sp:p08854 gb:m17158) (le:2645) (re:2854) (di:complement) U32817 U32817 g1574203 Haemophilus influenzae Rd 71421 -11537160 6500733302 molybdenum-pterin binding protein:mopi:probable molybdenum-pterin binding protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1370 HI1370 Haemophilus influenzae 727 -11537160

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880570	14465	36621	1233	411

Description

5000694418 moea:chle:hi1448 molybdopterin biosynthesis protein:chle:molybdopterin biosynthesis moea protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1448 HI1448 Haemophilus influenzae 727 -11537161 83997 moea:chle:hi1448 (de:molybdopterin biosynthesis moea protein) (db:swissprot) MOEA_HAEIN P45210 HAEMOPHILUS INFLUENZAE 727 -11537161 167004 moea:chle molybdopterin biosynthesis protein moea:molybdopterin-converting factor chle (db:pir2.dat) B64124 B64124 Haemophilus influenzae 727 -11537161 7500885757 hi1448 molybdopterin biosynthesis protein moea (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:m21151 sp:p12281 pid:145539 gb:u00096) (le:4341) (re:5555) (di:direct) U32823 U32823 g1574287 Haemophilus influenzae Rd 71421 -11537161 6500733303 moea:chle molybdopterin biosynthesis protein:chle:molybdopterin biosynthesis moea protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1448 HI1448 Haemophilus influenzae 727 -11537161

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880582	14466	36622	645	214

Description

5000694419 moeb:chln:hi1449 molybdopterin biosynthesis protein:chln:molybdopterin biosynthesis moeb protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1449 HI1449 Haemophilus influenzae 727 -11537162 83999 moeb:chln:hi1449 (de:molybdopterin biosynthesis moeb protein) (db:swissprot) MOEB_HAEIN P45211 HAEMOPHILUS INFLUENZAE 727 -11537162 167006 moeb:chln molybdopterin biosynthesis protein moeb (cl:molybdopterin biosynthesis protein moeb) (db:pir2.dat) C64124 C64124 Haemophilus influenzae 727 -11537162 7500885762 hi1449 molybdopterin biosynthesis protein moeb (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:m21151 sp:p12282 pid:145540 gb:u00096) (le:5559) (re:6290) (di:direct) U32823 U32823 g1574288 Haemophilus influenzae Rd 71421 -11537162 6500733304 moeb:chln molybdopterin biosynthesis protein:chln:molybdopterin biosynthesis moeb protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1449 HI1449 Haemophilus influenzae 727 -11537162

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880606	14467	36623	366	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880611	14468	36624	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880628	14469	36625	1182	393

Description

6500733305 moae:hi1673 molybdopterin converting factor subunit 2:mpt converting factor:molybdenum cofactor biosynthesis protein e (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1673 HI1673 Haemophilus influenzae 727 -11537163 83954 moae:hi1673 (de:subunit)) (db:swissprot) MOAE_HAEIN P45308 HAEMOPHILUS INFLUENZAE 727 -11537163 167007 molybdopterin-converting factor 16k chain (cl:molybdopterin-converting factor chain 2) (db:pir2.dat) H64135 H64135 Haemophilus influenzae 727 -11537163 7500885731 hi1673 molybdopterin converting factor:subunit 2 (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to gb:x70420 sp:p30749 pid:42012 gb:u00096) (le:6931) (re:7383) (di:complement) U32840 U32840 g1574523 Haemophilus influenzae Rd 71421 -11537163 5000694420 (de:(hi1673) (pn:molybdopterin:mpt converting factor, subunit 2:molybdenum cofactor biosynthesis protein e:molybdopterin converting factor, subunit 2:moae) (gn:moae) (gtcfc:9.11) (ec:) (moae_haein) (keggfc:11.2) (tigrfc:2.6) (db) HI1673 HI1673 Haemophilus influenzae 727 10026161

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880633	14470	36626	249	82

Description

6500733306 moad:hi1674 molybdopterin:mpt converting factor:subunit 1:molybdenum cofactor biosynthesis protein d (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1674 HI1674 Haemophilus influenzae 727 -11537164 83952 moad:hi1674 (de:subunit)) (db:swissprot) MOAD_HAEIN P45309 HAEMOPHILUS INFLUENZAE 727 -11537164 7500885728 hi1674 molybdopterin converting factor:subunit 1 (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to sp:p30748 pid:42011 gb:u00096) (le:7384) (re:7629) (di:complement) U32840 U32840 g1574524 Haemophilus influenzae Rd 71421 -11537164 5000694421 (de:(hi1674) (pn:molybdenum cofactor biosynthesis protein d:molybdopterin:mpt converting factor, subunit 1:moad) (gn:moad) (gtcfc:9.11) (ec:) (moad_haein) (keggfc:11.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae)) HI1674 HI1674 Haemophilus influenzae 727 10126725

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880644	14471	36627	300	99

Description

6500733307 moac:hi1675 molybdenum cofactor biosynthesis protein:molybdenum cofactor biosynthesis protein c (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1675 HI1675 Haemophilus influenzae 727 -11537165 83950 moac:hi1675 (de:molybdenum cofactor biosynthesis protein c) (db:swissprot) MOAC_HAEIN P45310 HAEMOPHILUS INFLUENZAE 727 -11537165 166999 moac molybdenum cofactor biosynthesis protein c (cl:molybdenum cofactor biosynthesis protein c) (db:pir2.dat) A64136 A64136 Haemophilus influenzae 727 -11537165 7500885725 hi1675 molybdenum cofactor biosynthesis protein c (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to gb:x70420 sp:p30747 pid:42010 gb:u00096) (le:7631) (re:8113) (di:complement) U32840 U32840 g1574525 Haemophilus influenzae Rd 71421 -11537165 5000694422 (de:(hi1675) (pn:molybdenum cofactor biosynthesis protein c:molybdenum cofactor biosynthesis protein:moac) (gn:moac) (gtcfc:9.11) (ec:) (moac_haein) (keggfc:11.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae)) HI1675 HI1675 Haemophilus influenzae 727 10026157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880645	14472	36628	582	193

Description

6500733308 moaa:hi1676 molybdenum cofactor biosynthesis protein a (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae) HI1676 HI1676 Haemophilus influenzae 727 -11537166 83947 moaa:hi1676 (de:molybdenum cofactor biosynthesis protein a) (db:swissprot) MOAA_HAEIN P45311 HAEMOPHILUS INFLUENZAE 727 -11537166 167000 molybdenum cofactor biosynthesis protein a (cl:haemophilus influenzae molybdenum cofactor biosynthesis protein a) (db:pir2.dat) B64136 B64136 Haemophilus influenzae 727 -11537166 7500885712 hi1676 molybdenum cofactor biosynthesis protein a (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to sp:p30745 pid:42008 gb:u00096) (le:8205) (re:9218) (di:complement) U32840 U32840 g1574526 Haemophilus influenzae Rd 71421 -11537166 5000694423 (de:(hi1676) (pn:molybdenum cofactor biosynthesis protein a:moaa) (gn:moaa) (gtcfc:9.11) (ec:) (moaa_haein) (keggfc:11.2) (tigrfc:2.6) (db:gtc-haemophilus influenzae)) HI1676 HI1676 Haemophilus influenzae 727 10026154

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880647	14473	36629	186	61

Description

6500733309 lipb:hi0027 lipoate-protein ligase b:lipoate biosynthesis protein b (gtcfc:9.12:9.6:9.7) (ec:6.-.-.-) (keggfc:9.7:9.13) (tigrfc:2.4) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-quinone biosynthesis:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabo... HI0027 HI0027 Haemophilus influenzae 727 -11537167 166953 lipb lipoate--protein ligase:b:lipoic acid metabolism protein lipb (ec:6.3.4.-) (db:pir2.dat) H64043 H64043 Haemophilus influenzae 727 -11537167 7500960711 hi0027 lipoate biosynthesis protein b lipb (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to gb:l07636 sp:p30976 pid:146622 gb:u00096) (le:5182) (re:5820) (di:complement) U32688 U32688 g1572972 Haemophilus influenzae Rd 71421 -11537167 5000694424 (de:(hi0027) (pn:lipoate-protein ligase b:lipoate biosynthesis protein b:lipb) (gn:lipb) (gtcfc:9.12) (ec:6.-.-.-) (lipb_haein) (keggfc:9.13) (tigrfc:2.4) (db:gtc-haemophilus influenzae)) HI0027 HI0027 Haemophilus influenzae 727 10088212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880648	14474	36630	189	62

Description

6500733310 mene:hi0194 o-succinylbenzoate-coenzyme a synthase:o-succinylbenzoic acid--coa ligase:osb-coa synthetase:o-succinylbenzoate-coa synthase (gtcfc:9.12) (ec:6.2.1.26) (keggfc:9.13) (tigrfc:2.5) (db:gtc-haemophilus influenzae) HI0194 HI0194 Haemophilus influenzae 727 -11537168 83448 mene:hi0194 (ec:6.2.1.26) (de:(o-succinylbenzoate-coa synthase)) (db:swissprot) MENE_HAEIN P44565 HAEMOPHILUS INFLUENZAE 727 -11537168 167047 4-chlorobenzoate--coa ligase homolog (cl:o-succinylbenzoate--coa ligase) (db:pir2.dat) F64053 F64053 Haemophilus influenzae 727 -11537168 7500885494 hi0194 o-succinylbenzoate--coa ligase mene (db:genpept-bct1) (de:haemophilus influenzae rd section 19 of 163 of the complete genome.) (nt:similar to gb:l35031 sp:p37353 pid:520813 gb:u00096) (le:6646) (re:8004) (di:direct) U32704 U32704 g1573152 Haemophilus influenzae Rd 71421 -11537168 5000694425 (de:(hi0194) (pn:o-succinylbenzoic acid--coa ligase:osb-coa synthetase:o-succinylbenzoate-coa synthase:o-succinylbenzoate-coenzyme a synthase:mene) (gn:mene) (gtcfc:9.12) (ec:6.2.1.26) (mene_haein) (keggfc:9.13) (tigrfc:2.5) (d)) HI0194 HI0194 Haemophilus influenzae 727 10025662

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880652	14475	36631	264	87

Description

6500733311 mend:hi0283 2-succinyl-6-hydroxy-2:4-cyclohexadiene-1-carboxylate synthase:shchc synthase / 2-oxoglutarate decarboxylase:alpha-ketoglutarate decarboxylase:kdc (gtcfc:9.12) (ec:4.1.1.71) (keggfc:9.13) (tigrfc:2.5) (db:gtc-haemophilus influenzae) HI0283 HI0283 Haemophilus influenzae 727 -11537169 83445 mend:hi0283 (ec:4.1.1.71) (de:ketoglutarate decarboxylase) (kdc)) (db:swissprot) MEND_HAEIN P44612 HAEMOPHILUS INFLUENZAE 727 -11537169 165964 2-succinyl-6-hydroxy-2:4-cyclohexadiene-1-carboxylate synthase homolog (cl:mend protein) (db:pir2.dat) D64059 D64059 Haemophilus influenzae 727 -11537169 7500885492 hi0283 2-succinyl-6-hydroxy-2 (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:similar to sp:p17109 gb:m21787 gb:l04464 pid:146815) (le:7121) (re:8827) (di:complement) U32714 U32714 g1573248 Haemophilus influenzae Rd 71421 -11537169 5000694426 (de:(hi0283) (pn:shchc synthase :2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase:mend) (gn:mend) (gtcfc:9.12) (ec:4.1.1.71) (mend_haein) (keggfc:9.13) (tigrfc:2.5) (db:gtc-haemophilus influenzae)) HI0283 HI0283 Haemophilus influenzae 727 10025659

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880667	14476	36632	732	243

Description

6500733312 menf:hi0285 isochorismate synthase:entc:menaquinone-specific isochorismate synthase (gtcfc:9.12) (ec:5.4.99.6) (keggfc:9.13) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0285 HI0285 Haemophilus influenzae 727 -11537170 83452 menf:hi0285 (ec:5.4.99.6) (de:menaquinone-specific isochorismate synthase,) (db:swissprot) MENF_HAEIN P44613 HAEMOPHILUS INFLUENZAE 727 -11537170 166930 probable isochorismate synthase (cl:isochorismate synthase) (ec:5.4.99.6) (db:pir2.dat) E64059 E64059 Haemophilus influenzae 727 -11537170 7500885496 hi0285 menaquinone-specific isochorismate synthase (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:similar to pid:1050907 gb:u00096 pid:1399684) (le:8843) (re:10135) (di:complement) U32714 U32714 g1573249 Haemophilus influenzae Rd 71421 -11537170 5000694427 (de:(hi0285) (pn:menaquinone-specific isochorismate synthase:isochorismate synthase:entc) (gn:menf) (gtcfc:9.12) (ec:5.4.99.6) (menf_haein) (keggfc:9.13) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0285 HI0285 Haemophilus influenzae 727 10025666

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880668	14477	36633	1386	462

Description

6500733313 dnag:hi0532 dna primase (gtcfc:9.12:10.8) (ec:2.7.7.-) (keggfc:9.13) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0532 HI0532 Haemophilus influenzae 727 -11537171 91036 dnag:hi0532 (ec:2.7.7.-) (de:dna primase,) (db:swissprot) PRIM_HAEIN Q08346 HAEMOPHILUS INFLUENZAE 727 -11537171 153213 dna primase (cl:dna primase) (ec:2.7.7.-) (db:pir2.dat) A64075 A64075 Haemophilus influenzae 727 -11537171 7500888462 hi0532 dna primase dnag (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:similar to gb:j01687 sp:p02923 gb:v00274 gb:v00346) (le:4835) (re:6616) (di:direct) U32735 U32735 g1573516 Haemophilus influenzae Rd 71421 -11537171 5000694376 (de:(hi0532) (pn:dna primase:dnag) (gn:dnag) (gtcfc:7.1:9.12) (ec:2.7.7.-) (prim_haein) (keggfc:4.4:9.13) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0532 HI0532 Haemophilus influenzae 727 10033145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880674	14478	36634	531	176

Description

GTC ORF with score 493 to: (fn:catalyzes the hydrolysis of glucosides) (db:genpept-pln1) (ec:3.2.1.21) (de:coccidioides immitis cytosolic beta-glucosidase (bgl1) gene,complete cds.) (nt:bgl1) (le:660:1500:1810) (re:1436:1751:3393) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880675	14479	36635	2043	680

Description

6500733314 menb:hi0968 dihydroxynaphthoic acid synthase:naphthoate synthase:dihydroxynaphthoic acid synthetase:dhna synthetase (gtcfc:9.12) (ec:4.1.3.36) (keggfc:9.13) (tigrfc:2.5) (db:gtc-haemophilus influenzae) HI0968 HI0968 Haemophilus influenzae 727 -11537172 83440 menb:hi0968 (ec:4.1.3.36) (de:(dhna synthetase)) (db:swissprot) MENB_HAEIN P44960 HAEMOPHILUS INFLUENZAE 727 -11537172 166095 menb naphthoate synthase:menb (cl:naphthoate synthase:enoyl-coa hydratase homology) (ec:4.1.3.36) (db:pir2.dat) B64105 B64105 Haemophilus influenzae 727 -11537172 7500885486 hi0968 naphthoate synthase menb (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:similar to gb:m93421 sp:p27290 pid:145740 gb:u00096) (le:9976) (re:10833) (di:direct) U32777 U32777 g1573991 Haemophilus influenzae Rd 71421 -11537172 5000694428 (de:(hi0968) (pn:naphthoate synthase:dihydroxynaphthoic acid synthetase:dhna synthetase:dihydroxynaphthoic acid synthase:menb) (gn:menb) (gtcfc:9.12) (ec:4.1.3.36) (menb_haein) (keggfc:9.13) (tigrfc:2.5) (db:gtc-haemophilus infl) HI0968 HI0968 Haemophilus influenzae 727 10025654

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880677	14480	36636	387	128

Description

GTC ORF with score 186 to: (sr:s.fibuligera (strain hut7212) dna, clones psfbetag(1,2,3,4)) (db:genpept-pln1) (de:s.fibuligera extracellular beta-glucosidase 2 (bgl2) gene, completecds.) (nt:beta-glucosidase 2 precursor) (le:422) (re:3064) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880678	14481	36637	345	115

Description

6500733315 menc:hi0969 2-carboxyphenyl-4-oxybutyric acid synthase:o-succinylbenzoate-coa synthase:osb synthase:4-:2-carboxyphenyl-4-oxybutyric acid synthase (gtcfc:9.12) (keggfc:14.2) (tigrfc:2.5) (db:gtc-haemophilus influenzae) HI0969 HI0969 Haemophilus influenzae 727 -11537173 83442 menc:hi0969 (de:4-oxybutyric acid synthase)) (db:swissprot) MENC_HAEIN P44961 HAEMOPHILUS INFLUENZAE 727 -11537173 165970 o-succinylbenzoate synthase (db:pir2.dat) C64105 C64105 Haemophilus influenzae 727 -11537173 7500885488 hi0969 o-succinylbenzoate-coa synthase menc (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:similar to gb:l07256 sp:p29208 pid:146811 gb:u00096) (le:10848) (re:11891) (di:direct) U32777 U32777 g1573992 Haemophilus influenzae Rd 71421 -11537173 5000694429 (de:(hi0969) (pn:o-succinylbenzoate-coa synthase:osb synthase:2"-carboxyphenyl-4-oxybutyric acid synthase:4-:2"-carboxyphenyl-4-oxybutyric acid synthase:menc) (gn:menc) (gtcfc:9.12) (ec:) (menc_haein) (keggfc:11.2) (tigrfc:2.5)) HI0969 HI0969 Haemophilus influenzae 727 10025656

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880690	14482	36638	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880694	14483	36639	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880697	14484	36640	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880713	14485	36641	1590	529

Description

GTC ORF with score 166 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c4d7.) (nt:spac4d7.09, probable translation initiation factor) (le:20500:20773:21140:21653) (re:20648:21043:21611:21795) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880717	14486	36642	204	67

Description

GTC ORF with score 121 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c4d7.) (nt:spac4d7.09, probable translation initiation factor) (le:20500:20773:21140:21653) (re:20648:21043:21611:21795) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880737	14487	36643	708	235

Description

GTC ORF with score 146 to: (db:genpept-inv) (de:caenorhabditis elegans unc-89 (unc-89) gene, complete cds.) (nt:giant ig superfamily member located in the middle) (le:4920:5656:5974:7518) (re:4969:5929:6110:7688) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880744	14488	36644	2250	749

Description

6500733316 hin0598:hi1189 coenzyme pqq synthesis protein iii:pqqiii:hypothetical protein (gtcfc:9.12) (keggfc:14.2) (tigrfc:2.5) (db:gtc-haemophilus influenzae) HI1189 HI1189 Haemophilus influenzae 727 -11537174 112285 hi1189 (de:hypothetical protein hi1189) (db:swissprot) YGCF_HAEIN P45097 HAEMOPHILUS INFLUENZAE 727 -11537174 166059 hypothetical protein hi1189 (db:pir2.dat) I64188 I64188 Haemophilus influenzae 727 -11537174 7500924062 hi1189 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to pid:1652793 percent ident: 32.65;) (le:7046) (re:7681) (di:complement) U32798 U32798 g1574116 Haemophilus influenzae Rd 71421 -11537174 5000694430 (de:(hi1189) (pn:hypothetical protein:coenzyme pqq synthesis protein iii:pqqiii) (gn:hin0598) (gtcfc:9.12) (ec:) (ygcf_haein) (keggfc:11.2) (tigrfc:2.5) (db:gtc-haemophilus influenzae)) HI1189 HI1189 Haemophilus influenzae 727 10054013

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880755	14489	36645	843	281

Description

6500733317 riba:hi0212 gtp cyclohydrolase ii (gtcfc:9.2) (ec:3.5.4.25) (keggfc:9.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HI0212 HI0212 Haemophilus influenzae 727 -11537175 73407 riba:hi0212 (ec:3.5.4.25) (de:gtp cyclohydrolase ii,) (db:swissprot) GCH2_HAEIN P44571 HAEMOPHILUS INFLUENZAE 727 -11537175 166175 riba gtp cyclohydrolase ii (cl:escherichia coli cyclohydrolase ii:cyclohydrolase homology) (ec:3.5.4.25) (db:pir2.dat) A64055 A64055 Haemophilus influenzae 727 -11537175 7500882253 hi0212 gtp cyclohydrolase ii riba (db:genpept-bct1) (de:haemophilus influenzae rd section 21 of 163 of the complete genome.) (nt:similar to sp:p25523 gb:x67876 pid:40897 pid:42738) (le:1414) (re:2088) (di:direct) U32706 U32706 g1573172 Haemophilus influenzae Rd 71421 -11537175 5000694433 (de:(hi0212) (pn:gtp cyclohydrolase ii:riba) (gn:riba) (gtcfc:9.2) (ec:3.5.4.25) (gch2_haein) (keggfc:9.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae)) HI0212 HI0212 Haemophilus influenzae 727 10015941

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880770	14490	36646	279	92

Description

6500733318 ribh:hi1303 ribe:6:7-dimethyl-8-ribityllumazine synthase:dmrl synthase:lumazine synthase:riboflavin synthase beta chain (gtcfc:9.2) (ec:2.5.1.9) (keggfc:9.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HI1303 HI1303 Haemophilus influenzae 727 -11537176 167140 ribh:ribe riboflavin synthase:beta chain:6:7-dimethyl-8-ribityllumazine synthase:lumazine synthase (ec:2.5.1.9) (db:pir2.dat) C64115 C64115 Haemophilus influenzae 727 -11537176 7500960730 hi1303 riboflavin synthase:beta chain ribh (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to sp:p25540 gb:x64395 pid:42150 gb:u00096) (le:1649) (re:2170) (di:direct) U32810 U32810 g1574762 Haemophilus influenzae Rd 71421 -11537176 5000694434 (de:(hi1303) (pn:6,7-dimethyl-8-ribityllumazine synthase:dmrl synthase:lumazine synthase:riboflavin synthase beta chain:ribe) (gn:ribh) (gtcfc:9.2) (ec:2.5.1.9) (risb_haein) (keggfc:9.2) (tigrfc:2.9) (db:gtc-haemophilus influenz) HI1303 HI1303 Haemophilus influenzae 727 10088292

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880771	14491	36647	573	190

Description

5000694435 ribe:ribc:hi1613 riboflavin synthase alha chain:ribc:riboflavin synthase alpha chain (gtcfc:9.2) (ec:2.5.1.9) (keggfc:9.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HI1613 HI1613 Haemophilus influenzae 727 -11537177 94479 ribe:ribc:hi1613 (ec:2.5.1.9) (de:riboflavin synthase alpha chain,) (db:swissprot) RISA_HAEIN P45273 HAEMOPHILUS INFLUENZAE 727 -11537177 167139 ribc riboflavin synthase:alpha chain (cl:riboflavin synthase alpha chain) (ec:2.5.1.9) (db:pir2.dat) E64132 E64132 Haemophilus influenzae 727 -11537177 7500889813 hi1613 riboflavin synthase:alpha chain ribe (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:similar to sp:p29015 gb:x69109 pid:42740 gb:u00096) (le:12992) (re:13606) (di:direct) U32834 U32834 g1574454 Haemophilus influenzae Rd 71421 -11537177 6500733319 ribe:ribc riboflavin synthase alha chain:ribc:riboflavin synthase alpha chain (gtcfc:9.2) (ec:2.5.1.9) (keggfc:9.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae) HI1613 HI1613 Haemophilus influenzae 727 -11537177

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880788	14492	36648	540	179

Description

6500733320 ribb:hi0764 3:4-dihydroxy-2-butanone 4-phosphate synthase:dhbp synthase (gtcfc:9.2) (keggfc:14.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HI0764 HI0764 Haemophilus influenzae 727 -11537178 94338 ribb:hi0764 (de:3,4-dihydroxy-2-butanone 4-phosphate synthase (dhbp synthase)) (db:swissprot) RIBB_HAEIN P44866 HAEMOPHILUS INFLUENZAE 727 -11537178 165965 3:4-dihydroxy-2-butanone 4-phosphate synthase (cl:3,4-dihydroxy-2-butanone 4-phosphate synthase:3,4-dihydroxy-2-butanone 4-phosphate synthase homology) (ec:5.4.99.-) (db:pir2.dat) E64091 E64091 Haemophilus influenzae 727 -11537178 7500889768 hi0764 3:4-dihydroxy-2-butanone 4-phosphate synthase (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to sp:p24199 gb:x66720 pid:455174 pid:49100) (le:7908) (re:8555) (di:direct) U32760 U32760 g1573772 Haemophilus influenzae Rd 71421 -11537178 5000694436 (de:(hi0764) (pn:dhbp synthase:3,4-dihydroxy-2-butanone 4-phosphate synthase:ribb) (gn:ribb) (gtcfc:9.2) (ec:) (ribb_haein) (keggfc:11.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae)) HI0764 HI0764 Haemophilus influenzae 727 10036318

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880791	14493	36649	1137	379

Description

5000694437 ribd:ribg:hi0944 riboflavin biosynthesis protein:ribg:riboflavin-specific deaminase (gtcfc:9.2) (keggfc:14.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HI0944 HI0944 Haemophilus influenzae 727 -11537179 94343 ribd:ribg:hi0944 (ec:3.5.4.-) (de:riboflavin-specific deaminase,) (db:swissprot) RIBD_HAEIN P44326 HAEMOPHILUS INFLUENZAE 727 -11537179 167138 ribd:ribg riboflavin-specific deaminase (ec:3.5.4.-) (db:pir2.dat) H64103 H64103 Haemophilus influenzae 727 -11537179 7500889770 hi0944 riboflavin biosynthesis protein ribd (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to sp:p25539 gb:x64395 pid:581147 gb:u00096) (le:15867) (re:16985) (di:direct) U32775 U32775 g1573964 Haemophilus influenzae Rd 71421 -11537179 6500733321 ribd:ribg riboflavin biosynthesis protein:ribg:riboflavin-specific deaminase (gtcfc:9.2) (keggfc:14.2) (tigrfc:2.9) (db:gtc-haemophilus influenzae) HI0944 HI0944 Haemophilus influenzae 727 -11537179

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880795	14494	36650	501	166

Description

6500733322 pdxh:hi0863 pyridoxamine phosphate oxidase:pyridoxamine 5-phosphate oxidase:pnp/pmp oxidase (gtcfc:9.3) (ec:1.4.3.5) (keggfc:9.3) (tigrfc:2.8) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6)) (keggfc:vitamin b6 metabolism) HI0863 HI0863 Haemophilus influenzae 727 -11537180 88904 pdxh:hi0863 (ec:1.4.3.5) (de:pyridoxamine 5'-phosphate oxidase, (pnp/pmp oxidase)) (db:swissprot) PDXH_HAEIN P44909 HAEMOPHILUS INFLUENZAE 727 -11537180 167126 pyridoxamine-phosphate oxidase homolog (cl:pyridoxamine-phosphate oxidase) (db:pir2.dat) H64098 H64098 Haemophilus influenzae 727 -11537180 7500887775 hi0863 pyridoxamine phosphate oxidase pdxh (db:genpept-bct1) (de:haemophilus influenzae rd section 83 of 163 of the complete genome.) (nt:similar to gb:m92351 sp:p28225 pid:148097 gb:u00096) (le:969) (re:1658) (di:direct) U32768 U32768 g1573880 Haemophilus influenzae Rd 71421 -11537180 5000694438 (de:(hi0863) (pn:pyridoxamine 5"-phosphate oxidase:pnp:pyridoxamine phosphate oxidase:pdxh) (gn:pdxh) (gtcfc:9.3) (ec:1.4.3.5) (pdxh_haein) (keggfc:9.3) (tigrfc:2.8) (db:gtc-haemophilus influenzae)) HI0863 HI0863 Haemophilus influenzae 727 10031031

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880803	14495	36651	570	189

Description

6500733323 coaa:hi0631 antothenate kinase:pantothenate kinase (gtcfc:9.5) (ec:2.7.1.33) (keggfc:9.5) (tigrfc:2.7) (db:gtc-haemophilus influenzae) HI0631 HI0631 Haemophilus influenzae 727 -11537181 65056 coaa:hi0631 (ec:2.7.1.33) (de:pantothenate kinase,) (db:swissprot) COAA_HAEIN P44793 HAEMOPHILUS INFLUENZAE 727 -11537181 138479 pantothenate kinase (cl:pantothenate kinase) (ec:2.7.1.33) (db:pir2.dat) I64082 I64082 Haemophilus influenzae 727 -11537181 7500878984 hi0631 pantothenate kinase coaa (db:genpept-bct1) (de:haemophilus influenzae rd section 61 of 163 of the complete genome.) (nt:similar to gb:m36321 sp:p15044 gb:m90071 pid:145560) (le:1108) (re:2043) (di:complement) U32746 U32746 g1573628 Haemophilus influenzae Rd 71421 -11537181 5000694439 (de:(hi0631) (pn:pantothenate kinase:antothenate kinase:coaa) (gn:coaa) (gtcfc:9.5) (ec:2.7.1.33) (coaa_haein) (keggfc:9.5) (tigrfc:2.7) (db:gtc-haemophilus influenzae)) HI0631 HI0631 Haemophilus influenzae 727 10007711

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880804	14496	36652	288	95

Description

6500733324 dfp:hi0953 pantothenate metabolism flavoprotein:dfp:protein (gtcfc:9.5:2.8) (keggfc:14.2) (tigrfc:2.7) (db:gtc-haemophilus influenzae) HI0953 HI0953 Haemophilus influenzae 727 -11537182 68311 dfp:hi0953 (de:dna/pantothenate metabolism flavoprotein homolog) (db:swissprot) DFP_HAEIN P44953 HAEMOPHILUS INFLUENZAE 727 -11537182 167068 dfp protein homolog (cl:pantothenate metabolism flavoprotein dfp) (db:pir2.dat) G64104 G64104 Haemophilus influenzae 727 -11537182 7500880202 hi0953 dna/pantothenate metabolism flavoprotein dfp (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p24285 pid:290489 gb:u00096) (le:6621) (re:7823) (di:direct) U32776 U32776 g1573978 Haemophilus influenzae Rd 71421 -11537182 5000694440 (de:(hi0953) (pn:protein :pantothenate metabolism flavoprotein:dfp) (gn:dfp) (gtcfc:9.5) (ec:) (_haein) (keggfc:11.2) (tigrfc:2.7) (db:gtc-haemophilus influenzae)) HI0953 HI0953 Haemophilus influenzae 727 10010903

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880809	14497	36653	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880810	14498	36654	558	185

Description

6500733325 biob:hi1022 biotin synthetase (gtcfc:9.6) (ec:2.8.1.-) (keggfc:9.6) (tigrfc:2.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1022 HI1022 Haemophilus influenzae 727 -11537183 61721 biob:hi1022 (ec:2.8.1.6) (de:biotin synthase, (biotin synthetase)) (db:swissprot) BIOB_HAEIN P44987 HAEMOPHILUS INFLUENZAE 727 -11537183 142470 biotin synthetase (cl:biotin synthetase) (ec:2.8.1.-) (db:pir2.dat) F64108 F64108 Haemophilus influenzae 727 -11537183 7500877811 hi1022 biotin synthetase biob (db:genpept-bct1) (de:haemophilus influenzae rd section 98 of 163 of the complete genome.) (nt:similar to gb:j04423 sp:p12996 pid:145425) (le:87) (re:1088) (di:direct) U32783 U32783 g1574054 Haemophilus influenzae Rd 71421 -11537183 5000694441 (de:(hi1022) (pn:biotin synthetase:biob) (gn:biob) (gtcfc:9.6) (ec:2.8.1.-) (biob_haein) (keggfc:9.6) (tigrfc:2.1) (db:gtc-haemophilus influenzae)) HI1022 HI1022 Haemophilus influenzae 727 10004429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880815	14499	36655	540	179

Description

6500733326 biod-a:hi1445 dethiobiotin synthetase:biod:probable dethiobiotin synthetase 1:dethiobiotin synthase 1:dtb synthetase 1:dtbs 1 (gtcfc:9.6) (ec:6.3.3.3) (keggfc:9.6) (tigrfc:2.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1445 HI1445 Haemophilus influenzae 727 -11537184 61687 biod-a:hi1445 (ec:6.3.3.3) (de:1) (dtb synthetase 1) (dtbs 1)) (db:swissprot) BID1_HAEIN P45209 HAEMOPHILUS INFLUENZAE 727 -11537184 166090 dethiobiotin synthetase homolog hi1445 (cl:dethiobiotin synthase) (db:pir2.dat) I64123 I64123 Haemophilus influenzae 727 -11537184 7500877794 hi1445 dethiobiotin synthase biod-1 (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:s68059 sp:p13000 pid:490223) (le:2389) (re:3117) (di:complement) U32823 U32823 g1574285 Haemophilus influenzae Rd 71421 -11537184 5000694442 (de:(hi1445) (pn:probable dethiobiotin synthetase 1:dethiobiotin synthase 1:dtb synthetase 1:dtbs 1:dethiobiotin synthetase:biod) (gn:biod-a) (gtcfc:9.6) (ec:6.3.3.3) (bid1_haein) (keggfc:9.6) (tigrfc:2.1) (db:gtc-haemophilus in) HI1445 HI1445 Haemophilus influenzae 727 10004396

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880819	14500	36656	474	158

Description

6500733327 biod-b:hi1550 dethiobiotin synthase:biod:probable dethiobiotin synthetase 2:dethiobiotin synthase 2:dtb synthetase 2:dtbs 2 (gtcfc:9.6) (ec:6.3.3.3) (keggfc:9.6) (tigrfc:2.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1550 HI1550 Haemophilus influenzae 727 -11537185 61688 biod-b:hi1550 (ec:6.3.3.3) (de:2) (dtb synthetase 2) (dtbs 2)) (db:swissprot) BID2_HAEIN P45248 HAEMOPHILUS INFLUENZAE 727 -11537185 166089 dethiobiotin synthase homolog hi1550 (cl:dethiobiotin synthase) (db:pir2.dat) B64129 B64129 Haemophilus influenzae 727 -11537185 7500877795 hi1550 dethiobiotin synthase biod-2 (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:m29292 sp:p22818 pid:551693 percent) (le:5517) (re:6092) (di:complement) U32830 U32830 g1574395 Haemophilus influenzae Rd 71421 -11537185 5000694443 (de:(hi1550) (pn:probable dethiobiotin synthetase 2:dethiobiotin synthase 2:dtb synthetase 2:dtbs 2:dethiobiotin synthase:biod) (gn:biod-b) (gtcfc:9.6) (ec:6.3.3.3) (bid2_haein) (keggfc:9.6) (tigrfc:2.1) (db:gtc-haemophilus infl) HI1550 HI1550 Haemophilus influenzae 727 10004397

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880831	14501	36657	939	312

Description

GTC ORF with score 126 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1537.) (nt:unnamed protein product) (le:<1) (re:854) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880844	14502	36658	219	73

Description

6500733328 biof:hi1553 7-keto-8-aminopelargonic acid synthetase:8-amino-7-oxononanoate synthase:7-keto-8-amino-pelargonic acid synthetase:7-kap synthetase:l-alanine--pimelyl coa ligase (gtcfc:9.6) (ec:2.3.1.47) (keggfc:9.6) (tigrfc:2.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1553 HI1553 Haemophilus influenzae 727 -11537186 61740 biof:hi1553 (ec:2.3.1.47) (de:ligase)) (db:swissprot) BIOF_HAEIN P44422 HAEMOPHILUS INFLUENZAE 727 -11537186 165976 8-amino-7-oxononanoate synthase homolog (cl:5-aminolevulinate synthase) (db:pir2.dat) D64129 D64129 Haemophilus influenzae 727 -11537186 7500877831 hi1553 8-amino-7-oxononanoate synthase biof (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to sp:p53556 pid:1277027 pid:2293185) (le:7529) (re:8671) (di:complement) U32830 U32830 g1574397 Haemophilus influenzae Rd 71421 -11537186 5000694444 (de:(hi1553) (pn:8-amino-7-oxononanoate synthase:7-keto-8-amino-pelargonic acid synthetase:7-kap synthetase:l-alanine--pimelyl coa ligase:7-keto-8-aminopelargonic acid synthetase:biof) (gn:biof) (gtcfc:9.6) (ec:2.3.1.47) (biof_hae) HI1553 HI1553 Haemophilus influenzae 727 10004448

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880848	14503	36659	1011	336

Description

6500733329 bioa:hi1554 adenosylmethionine-8-amino-7-oxononanoate aminotransferase:7:8-diamino-pelargonic acid aminotransferase:dapa aminotransferase (gtcfc:9.6) (ec:2.6.1.62) (keggfc:9.6) (tigrfc:2.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1554 HI1554 Haemophilus influenzae 727 -11537187 61710 bioa:hi1554 (ec:2.6.1.62) (de:aminotransferase)) (db:swissprot) BIOA_HAEIN P44426 HAEMOPHILUS INFLUENZAE 727 -11537187 138404 adenosylmethionine--8-amino-7-oxononanoate transaminase (cl:ornithine--oxo-acid aminotransferase) (ec:2.6.1.62) (db:pir2.dat) E64129 E64129 Haemophilus influenzae 727 -11537187 7500877800 hi1554 adenosylmethionine-8-amino-7-oxononanoate (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:j04423 sp:p12995 pid:457106) (le:8680) (re:9972) (di:complement) U32830 U32830 g1574398 Haemophilus influenzae Rd 71421 -11537187 5000694445 (de:(hi1554) (pn:adenosylmethionine-8-amino-7-oxononanoate aminotransferase:dapa aminotransferase:7,8-diamino-pelargonic acid aminotransferase:bioa) (gn:bioa) (gtcfc:9.6) (ec:2.6.1.62) (bioa_haein) (keggfc:9.6) (tigrfc:2.1) (db:) HI1554 HI1554 Haemophilus influenzae 727 10004419

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880869	14504	36660	279	93

Description

6500733330 folk:hi0064
7:8-dihydro-6-hydroxymethylpterin-pyrophosphokinase:2-amino-4-hydroxy-6-hydr
oxymethyldihydropteridine
pyrophosphokinase:7:8-dihydro-6-hydroxymethylpterin-pyrophosphokinase:hppk:6
-hydroxymethyl-7:8-dihydropterin pyrophosphokinase:pppk (gtcfc:9.6)
(ec:2.7.6.3) (keggfc:9.7) (tigrfc:2.2) (db:gtc-haemophilus influenzae)
(gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and
folate biosynthesis) HI0064 HI0064 Haemophilus influenzae 727 -11537188
77551 folk:hi0064 (ec:2.7.6.3) (de:(hppk)
(6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase) (pppk)) (db:swissprot)
HPPK_HAEIN P43777 HAEMOPHILUS INFLUENZAE 727 -11537188 7500883498 hi0064
2-amino-4-hydroxy-6- (db:genpept-bct1) (de:haemophilus influenzae rd section
6 of 163 of the complete genome.) (nt:similar to gb:d26562 sp:p26281
gb:l06495 pid:146013) (le:10297) (re:10779) (di:direct) U32691 U32691
g1573012 Haemophilus influenzae Rd 71421 -11537188 5000694446 (de:(hi0064)
(pn:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine
pyrophosphokinase:7,8-dihydro-6-hydroxymethylpterin-
pyrophosphokinase:hppk:6-hydroxymethyl-7,8-dihydropterin
pyrophosphokinase:pppk:7,8-dihydro-6-hydroxymethylpterin-py) HI0064 HI0064
Haemophilus influenzae 727 10019911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880887	14505	36661	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880888	14506	36662	309	102

Description

6500733331 ntpa:hi0316 hypothetical protein:gb:d10165_1:datp pyrophosphohydrolase (gtcfc:9.6:14.1) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:15.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:unknown-hypothetical) HI0316 HI0316 Haemophilus influenzae 727 -11537189 86616 ntpa:hi0316 (ec:3.6.1.-) (de:datp pyrophosphohydrolase,) (db:swissprot) NTPA_HAEIN P44635 HAEMOPHILUS INFLUENZAE 727 -11537189 166360 hypothetical protein hi0316 (cl:mutt domain homology) (db:pir2.dat) H64147 H64147 Haemophilus influenzae 727 -11537189 7500886629 hi0316 datp pyrophosphohydrolase ntpa (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:d10165 sp:p24236 pid:581152) (le:1581) (re:2057) (di:complement) U32717 U32717 g1573286 Haemophilus influenzae Rd 71421 -11537189 5000694447 (de:(hi0316) (pn:datp pyrophosphohydrolase:hypothetical protein:gb:d10165_1) (gn:ntpa) (gtcfc:9.6) (ec:3.6.1.-) (ntpa_haein) (keggfc:9.7) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0316 HI0316 Haemophilus influenzae 727 10028780

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880889	14507	36663	1446	481

Description

6500733332 rep:hi0649 rep helicase:single-stranded dna-dependent atpase:atp-dependent dna helicase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HI0649 HI0649 Haemophilus influenzae 727 -11537190 93973 rep:hi0649 (ec:3.6.1.-) (de:atp-dependent dna helicase rep,) (db:swissprot) REP_HAEIN P44804 HAEMOPHILUS INFLUENZAE 727 -11537190 7500889638 hi0649 atp-dependent dna helicase rep (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p09980 gb:x04794 pid:148182) (le:1972) (re:3984) (di:complement) U32748 U32748 g1573648 Haemophilus influenzae Rd 71421 -11537190 5000694448 (de:(hi0649) (pn:atp-dependent dna helicase :rep helicase, single-stranded dna-dependent atpase:rep) (gn:rep) (gtcfc:9.6) (ec:3.6.1.-) (rep_haein) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0649 HI0649 Haemophilus influenzae 727 10035957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880893	14508	36664	324	107

Description

5000694449 fola:folh:hi0899 dehydrofolate reductase:type i:fola:dihydrofolate reductase type i (gtcfc:9.6) (ec:1.5.1.3) (keggfc:9.7:9.8) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI0899 HI0899 Haemophilus influenzae 727 -11537191 69426 fola:folh:hi0899 (ec:1.5.1.3) (de:dihydrofolate reductase,) (db:swissprot) DYR_HAEIN P43791 HAEMOPHILUS INFLUENZAE 727 -11537191 136629 folh dihydrofolate reductase (cl:type i dihydrofolate reductase:type i dihydrofolate reductase homology) (ec:1.5.1.3) (db:pir2.dat) C64101 C64101 Haemophilus influenzae 727 -11537191 7500880746 hi0899 dihydrofolate reductase fola (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p00379 gb:j01609 gb:v00276) (le:122) (re:604) (di:complement) U32772 U32772 g1573919 Haemophilus influenzae Rd 71421 -11537191 6500733333 fola:folh dehydrofolate reductase:type i:fola:dihydrofolate reductase type i (gtcfc:9.6) (ec:1.5.1.3) (keggfc:9.7:9.8) (tigrfc:2.2) (db:gtc-haemophilus influenzae) HI0899 HI0899 Haemophilus influenzae 727 -11537191

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880897	14509	36665	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880900	14510	36666	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880901	14511	36667	615	205

Description

GTC ORF with score 96 to: (db:genpept-pln1) (de:emericella nidulans acetate regulatory dna binding protein facb(facb) gene, complete cds.) (nt:description: facb acetate regulatory gene) (le:1363:1906:2274:2607) (re:1846:2219:2554:2964) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880908	14512	36668	372	123

Description

GTC ORF with score 107 to: (sr:nocardioides sp. (strain:kp7) dna) (db:genpept-bct1) (de:nocardioides sp. genes for 2-carboxybenzaldehyde dehydrogenase,trans-2'-carboxybenzalpyruvate hydratase-aldolase and 5 orfs,complete cds.) (le:6724) (re:7887) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880909	14513	36669	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880929	14514	36670	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880936	14515	36671	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880943	14516	36672	789	262

Description

6500733334 mutt:hi0910 mutator mutt:at-gc transversion:mutator protein:7:8-dihydro-8-oxoguanine-triphosphatase:8-oxo-dgtpase:dgtp pyrophosphohydrolase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HI0910 HI0910 Haemophilus influenzae 727 -11537192 84751 mutt:hi0910 (ec:3.6.1.-) (de:(8-oxo-dgtpase), (dgtp pyrophosphohydrolase)) (db:swissprot) MUTT_HAEIN P44932 HAEMOPHILUS INFLUENZAE 727 -11537192 7500886171 hi0910 mutator mutt protein mutt (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p08337 gb:m20791 gb:x04831) (le:9092) (re:9502) (di:direct) U32772 U32772 g1573927 Haemophilus influenzae Rd 71421 -11537192 5000694450 (de:(hi0910) (pn:mutator protein:7,8-dihydro-8-oxoguanine-triphosphatase:8-oxo-dgtpase:dgtp pyrophosphohydrolase:mutator mutt:at-gc transversion) (gn:mutt) (gtcfc:9.6) (ec:3.6.1.-) (mutt_haein) (keggfc:9.7) (tigrfc:10.2) (db:gt) HI0910 HI0910 Haemophilus influenzae 727 10026942

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880955	14517	36673	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880956	14518	36674	291	96

Description

5000694451 uvrd:mutb:hi1188 mutb1:dna helicase ii (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HI1188 HI1188 Haemophilus influenzae 727 -11537193 104053 uvrd:mutb:hi1188 (ec:3.6.1.-) (de:dna helicase ii,) (db:swissprot) UVRD_HAEIN Q02322 HAEMOPHILUS INFLUENZAE 727 -11537193 141451 helicase:ii (cl:helicase ii) (ec:3.6.1.-) (db:pir2.dat) H64188 H64188 Haemophilus influenzae 727 -11537193 7500893924 hi1188 dna helicase ii uvrd (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to gb:m99049 sp:q02322 percent ident:) (le:4252) (re:6435) (di:complement) U32798 U32798 g1574115 Haemophilus influenzae Rd 71421 -11537193 6500733335 uvrd:mutb mutb1:dna helicase ii (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1188 HI1188 Haemophilus influenzae 727 -11537193

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880964	14519	36675	1617	538

Description

GTC ORF with score 823 to: (fn:processing of pre-ribosomal rna) (sr:baker's yeast) (db:genpept-pln1) (de:s.cerevisiae chromosome xiii cosmid 9959.) (nt:ym9959.11c, unknown, len: 1729, cai: 0.24) (le:16981) (re:22170) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880965	14520	36676	591	196

Description

6500733336 folc:hi1261 folylpolyglutamate synthase:folylpoly-gamma-glutamate synthetase:fpgs (gtcfc:9.6) (ec:6.3.2.17) (keggfc:9.7) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1261 HI1261 Haemophilus influenzae 727 -11537194 72232 folc:hi1261 (ec:6.3.2.17) (de:synthetase) (fpgs)) (db:swissprot) FOLC_HAEIN P43775 HAEMOPHILUS INFLUENZAE 727 -11537194 142394 tetrahydrofolylpolyglutamate synthase:dihydrofolate synthase (cl:folylpolyglutamate synthase) (ec:6.3.2.17:6.3.2.12) (db:pir2.dat) C64113 C64113 Haemophilus influenzae 727 -11537194 7500881707 hi1261 folylpolyglutamate synthase/dihydrofolate (db:genpept-bct1) (de:haemophilus influenzae rd section 121 of 163 of the completegenome.) (nt:similar to gb:m68934 sp:p08192 gb:m32445 pid:146009) (le:1010) (re:2323) (di:direct) U32806 U32806 g1574719 Haemophilus influenzae Rd 71421 -11537194 5000694452 (de:(hi1261) (pn:folylpoly-gamma-glutamate synthetase:fpgs:folylpolyglutamate synthase:folc) (gn:folc) (gtcfc:9.6) (ec:6.3.2.17) (folc_haein) (keggfc:9.7) (tigrfc:2.2) (db:gtc-haemophilus influenzae)) HI1261 HI1261 Haemophilus influenzae 727 10014783

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880987	14521	36677	801	266

Description

5000694453 hi1464:folp-a:hi1336:folp-b:hi1336 folp:dihydropteroate synthase:dhps:dihydropteroate pyrophosphorylase (gtcfc:9.6) (ec:2.5.1.15) (keggfc:9.7) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1336 HI1336 Haemophilus influenzae 727 -11537195 68581 folp-a:hi1336:folp-b:hi1464 (ec:2.5.1.15) (de:pyrophosphorylase)) (db:swissprot) DHPS_HAEIN P43776 HAEMOPHILUS INFLUENZAE 727 -11537195 138212 dihydropteroate synthase (cl:dihydropteroate synthase:dihydropteroate synthase homology) (ec:2.5.1.15) (db:pir2.dat) E64117 E64117 Haemophilus influenzae 727 -11537195 7500880279 hi1336 dihydropteroate synthase folp-1 (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to gb:l06494 sp:p26282 gb:u01376 gb:x68776) (le:86) (re:913) (di:direct) U32813 U32813 g1574797 Haemophilus influenzae Rd 71421 -11537195 7500880280 hi1464 dihydropteroate synthase folp-2 (db:genpept-bct1) (de:haemophilus influenzae rd section 139 of 163 of the completegenome.) (nt:similar to gb:l06494 sp:p26282 gb:u01376 gb:x68776) (le:6509) (re:7336) (di:complement) U32824 U32824 g1574304 Haemophilus influenzae Rd 71421 -11537195 6500733337 hi1464:folp-a:hi1336:folp-b folp:dihydropteroate synthase:dhps:dihydropteroate pyrophosphorylase (gtcfc:9.6) (ec:2.5.1.15) (keggfc:9.7) (tigrfc:2.2) (db:gtc-haemophilus influenzae) HI1336 HI1336 Haemophilus influenzae 727 -11537195

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501880991	14522	36678	1584	527

Description

6500733338 fole:hi1447 gtp cyclohydrolase i:gtp-ch-i (gtcfc:9.6) (ec:3.5.4.16) (keggfc:9.7) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1447 HI1447 Haemophilus influenzae 727 -11537196 73391 fole:hi1447 (ec:3.5.4.16) (de:gtp cyclohydrolase i, (gtp-ch-i)) (db:swissprot) GCH1_HAEIN P43866 HAEMOPHILUS INFLUENZAE 727 -11537196 166174 gtp cyclohydrolase i (cl:gtp cyclohydrolase i) (ec:3.5.4.16) (db:pir2.dat) A64124 A64124 Haemophilus influenzae 727 -11537196 7500882243 hi1447 gtp cyclohydrolase i fole (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:u00007 sp:p27511 gb:x63910 pid:312964) (le:3547) (re:4203) (di:complement) U32823 U32823 g1574286 Haemophilus influenzae Rd 71421 -11537196 5000694454 (de:(hi1447) (pn:gtp-ch-i:gtp cyclohydrolase i:fole) (gn:fole) (gtcfc:9.6) (ec:3.5.4.16) (gch1_haein) (keggfc:9.7) (tigrfc:2.2) (db:gtc-haemophilus influenzae)) HI1447 HI1447 Haemophilus influenzae 727 10015925

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881006	14523	36679	363	120

Description

6500733339 dnab:hi1574 replicative dna helicase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HI1574 HI1574 Haemophilus influenzae 727 -11537197 68854 dnab:hi1574 (ec:3.6.1.-) (de:replicative dna helicase,) (db:swissprot) DNAB_HAEIN P45256 HAEMOPHILUS INFLUENZAE 727 -11537197 154421 dnab dnab protein:replicative dna helicase (cl:phage p22 gene 12 protein) (db:pir2.dat) D64130 D64130 Haemophilus influenzae 727 -11537197 7500880404 hi1574 replicative dna helicase dnab (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the completegenome.) (nt:similar to sp:p03005 gb:k01174 gb:l02312 pid:145763) (le:9639) (re:11153) (di:direct) U32831 U32831 g1574411 Haemophilus influenzae Rd 71421 -11537197 5000694455 (de:(hi1574) (pn:replicative dna helicase:dnab) (gn:dnab) (gtcfc:9.6) (ec:3.6.1.-) (dnab_haein) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1574 HI1574 Haemophilus influenzae 727 10011439

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881015	14524	36680	570	189

Description

6500733340 recg:hi1740 dna recombinase:atp-dependent dna helicase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HI1740 HI1740 Haemophilus influenzae 727 -11537198 93810 recg:hi1740 (ec:3.6.1.-) (de:atp-dependent dna helicase recg,) (db:swissprot) RECG_HAEIN P43809 HAEMOPHILUS INFLUENZAE 727 -11537198 166108 recg recg protein (cl:dna helicase recg:dead/h box helicase homology) (db:pir2.dat) E64139 E64139 Haemophilus influenzae 727 -11537198 7500889576 hi1740 atp-dependent dna helicase recg (db:genpept-bct1) (de:haemophilus influenzae rd section 162 of 163 of the completegenome.) (nt:similar to gb:l10328 sp:p24230 gb:x59550 pid:147545) (le:8231) (re:10312) (di:complement) U32847 U32847 g1574599 Haemophilus influenzae Rd 71421 -11537198 5000694456 (de:(hi1740) (pn:atp-dependent dna helicase :dna recombinase:recg) (gn:recg) (gtcfc:9.6) (ec:3.6.1.-) (recg_haein) (keggfc:9.7) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1740 HI1740 Haemophilus influenzae 727 10035801

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881020	14525	36681	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881038	14526	36682	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881039	14527	36683	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881053	14528	36684	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881061	14529	36685	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881064	14530	36686	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881066	14531	36687	639	212

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881068	14532	36688	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881075	14533	36689	1176	391

Description

6500733341 bisc:hi0643 biotin sulfoxide reductase:probable biotin sulfoxide reductase:bds reductase:bso reductase (gtcfc:9.6) (ec:1.-.-.-) (keggfc:14.1) (tigrfc:2.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI0643 HI0643 Haemophilus influenzae 727 -11537199 61757 bisc:hi0643 (ec:1.-.-.-) (de:(bso reductase)) (db:swissprot) BISC_HAEIN P44798 HAEMOPHILUS INFLUENZAE 727 -11537199 166031 biotin sulfoxide reductase (cl:trimethylamine-n-oxide reductase) (ec:1.8.4.-) (db:pir2.dat) H64083 H64083 Haemophilus influenzae 727 -11537199 7500877843 hi0643 biotin sulfoxide reductase bisc (db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the complete genome.) (nt:similar to sp:p46923 pid:1045667 gb:u00096) (le:5877) (re:8354) (di:complement) U32747 U32747 g1573641 Haemophilus influenzae Rd 71421 -11537199 5000694431 (de:(hi0643) (pn:probable biotin sulfoxide reductase:bso reductase:biotin sulfoxide reductase:bds reductase:bisc) (gn:bisc) (gtcfc:9.13:9.6:9.8) (ec:1.-.-.-) (bisc_haein) (keggfc:11.1) (tigrfc:2.1) (db:gtc-haemophilus influenzae) HI0643 HI0643 Haemophilus influenzae 727 10004465

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881076	14534	36690	765	255

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881077	14535	36691	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881090	14536	36692	306	101

Description

6500733342 bioc:hi1551 biotin synthesis protein:putative biotin synthesis protein (gtcfc:9.6) (keggfc:14.2) (tigrfc:2.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1551 HI1551 Haemophilus influenzae 727 -11537200 61728 bioc:hi1551 (de:putative biotin synthesis protein bioc) (db:swissprot) BIOC_HAEIN P45249 HAEMOPHILUS INFLUENZAE 727 -11537200 166032 biotin synthesis protein homolog (cl:bioc homology) (db:pir2.dat) C64129 C64129 Haemophilus influenzae 727 -11537200 7500877827 hi1551 biotin synthesis protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:j04423 sp:p12999 pid:145427) (le:6102) (re:6884) (di:complement) U32830 U32830 g1574396 Haemophilus influenzae Rd 71421 -11537200 5000694432 (de:(hi1551) (pn:putative biotin synthesis protein :biotin synthesis protein:bioc) (gn:bioc) (gtcfc:9.13:9.6:9.8) (ec:) (bioc_haein) (keggfc:11.2) (tigrfc:2.1) (db:gtc-haemophilus influenzae)) HI1551 HI1551 Haemophilus influenzae 727 10004436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881091	14537	36693	357	118

Description

5000694457 aminodeoxychorismate lyase:pabc:hypothetical protein (gtcfc:9.6) (keggfc:14.2) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI0457 HI0457 Haemophilus influenzae 727 -11537201 110667 hi0457 (de:hypothetical protein hi0457) (db:swissprot) YCEG_HAEIN P44720 HAEMOPHILUS INFLUENZAE 727 -11537201 165995 yceg protein homolog hi0457 (cl:yceg protein) (db:pir2.dat) E64069 E64069 Haemophilus influenzae 727 -11537201 7500921683 hi0457 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1510185 pid:1787339) (le:5602) (re:6645) (di:complement) U32728 U32728 g1573431 Haemophilus influenzae Rd 71421 -11537201 6500733343 aminodeoxychorismate lyase:pabc:hypothetical protein (gtcfc:9.6) (keggfc:14.2) (tigrfc:2.2) (db:gtc-haemophilus influenzae) HI0457 HI0457 Haemophilus influenzae 727 -11537201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881092	14538	36694	2025	675

Description

6500733344 pabb:hi1170 p-aminobenzoate synthetase (gtcfc:9.6) (keggfc:14.2) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1170 HI1170 Haemophilus influenzae 727 -11537202 167065 p-aminobenzoate synthase component i homolog (db:pir2.dat) F64187 F64187 Haemophilus influenzae 727 -11537202 7500960722 hi1170 h. influenzae predicted coding region hi1170 (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1077) (re:2063) (di:complement) U32797 U32797 g1574097 Haemophilus influenzae Rd 71421 -11537202 5000694458 (de:(hi1170) (pn:p-aminobenzoate synthetase:pabb) (gn:pabb) (gtcfc:9.6:9.8) (ec:) (keggfc:11.2) (tigrfc:2.2) (db:gtc-haemophilus influenzae)) HI1170 HI1170 Haemophilus influenzae 727 10088275

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881095	14539	36695	564	187

Description

5000694459 deda protein:deda:hypothetical protein (gtcfc:9.6) (keggfc:14.2) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI1629 HI1629 Haemophilus influenzae 727 -11537203 112085 hi1629 (de:hypothetical protein hi1629) (db:swissprot) YG29_HAEIN P45280 HAEMOPHILUS INFLUENZAE 727 -11537203 166084 hypothetical protein hi1629 (db:pir2.dat) D64133 D64133 Haemophilus influenzae 727 -11537203 7500923703 hi1629 deda protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:similar to gb:m68934 sp:p09548 gb:x02743 pid:146363) (le:934) (re:1572) (di:complement) U32836 U32836 g1574476 Haemophilus influenzae Rd 71421 -11537203 6500733345 deda protein:deda:hypothetical protein (gtcfc:9.6) (keggfc:14.2) (tigrfc:2.2) (db:gtc-haemophilus influenzae) HI1629 HI1629 Haemophilus influenzae 727 -11537203

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881099	14540	36696	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881101	14541	36697	537	178

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881105	14542	36698	330	109

Description

6500733346 lipa:hi0026 lipoate biosynthesis protein a:lipoic acid synthetase:lip-syn (gtcfc:9.7) (keggfc:14.2) (tigrfc:2.4) (db:gtc-haemophilus influenzae) HI0026 HI0026 Haemophilus influenzae 727 -11537204 82173 lipa:hi0026 (de:lipoic acid synthetase (lip-syn) (lipoate synthase)) (db:swissprot) LIPA_HAEIN P44463 HAEMOPHILUS INFLUENZAE 727 -11537204 166952 lipoic acid synthase (cl:lipoic acid synthase) (ec:2.8.1.-) (db:pir2.dat) G64043 G64043 Haemophilus influenzae 727 -11537204 7500885026 hi0026 lipoate biosynthesis protein a lipa (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to gb:l07636 sp:p25845 pid:146617) (le:4166) (re:5128) (di:complement) U32688 U32688 g1572971 Haemophilus influenzae Rd 71421 -11537204 5000694460 (de:(hi0026) (pn:lipoic acid synthetase:lip-syn:lipoate biosynthesis protein a:lipa) (gn:lipa) (gtcfc:9.7) (ec:) (lipa_haein) (keggfc:11.2) (tigrfc:2.4) (db:gtc-haemophilus influenzae)) HI0026 HI0026 Haemophilus influenzae 727 10024405

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881112	14543	36699	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881117	14544	36700	450	149

Description

GTC ORF with score 153 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0143.) (nt:unnamed protein product) (le:<1) (re:951) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881127	14545	36701	945	314

Description

5000694471 dna binding protein:probable:hypothetical transcriptional regulator hi0186 (gtcfc:10.1) (keggfc:14.2) (tigrfc:12.3) (db:gtc-haemophilus influenzae) HI0186 HI0186 Haemophilus influenzae 727 -11537205 108951 hi0186 (de:hypothetical transcriptional regulator hi0186) (db:swissprot) Y186_HAEIN P44558 HAEMOPHILUS INFLUENZAE 727 -11537205 166100 probable dna-binding protein homolog (cl:transcription repressor glnr) (db:pir2.dat) I64052 I64052 Haemophilus influenzae 727 -11537205 7500894839 hi0186 transcriptional regulator:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 19 of 163 of the complete genome.) (nt:similar to gb:d26185 sp:p37510 pid:467364) (le:92) (re:499) (di:direct) U32704 U32704 g1573144 Haemophilus influenzae Rd 71421 -11537205 6500733347 dna binding protein:probable:hypothetical transcriptional regulator hi0186 (gtcfc:10.1) (keggfc:14.2) (tigrfc:12.3) (db:gtc-haemophilus influenzae) HI0186 HI0186 Haemophilus influenzae 727 -11537205

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881128	14546	36702	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881135	14547	36703	891	296

Description

GTC ORF with score 214 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f10e7.) (nt:coded for by c. elegans cdna yk20f8.5; coded for by) (le:900:1176:1685) (re:1126:1637:1769) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881138	14548	36704	195	64

Description

6500733348 hupa:hi0430 dna-binding protein hu-alpha:ns2:hu-2 (gtcfc:10.1) (keggfc:14.2) (tigrfc:12.3) (db:gtc-haemophilus influenzae) HI0430 HI0430 Haemophilus influenzae 727 -11537206 148283 hupa dna-binding protein hu-2:dna-binding protein ns2 (cl:bacterial dna-binding protein) (db:pir2.dat) E64067 E64067 Haemophilus influenzae 727 -11537206 7500954782 hi0430 dna-binding protein hu-alpha hupa (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to sp:p02342 gb:d12624 gb:x05994 pid:216565) (le:6451) (re:6861) (di:complement) U32726 U32726 g1573405 Haemophilus influenzae Rd 71421 -11537206 5000694472 (de:(hi0430) (pn:dna-binding protein hu-alpha:dna-binding protein hu-alpha:ns2:hu-2) (gn:hupa) (gtcfc:10.1) (ec:) (dbha_haein) (keggfc:11.2) (tigrfc:12.3) (db:gtc-haemophilus influenzae)) HI0430 HI0430 Haemophilus influenzae 727 10077607

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881139	14549	36705	315	104

Description

6500733349 rdgb:hi1491 dna-binding protein (gtcfc:10.1) (keggfc:14.2) (tigrfc:12.3) (db:gtc-haemophilus influenzae) HI1491 HI1491 Haemophilus influenzae 727 -11537207 7500976290 hi1491 dna-binding protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:similar to gb:l32173 pid:476018 sp:q47588 percent) (le:4178) (re:4396) (di:direct) U32826 U32826 g1574325 Haemophilus influenzae Rd 71421 -11537207 5000694473 (de:(hi1491) (pn:dna-binding protein:rdgb) (gn:rdgb) (gtcfc:10.1) (ec:) (keggfc:11.2) (tigrfc:12.3) (db:gtc-haemophilus influenzae)) HI1491 HI1491 Haemophilus influenzae 727 10126720

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881144	14550	36706	1299	432

Description

6500733350 hns:hi1587 dna-binding protein h-ns:dna-binding protein h-ns homolog (gtcfc:10.1) (keggfc:14.2) (tigrfc:12.3) (db:gtc-haemophilus influenzae) HI1587 HI1587 Haemophilus influenzae 727 -11537208 77437 hns:hi1587 (de:dna-binding protein h-ns homolog) (db:swissprot) HNS_HAEIN P43841 HAEMOPHILUS INFLUENZAE 727 -11537208 166112 dna-binding protein h-ns homolog hi1587 (db:pir2.dat) D64131 D64131 Haemophilus influenzae 727 -11537208 7500883447 hi1587 dna-binding protein h-ns hns (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to gb:x07688 sp:p08936 gb:x57231 gb:x59940) (le:9704) (re:10108) (di:direct) U32832 U32832 g1574428 Haemophilus influenzae Rd 71421 -11537208 5000694474 (de:(hi1587) (pn:dna-binding protein h-ns homolog:dna-binding protein h-ns:hns) (gn:hns) (gtcfc:10.1) (ec:) (hns_haein) (keggfc:11.2) (tigrfc:12.3) (db:gtc-haemophilus influenzae)) HI1587 HI1587 Haemophilus influenzae 727 10019798

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881145	14551	36707	1011	337

Description

6500733351 xtha:hi0041 exodeoxyribonuclease iii:exonuclease iii (gtcfc:10.10) (ec:3.1.11.2) (keggfc:14.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI0041 HI0041 Haemophilus influenzae 727 -11537209 70773 xtha:hi0041 (ec:3.1.11.2) (de:exodeoxyribonuclease iii, (exonuclease iii) (exo iii)) (db:swissprot) EX3_HAEIN P44318 HAEMOPHILUS INFLUENZAE 727 -11537209 139828 exodeoxyribonuclease iii (cl:exodeoxyribonuclease iii) (ec:3.1.11.2) (db:pir2.dat) H64044 H64044 Haemophilus influenzae 727 -11537209 7500881214 hi0041 exodeoxyribonuclease iii xtha (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to gb:m22592 sp:p09030 gb:x13002 pid:148277) (le:7377) (re:8180) (di:complement) U32689 U32689 g1572987 Haemophilus influenzae Rd 71421 -11537209 5000694462 (de:(hi0041) (pn:exodeoxyribonuclease iii:exonuclease iii:xtha) (gn:xtha) (gtcfc:10.10) (ec:3.1.11.2) (ex3_haein) (keggfc:11.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae)) HI0041 HI0041 Haemophilus influenzae 727 10013348

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881168	14552	36708	855	284

Description

6500733352 uvrc:hi0057 excinuclease abc subunit c (gtcfc:10.10) (keggfc:14.2) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI0057 HI0057 Haemophilus influenzae 727 -11537210 104049 uvrc:hi0057 (de:excinuclease abc subunit c) (db:swissprot) UVRC_HAEIN P44489 HAEMOPHILUS INFLUENZAE 727 -11537210 154710 excinuclease abc chain c:excision endonuclease abc::chain c:uvrc protein (cl:excinuclease abc chain c) (ec:3.1.-.-) (db:pir2.dat) F64045 F64045 Haemophilus influenzae 727 -11537210 7500893912 hi0057 excinuclease abc:subunit c uvrc (db:genpept-bct1) (de:haemophilus influenzae rd section 6 of 163 of the complete genome.) (nt:similar to sp:p07028 gb:x03691 pid:43290 gb:u00096) (le:79) (re:1908) (di:complement) U32691 U32691 g1573005 Haemophilus influenzae Rd 71421 -11537210 5000694463 (de:(hi0057) (pn:excinuclease abc subunit c:uvrc) (gn:uvrc) (gtcfc:10.10) (ec:) (uvrc_haein) (keggfc:11.2) (tigrfc:10.1) (db:gtc-haemophilus influenzae)) HI0057 HI0057 Haemophilus influenzae 727 10045819

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881169	14553	36709	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881203	14554	36710	3156	1051

Description

6500733353 xsea:hi0397 exonuclease vii:large subunit:exodeoxyribonuclease large subunit:exonuclease vii large subunit (gtcfc:10.10) (ec:3.1.11.6) (keggfc:14.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI0397 HI0397 Haemophilus influenzae 727 -11537211 70782 xsea:hi0397 (ec:3.1.11.6) (de:large subunit)) (db:swissprot) EX7L_HAEIN P43913 HAEMOPHILUS INFLUENZAE 727 -11537211 139829 exodeoxyribonuclease vii:large chain (cl:exodeoxyribonuclease vii) (ec:3.1.11.6) (db:pir2.dat) D64065 D64065 Haemophilus influenzae 727 -11537211 7500881226 hi0397 exodeoxyribonuclease vii:large subunit xsea (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to gb:j02599 sp:p04994 pid:148275 gb:u00096) (le:4613) (re:5932) (di:direct) U32723 U32723 g1573368 Haemophilus influenzae Rd 71421 -11537211 5000694464 (de:(hi0397) (pn:exodeoxyribonuclease large subunit:exonuclease vii large subunit:exonuclease vii, large subunit:xsea) (gn:xsea) (gtcfc:10.10) (ec:3.1.11.6) (ex7l_haein) (keggfc:11.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI0397 HI0397 Haemophilus influenzae 727 10013357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881212	14555	36711	2412	803

Description

6500733354 recc:hi0942 exodeoxyribonuclease v:exodeoxyribonuclease v gamma chain (gtcfc:10.10) (ec:3.1.11.5) (keggfc:14.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI0942 HI0942 Haemophilus influenzae 727 -11537212 70779 recc:hi0942 (ec:3.1.11.5) (de:exodeoxyribonuclease v gamma chain,) (db:swissprot) EX5C_HAEIN P44945 HAEMOPHILUS INFLUENZAE 727 -11537212 166120 exodeoxyribonuclease v 125k chain homolog (db:pir2.dat) G64103 G64103 Haemophilus influenzae 727 -11537212 7500881222 hi0942 exodeoxyribonuclease v:gamma chain recc (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to sp:p07648 pid:42689 pid:882714 gb:u00096) (le:11995) (re:15360) (di:direct) U32775 U32775 g1573962 Haemophilus influenzae Rd 71421 -11537212 5000694465 (de:(hi0942) (pn:exodeoxyribonuclease v gamma chain:exodeoxyribonuclease v:recc) (gn:recc) (gtcfc:10.10) (ec:3.1.11.5) (ex5c_haein) (keggfc:11.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae)) HI0942 HI0942 Haemophilus influenzae 727 10013354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881213	14556	36712	312	103

Description

6500733355 recj:hi1214 single-stranded-dna-specific exonuclease (gtcfc:10.10) (ec:3.1.-.-) (keggfc:14.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI1214 HI1214 Haemophilus influenzae 727 -11537213 93813 recj:hi1214 (ec:3.1.-.-) (de:single-stranded-dna-specific exonuclease recj,) (db:swissprot) RECJ_HAEIN P45112 HAEMOPHILUS INFLUENZAE 727 -11537213 167164 single-stranded-dna-specific exonuclease (ec:3.1.-.-) (db:pir2.dat) F64110 F64110 Haemophilus influenzae 727 -11537213 7500889578 hi1214 single-stranded-dna-specific exonuclease recj (db:genpept-bct1) (de:haemophilus influenzae rd section 116 of 163 of the completegenome.) (nt:similar to gb:m54884 sp:p21893 pid:147550) (le:175) (re:1902) (di:direct) U32801 U32801 g1574144 Haemophilus influenzae Rd 71421 -11537213 5000694466 (de:(hi1214) (pn:single-stranded-dna-specific exonuclease :single-stranded-dna-specific exonuclease:recj) (gn:recj) (gtcfc:10.10) (ec:3.1.-.-) (recj_haein) (keggfc:11.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae)) HI1214 HI1214 Haemophilus influenzae 727 10035804

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881221	14557	36713	282	93

Description

6500733356 recb:hi1321 exodeoxyribonuclease v:exodeoxyribonuclease v beta chain (gtcfc:10.10) (ec:3.1.11.5) (keggfc:14.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI1321 HI1321 Haemophilus influenzae 727 -11537214 70777 recb:hi1321 (ec:3.1.11.5) (de:exodeoxyribonuclease v beta chain,) (db:swissprot) EX5B_HAEIN P45157 HAEMOPHILUS INFLUENZAE 727 -11537214 166119 exodeoxyribonuclease v 135k chain homolog (db:pir2.dat) D64116 D64116 Haemophilus influenzae 727 -11537214 7500881220 hi1321 exodeoxyribonuclease v:beta chain recb (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:similar to sp:p08394 gb:x04581 gb:x04582 pid:42682) (le:3916) (re:7551) (di:direct) U32811 U32811 g1574781 Haemophilus influenzae Rd 71421 -11537214 5000694467 (de:(hi1321) (pn:exodeoxyribonuclease v beta chain:exodeoxyribonuclease v:recb) (gn:recb) (gtcfc:10.10) (ec:3.1.11.5) (ex5b_haein) (keggfc:11.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae)) HI1321 HI1321 Haemophilus influenzae 727 10013352

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881222	14558	36714	411	136

Description

6500733357 recd:hi1322 exodeoxyribonuclease v:exodeoxyribonuclease v alpha chain (gtcfc:10.10) (ec:3.1.11.5) (keggfc:14.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI1322 HI1322 Haemophilus influenzae 727 -11537215 70775 recd:hi1322 (ec:3.1.11.5) (de:exodeoxyribonuclease v alpha chain,) (db:swissprot) EX5A_HAEIN P45158 HAEMOPHILUS INFLUENZAE 727 -11537215 166121 exodeoxyribonuclease v 67k chain homolog (db:pir2.dat) E64116 E64116 Haemophilus influenzae 727 -11537215 7500881218 hi1322 exodeoxyribonuclease v:alpha chain recd (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:similar to sp:p04993 gb:x04581 gb:x04582 pid:42683) (le:7551) (re:9473) (di:direct) U32811 U32811 g1574782 Haemophilus influenzae Rd 71421 -11537215 5000694468 (de:(hi1322) (pn:exodeoxyribonuclease v alpha chain:exodeoxyribonuclease v:recd) (gn:recd) (gtcfc:10.10) (ec:3.1.11.5) (ex5a_haein) (keggfc:11.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae)) HI1322 HI1322 Haemophilus influenzae 727 10013350

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881248	14559	36715	393	130

Description

6500733358 sbcb:hi1377 exodeoxyribonuclease i:exonuclease i:dna deoxyribophosphodiesterase:drpase (gtcfc:10.10) (ec:3.1.11.1) (keggfc:14.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI1377 HI1377 Haemophilus influenzae 727 -11537216 70771 sbcb:hi1377 (ec:3.1.11.1) (de:deoxyribophosphodiesterase) (drpase)) (db:swissprot) EX1_HAEIN P45188 HAEMOPHILUS INFLUENZAE 727 -11537216 139827 exodeoxyribonuclease i (cl:exodeoxyribonuclease i) (ec:3.1.11.1) (db:pir2.dat) E64120 E64120 Haemophilus influenzae 727 -11537216 7500881213 hi1377 exodeoxyribonuclease i sbcb (db:genpept-bct1) (de:haemophilus influenzae rd section 133 of 163 of the completegenome.) (nt:similar to sp:p04995 gb:j02641 gb:u00009 pid:405954) (le:1865) (re:3286) (di:direct) U32818 U32818 g1574211 Haemophilus influenzae Rd 71421 -11537216 5000694469 (de:(hi1377) (pn:exonuclease i:dna deoxyribophosphodiesterase:drpase:exodeoxyribonuclease i:sbcb) (gn:sbcb) (gtcfc:10.10) (ec:3.1.11.1) (ex1_haein) (keggfc:11.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae)) HI1377 HI1377 Haemophilus influenzae 727 10013346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881266	14560	36716	654	217

Description

6500733359 nth:hi1689 endonuclease iii:dna-:apurinic or apyrimidinic site lyase (gtcfc:10.10) (ec:4.2.99.18) (keggfc:14.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae) HI1689 HI1689 Haemophilus influenzae 727 -11537217 70154 nth:hi1689 (ec:4.2.99.18) (de:lyase)) (db:swissprot) END3_HAEIN P44319 HAEMOPHILUS INFLUENZAE 727 -11537217 166117 deoxyribonuclease pyrimidine dimer::endonuclease iii (cl:apurinic/apyrimidinic endonuclease class ii) (ec:3.1.25.1) (db:pir2.dat) G64136 G64136 Haemophilus influenzae 727 -11537217 7500881014 hi1689 endonuclease iii nth (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to gb:j02857 sp:p20625 pid:146972 gb:u00096) (le:123) (re:758) (di:direct) U32842 U32842 g1574542 Haemophilus influenzae Rd 71421 -11537217 5000694470 (de:(hi1689) (pn:dna-:apurinic or apyrimidinic site lyase:endonuclease iii:nth) (gn:nth) (gtcfc:10.10) (ec:4.2.99.18) (end3_haein) (keggfc:11.1) (tigrfc:10.1) (db:gtc-haemophilus influenzae)) HI1689 HI1689 Haemophilus influenzae 727 10012732

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881273	14561	36717	624	207

Description

6500733360 hflk:hi0151 protease specific for phage lambda cii repressor:protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0151 HI0151 Haemophilus influenzae 727 -11537218 76912 hflk:hi0151 (de:hflk protein) (db:swissprot) HFLK_HAEIN P44546 HAEMOPHILUS INFLUENZAE 727 -11537218 167112 hflk probable integral membrane proteinase:hflk (ec:3.4.-.-) (db:pir2.dat) A64051 A64051 Haemophilus influenzae 727 -11537218 7500883239 hi0151 hflk protein hflk (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:similar to sp:p25662 gb:u00005 pid:436157) (le:1453) (re:2685) (di:complement) U32701 U32701 g1573108 Haemophilus influenzae Rd 71421 -11537218 5000694475 (de:(hi0151) (pn:protein:protease specific for phage lambda cii repressor:hflk) (gn:hflk) (gtcfc:10.11) (ec:) (hflk_haein) (keggfc:11.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI0151 HI0151 Haemophilus influenzae 727 10019274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881277	14562	36718	951	316

Description

6500733361 prlc:hi0214 oligopeptidase a (gtcfc:10.11) (ec:3.4.24.70) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0214 HI0214 Haemophilus influenzae 727 -11537219 87735 prlc:hi0214 (ec:3.4.24.70) (de:oligopeptidase a,) (db:swissprot) OPDA_HAEIN P44573 HAEMOPHILUS INFLUENZAE 727 -11537219 167048 thimet oligopeptidase (cl:peptidyl-dipeptidase dcp) (ec:3.4.24.15) (db:pir2.dat) C64055 C64055 Haemophilus influenzae 727 -11537219 7500887188 hi0214 oligopeptidase a prlc (db:genpept-bct1) (de:haemophilus influenzae rd section 21 of 163 of the complete genome.) (nt:similar to sp:p27298 gb:m93984 pid:451277) (le:4427) (re:6472) (di:direct) U32706 U32706 g1573174 Haemophilus influenzae Rd 71421 -11537219 5000694476 (de:(hi0214) (pn:oligopeptidase a:prlc) (gn:prlc) (gtcfc:10.11) (ec:3.4.24.70) (opda_haein) (keggfc:11.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI0214 HI0214 Haemophilus influenzae 727 10029877

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881283	14563	36719	441	146

Description

6500733362 hap:igai:hi0248 iga1 protease:adhesion and penetration protein precursor (gtcfc:11.3:13.8) (ec:3.4.21.-) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0248 HI0248 Haemophilus influenzae 727 -11537220 166915 iga-specific metalloendopeptidase type 1 homolog (db:pir2.dat) C64057 C64057 Haemophilus influenzae 727 -11537220 5000694477 (de:(hi0248) (pn:adhesion and penetration protein precursor :iga1 protease:igai) (gn:hap) (gtcfc:10.11) (ec:3.4.21.-) (hap1_haein) (keggfc:11.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI0248 HI0248 Haemophilus influenzae 727 10088197

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881290	14564	36720	357	118

Description

6500733363 gcp:hi0530 sialoglycoprotease:probable o-sialoglycoprotein endopeptidase:glycoprotease (gtcfc:10.11) (ec:3.4.24.57) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0530 HI0530 Haemophilus influenzae 727 -11537221 73423 gcp:hi0530 (ec:3.4.24.57) (de:(glycoprotease)) (db:swissprot) GCP_HAEIN P43764 HAEMOPHILUS INFLUENZAE 727 -11537221 157275 o-sialoglycoprotein endopeptidase::sialoglycoproteinase (cl:o-sialoglycoprotein endopeptidase) (ec:3.4.24.57) (db:pir2.dat) H64074 H64074 Haemophilus influenzae 727 -11537221 7500882262 hi0530 o-sialoglycoprotein endopeptidase gcp (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:similar to sp:p36175 pid:561690 percent ident:) (le:3226) (re:4254) (di:complement) U32735 U32735 g1573514 Haemophilus influenzae Rd 71421 -11537221 5000694478 (de:(hi0530) (pn:probable o-sialoglycoprotein endopeptidase:glycoprotease:sialoglycoprotease:gcp) (gn:gcp) (gtcfc:10.11) (ec:3.4.24.57) (gcp_haein) (keggfc:11.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI0530 HI0530 Haemophilus influenzae 727 10015957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881310	14565	36721	201	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881316	14566	36722	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881320	14567	36723	576	191

Description

6500733364 tig:hi0713 trigger factor:tf (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0713 HI0713 Haemophilus influenzae 727 -11537222 101512 tig:hi0713 (de:trigger factor (tf)) (db:swissprot) TIG_HAEIN P44837 HAEMOPHILUS INFLUENZAE 727 -11537222 167225 tig trigger factor (cl:trigger factor) (db:pir2.dat) C64088 C64088 Haemophilus influenzae 727 -11537222 7500893181 hi0713 trigger factor tig (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to gb:m34066 sp:p22257 gb:x17642 pid:145555) (le:4360) (re:5658) (di:direct) U32754 U32754 g1573715 Haemophilus influenzae Rd 71421 -11537222 5000694479 (de:(hi0713) (pn:tf:trigger factor:tig) (gn:tig) (gtcfc:10.11) (ec:) (tig_haein) (keggfc:11.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI0713 HI0713 Haemophilus influenzae 727 10043348

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881321	14568	36724	1578	525

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881322	14569	36725	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881324	14570	36726	318	106

Description

6500733365 clpp:hi0714 atp-dependent clp protease proteolytic component:atp-dependent clp protease proteolytic subunit:endopeptidase clp (gtcfc:10.11) (ec:3.4.21.92) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0714 HI0714 Haemophilus influenzae 727 -11537223 64826 clpp:hi0714 (ec:3.4.21.92) (de:(endopeptidase clp)) (db:swissprot) CLPP_HAEIN P43867 HAEMOPHILUS INFLUENZAE 727 -11537223 166018 clpp atp-dependent clp proteinase:chain p (cl:atp-dependent clp proteinase chain p) (ec:3.4.21.-) (db:pir2.dat) D64088 D64088 Haemophilus influenzae 727 -11537223 7500878871 hi0714 atp-dependent clp protease:proteolytic subunit (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to gb:j05534 sp:p19245 pid:145556 gb:u00096) (le:5781) (re:6362) (di:direct) U32754 U32754 g1573716 Haemophilus influenzae Rd 71421 -11537223 5000694480 (de:(hi0714) (pn:atp-dependent clp protease proteolytic subunit:endopeptidase clp:atp-dependent clp protease proteolytic component:clpp) (gn:clpp) (gtcfc:10.11) (ec:3.4.21.92) (clpp_haein) (keggfc:11.1) (tigrfc:12.2) (db:gtc-hae) HI0714 HI0714 Haemophilus influenzae 727 10007487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881353	14571	36727	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881354	14572	36728	747	248

Description

6500733366 clpx:hi0715 atp-dependent protease atpase subunit:atp-dependent clp protease atp-binding subunit (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0715 HI0715 Haemophilus influenzae 727 -11537224 64842 clpx:hi0715 (de:atp-dependent clp protease atp-binding subunit clpx) (db:swissprot) CLPX_HAEIN P44838 HAEMOPHILUS INFLUENZAE 727 -11537224 166021 clpx atp-dependent clp proteinase:regulatory chain x (ec:3.4.21.-) (db:pir2.dat) E64088 E64088 Haemophilus influenzae 727 -11537224 7500878878 hi0715 atp-dependent clp protease:atp-binding subunit (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to gb:l18867 sp:p33138 gb:z23278 pid:347729) (le:6372) (re:7607) (di:direct) U32754 U32754 g1573717 Haemophilus influenzae Rd 71421 -11537224 5000694481 (de:(hi0715) (pn:atp-dependent clp protease atp-binding subunit :atp-dependent protease atpase subunit:clpx) (gn:clpx) (gtcfc:10.11) (ec:) (clpx_haein) (keggfc:11.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI0715 HI0715 Haemophilus influenzae 727 10007503

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881356	14573	36729	447	149

Description

5000694482 proline dipeptidase:pepq:hypothetical protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0722 HI0722 Haemophilus influenzae 727 -11537225 113308 hi0722 (de:hypothetical protein hi0722) (db:swissprot) YIGZ_HAEIN P44842 HAEMOPHILUS INFLUENZAE 727 -11537225 167109 conserved hypothetical protein hi0722 (cl:hypothetical protein hi0722) (db:pir2.dat) I64088 I64088 Haemophilus influenzae 727 -11537225 7500937467 hi0722 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 70 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1790283 percent ident:) (le:1362) (re:1982) (di:direct) U32755 U32755 g1573725 Haemophilus influenzae Rd 71421 -11537225 6500733367 proline dipeptidase:pepq:hypothetical protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0722 HI0722 Haemophilus influenzae 727 -11537225

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881388	14574	36730	906	301

Description

6500733368 pepp:hi0816 aminopeptidase p:xaa-pro aminopeptidase:x-pro aminopeptidase:aminopeptidase p ii:app-ii:aminoacylproline aminopeptidase (gtcfc:10.11) (ec:3.4.11.9) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0816 HI0816 Haemophilus influenzae 727 -11537226 59402 pepp:hi0816 (ec:3.4.11.9) (de:(aminopeptidase p ii) (app-ii) (aminoacylproline aminopeptidase)) (db:swissprot) AMPP_HAEIN P44881 HAEMOPHILUS INFLUENZAE 727 -11537226 140286 x-pro aminopeptidase:ii (cl:aminopeptidase p) (ec:3.4.11.9) (db:pir2.dat) B64096 B64096 Haemophilus influenzae 727 -11537226 7500876866 hi0816 aminopeptidase p pepp (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to gb:d00398 sp:p15034 pid:216529) (le:651) (re:1943) (di:complement) U32764 U32764 g1573829 Haemophilus influenzae Rd 71421 -11537226 5000694483 (de:(hi0816) (pn:xaa-pro aminopeptidase:x-pro aminopeptidase:aminopeptidase p ii:app-ii:aminoacylproline aminopeptidase:aminopeptidase p:pepp) (gn:pepp) (gtcfc:10.11) (ec:3.4.11.9) (ampp_haein) (keggfc:11.1) (tigrfc:12.2) (db:gt) HI0816 HI0816 Haemophilus influenzae 727 10002139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881389	14575	36731	231	76

Description

6500733369 clpb:hi0859 atp-dependent protease binding subunit:protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0859 HI0859 Haemophilus influenzae 727 -11537227 64808 clpb:hi0859 (de:clpb protein) (db:swissprot) CLPB_HAEIN P44403 HAEMOPHILUS INFLUENZAE 727 -11537227 140611 atp-dependent clp proteinase:regulatory chain b (cl:atp-dependent clp proteinase chain a) (ec:3.4.21.-) (db:pir2.dat) F64098 F64098 Haemophilus influenzae 727 -11537227 7500878853 hi0859 atp-dependent clp protease:atpase subunit (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to gb:m29364 sp:p03815 gb:v00350 gb:x57620) (le:7438) (re:10008) (di:direct) U32767 U32767 g1573874 Haemophilus influenzae Rd 71421 -11537227 5000694484 (de:(hi0859) (pn:protein:atp-dependent protease binding subunit:clpb) (gn:clpb) (gtcfc:10.11) (ec:) (clpb_haein) (keggfc:11.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI0859 HI0859 Haemophilus influenzae 727 10007469

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881394	14576	36732	378	125

Description

5000694485 iga:iga1:hi0990 iga1:immunoglobulin a1 protease precursor:iga1 protease (gtcfc:10.11) (ec:3.4.21.72) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0990 HI0990 Haemophilus influenzae 727 -11537228 78977 iga:iga1:hi0990 (ec:3.4.21.72) (de:immunoglobulin a1 protease precursor, (iga1 protease)) (db:swissprot) IGA0_HAEIN P44969 HAEMOPHILUS INFLUENZAE 727 -11537228 166912 iga-specific metalloendopeptidase:type 1:immunoglobulin a1 proteinase type 1:immunoglobulin a1 proteinase type 1 (sr:strain rd kw20, , strain rd kw20) (sr:strain rd kw20,) (ec:3.4.24.13) (db:pir2.dat) H64106 H64106 Haemophilus influenzae 727 -11537228 7500883975 hi0990 immunoglobin a1 protease iga1 (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:similar to gb:m87489 percent ident: 99.82;) (le:9979) (re:15063) (di:complement) U32779 U32779 g1574019 Haemophilus influenzae Rd 71421 -11537228 6500733370 iga:iga1 iga1:immunoglobulin a1 protease precursor:iga1 protease (gtcfc:10.11) (ec:3.4.21.72) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0990 HI0990 Haemophilus influenzae 727 -11537228

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881395	14577	36733	600	199

Description

6500733371 htra:hi1259 probable periplasmic serine protease do/hhoa-like precursor (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.2:12.13) (db:gtc-haemophilus influenzae) HI1259 HI1259 Haemophilus influenzae 727 -11537229 78017 hi1259 (de:probable periplasmic serine protease do/hhoa-like precursor) (db:swissprot) HTOA_HAEIN P45129 HAEMOPHILUS INFLUENZAE 727 -11537229 167083 htra heat shock protein htra:periplasmic serine proteinase do homolog (db:pir2.dat) A64113 A64113 Haemophilus influenzae 727 -11537229 7500883597 hi1259 periplasmic serine protease (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:similar to sp:p39099 pid:558912 pid:606173) (le:10955) (re:12355) (di:complement) U32805 U32805 g1574189 Haemophilus influenzae Rd 71421 -11537229 5000694486 (de:(hi1259) (pn:probable periplasmic serine protease do:periplasmic serine protease do and heat shock protein:htra) (gtcfc:10.11) (ec:) (htoa_haein) (keggfc:11.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI1259 HI1259 Haemophilus influenzae 727 10020356

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881396	14578	36734	615	204

Description

6500733372 lonb:hi1324 lon protease:protease la homolog (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI1324 HI1324 Haemophilus influenzae 727 -11537230 82314 lon-b:hi1324 (ec:3.4.21.-) (de:protease la homolog,) (db:swissprot) LONH_HAEIN P43865 HAEMOPHILUS INFLUENZAE 727 -11537230 166962 endopeptidase la homolog hi1324 (cl:hypothetical protein b0955) (db:pir2.dat) F64116 F64116 Haemophilus influenzae 727 -11537230 7500885096 hi1324 lon protease:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:similar to gb:d00863 sp:p36772 pid:402504 percent) (le:79) (re:1884) (di:direct) U32812 U32812 g1574785 Haemophilus influenzae Rd 71421 -11537230 5000694487 (de:(hi1324) (pn:protease la homolog:lon protease:lon) (gn:lon-b) (gtcfc:10.11) (ec:3.4.21.-) (lonh_haein) (keggfc:11.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI1324 HI1324 Haemophilus influenzae 727 10024544

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881397	14579	36735	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881401	14580	36736	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881403	14581	36737	417	138

Description

6500733373 pept:hi1348 peptidase t:aminotripeptidase:tripeptidase (gtcfc:10.11) (ec:3.4.11.-) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI1348 HI1348 Haemophilus influenzae 727 -11537231 89033 pept:hi1348 (ec:3.4.11.-) (de:peptidase t, (aminotripeptidase) (tripeptidase)) (db:swissprot) PEPT_HAEIN P45172 HAEMOPHILUS INFLUENZAE 727 -11537231 167075 pept aminotripeptidase::peptidase t (ec:3.4.11.-) (db:pir2.dat) C64118 C64118 Haemophilus influenzae 727 -11537231 7500887829 hi1348 peptidase t pept (db:genpept-bct1) (de:haemophilus influenzae rd section 129 of 163 of the completegenome.) (nt:similar to sp:p29745 gb:u00096 pid:1651556) (le:165) (re:1403) (di:direct) U32814 U32814 g1574810 Haemophilus influenzae Rd 71421 -11537231 5000694488 (de:(hi1348) (pn:aminotripeptidase:tripeptidase:peptidase t:pept) (gn:pept) (gtcfc:10.11) (ec:3.4.11.-) (pept_haein) (keggfc:11.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI1348 HI1348 Haemophilus influenzae 727 10031159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881409	14582	36738	1356	451

Description

6500733374 sms:hi1597 atp-dependent protease:protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI1597 HI1597 Haemophilus influenzae 727 -11537232 166020 sms sms protein (cl:dna repair protein sms) (db:pir2.dat) I64131 I64131 Haemophilus influenzae 727 -11537232 7500960736 hi1597 dna repair protein rada (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:similar to sp:p24554 gb:x63155 pid:537229) (le:7647) (re:9074) (di:complement) U32833 U32833 g1574440 Haemophilus influenzae Rd 71421 -11537232 5000694489 (de:(hi1597) (pn:protein:atp-dependent protease:sms) (gn:sms) (gtcfc:10.11) (ec:) (sms_haein) (keggfc:11.2) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI1597 HI1597 Haemophilus influenzae 727 10088058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881423	14583	36739	237	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881448	14584	36740	927	308

Description

GTC ORF with score 126 to: (or:Homo sapiens) (sr:human) (db:genpept-pri2) (de:human chromosome 12p13 sequence, complete sequence.) (nt:human dentatorubral and pallidoluysian atrophy) (le:146011:146185:146474) (re:146037:146322:146587) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881450	14585	36741	2625	874

Description

6500733375 pepn:hi1614 aminopeptidase n:alpha-aminoacylpeptide hydrolase (gtcfc:10.11) (ec:3.4.11.2) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI1614 HI1614 Haemophilus influenzae 727 -11537233 59392 pepn:hi1614 (ec:3.4.11.2) (de:aminopeptidase n, (alpha-aminoacylpeptide hydrolase)) (db:swissprot) AMPN_HAEIN P45274 HAEMOPHILUS INFLUENZAE 727 -11537233 140285 pepn membrane alanyl aminopeptidase (cl:microsomal aminopeptidase) (ec:3.4.11.2) (db:pir2.dat) F64132 F64132 Haemophilus influenzae 727 -11537233 7500876861 hi1614 aminopeptidase n pepn (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:similar to gb:m15273 sp:p04825 gb:m15676 gb:x04020) (le:66) (re:2675) (di:complement) U32835 U32835 g1574460 Haemophilus influenzae Rd 71421 -11537233 5000694490 (de:(hi1614) (pn:alpha-aminoacylpeptide hydrolase:aminopeptidase n:pepn) (gn:pepn) (gtcfc:10.11) (ec:3.4.11.2) (ampn_haein) (keggfc:11.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI1614 HI1614 Haemophilus influenzae 727 10002129

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881453	14586	36742	684	227

Description

6500733376 pepa:hi1705 aminopeptidase a/i (gtcfc:10.11) (ec:3.4.11.1) (keggfc:14.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI1705 HI1705 Haemophilus influenzae 727 -11537234 59352 pepa:hi1705 (ec:3.4.11.1) (de:aminopeptidase a/i,) (db:swissprot) AMPA_HAEIN P45334 HAEMOPHILUS INFLUENZAE 727 -11537234 140281 leucyl aminopeptidase:a (cl:cytosol aminopeptidase) (ec:3.4.11.1) (db:pir2.dat) C64137 C64137 Haemophilus influenzae 727 -11537234 7500876828 hi1705 aminopeptidase a/i pepa (db:genpept-bct1) (de:haemophilus influenzae rd section 158 of 163 of the completegenome.) (nt:similar to sp:p11648 gb:x15130 pid:1054725) (le:5807) (re:7282) (di:direct) U32843 U32843 g1574559 Haemophilus influenzae Rd 71421 -11537234 5000694491 (de:(hi1705) (pn:aminopeptidase a:aminopeptidase a) (gn:pepa) (gtcfc:10.11) (ec:3.4.11.1) (ampa_haein) (keggfc:11.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI1705 HI1705 Haemophilus influenzae 727 10002090

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881457	14587	36743	453	150

Description

6500733377 pcnb:hi0063 plasmid copy number control protein:probable poly:a polymerase:pap (gtcfc:10.2) (ec:2.7.7.19) (keggfc:14.1) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0063 HI0063 Haemophilus influenzae 727 -11537235 88821 pcnb:hi0063 (ec:2.7.7.19) (de:probable poly(a) polymerase, (pap)) (db:swissprot) PCNB_HAEIN P44439 HAEMOPHILUS INFLUENZAE 727 -11537235 167094 pcnb polynucleotide adenylyltransferase::plasmid copy number control protein (ec:2.7.7.19) (db:pir2.dat) B64046 B64046 Haemophilus influenzae 727 -11537235 7500887736 hi0063 poly a polymerase pcnb (db:genpept-bct1) (de:haemophilus influenzae rd section 6 of 163 of the complete genome.) (nt:similar to sp:p13685 gb:d26562 gb:m20574 gb:s48039) (le:8930) (re:10288) (di:direct) U32691 U32691 g1573011 Haemophilus influenzae Rd 71421 -11537235 5000694492 (de:(hi0063) (pn:probable poly:a polymerase:pap:plasmid copy number control protein:pcnb) (gn:pcnb) (gtcfc:10.2) (ec:2.7.7.19) (pcnb_haein) (keggfc:11.1) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0063 HI0063 Haemophilus influenzae 727 10030948

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881464	14588	36744	2454	817

Description

6500733378 dead:hi0231 atp-dependent rna helicase:atp-dependent rna helicase homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0231 HI0231 Haemophilus influenzae 727 -11537236 68167 dead:hi0231 (de:atp-dependent rna helicase dead homolog) (db:swissprot) DEAD_HAEIN P44586 HAEMOPHILUS INFLUENZAE 727 -11537236 166022 probable atp-dependent rna helicase (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) F64056 F64056 Haemophilus influenzae 727 -11537236 7500880123 hi0231 atp-dependent rna helicase dead (db:genpept-bct1) (de:haemophilus influenzae rd section 24 of 163 of the complete genome.) (nt:similar to sp:p23304 gb:m63288 gb:u03750 pid:432406) (le:6034) (re:7875) (di:direct) U32709 U32709 g1573195 Haemophilus influenzae Rd 71421 -11537236 5000694493 (de:(hi0231) (pn:atp-dependent rna helicase homolog:atp-dependent rna helicase:dead) (gn:dead) (gtcfc:10.2) (ec:) (dead_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0231 HI0231 Haemophilus influenzae 727 10010760

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881472	14589	36745	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881474	14590	36746	525	174

Description

6500733379 rho:hi0295 transcription termination factor rho:transcription termination factor (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0295 HI0295 Haemophilus influenzae 727 -11537237 94310 rho:hi0295 (de:transcription termination factor rho) (db:swissprot) RHO_HAEIN P44619 HAEMOPHILUS INFLUENZAE 727 -11537237 154390 transcription termination factor rho (cl:transcription termination factor rho) (db:pir2.dat) B64060 B64060 Haemophilus influenzae 727 -11537237 7500889758 hi0295 transcription termination factor rho (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p03002 gb:m12779 pid:147607) (le:7988) (re:9250) (di:direct) U32715 U32715 g1573263 Haemophilus influenzae Rd 71421 -11537237 5000694494 (de:(hi0295) (pn:transcription termination factor :transcription termination factor rho:rho) (gn:rho) (gtcfc:10.2) (ec:) (rho_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0295 HI0295 Haemophilus influenzae 727 10036290

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881475	14591	36747	600	199

Description

6500733380 srmb:hi0422 atp-dependent rna helicase:atp-dependent rna helicase homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0422 HI0422 Haemophilus influenzae 727 -11537238 99474 srmb:hi0422 (de:atp-dependent rna helicase srmb homolog) (db:swissprot) SRMB_HAEIN P44701 HAEMOPHILUS INFLUENZAE 727 -11537238 166024 atp-dependent rna helicase homolog (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) H64066 H64066 Haemophilus influenzae 727 -11537238 7500892080 hi0422 atp-dependent rna helicase srmb (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:similar to gb:d13169 sp:p21507 gb:x14152 pid:285777) (le:6951) (re:8270) (di:complement) U32725 U32725 g1573394 Haemophilus influenzae Rd 71421 -11537238 5000694495 (de:(hi0422) (pn:atp-dependent rna helicase homolog:atp-dependent rna helicase:srmb) (gn:srmb) (gtcfc:10.2) (ec:) (srmb_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0422 HI0422 Haemophilus influenzae 727 10041332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881482	14592	36748	267	88

Description

6500733381 greb:hi0569 transcription elongation factor:transcript cleavage factor greb (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0569 HI0569 Haemophilus influenzae 727 -11537239 74481 greb:hi0569 (de:greb)) (db:swissprot) GREB_HAEIN P43882 HAEMOPHILUS INFLUENZAE 727 -11537239 167201 transcription elongation factor greb homolog (cl:transcription elongation factor greb) (db:pir2.dat) B64078 B64078 Haemophilus influenzae 727 -11537239 7500882727 hi0569 transcription elongation factor greb (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to sp:p30128 pid:606340 gb:u00096) (le:8767) (re:9243) (di:direct) U32738 U32738 g1573556 Haemophilus influenzae Rd 71421 -11537239 5000694496 (de:(hi0569) (pn:transcription elongation factor :transcript cleavage factor greb:transcription elongation factor:greb) (gn:greb) (gtcfc:10.2) (ec:) (greb_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0569 HI0569 Haemophilus influenzae 727 10016997

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881486	14593	36749	228	75

Description

6500733382 hepa:hi0616 atp-dependent helicase:probable atp-dependent helicase homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0616 HI0616 Haemophilus influenzae 727 -11537240 76798 hepa:hi0616 (de:hepa)) (db:swissprot) HEPA_HAEIN P44781 HAEMOPHILUS INFLUENZAE 727 -11537240 166019 atp-dependent helicase hepa homolog hi0616 (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) H64081 H64081 Haemophilus influenzae 727 -11537240 7500883215 hi0616 atp-dependent helicase hepa (db:genpept-bct1) (de:haemophilus influenzae rd section 59 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1786245 percent ident:) (le:1068) (re:3839) (di:direct) U32744 U32744 g1573610 Haemophilus influenzae Rd 71421 -11537240 5000694497 (de:(hi0616) (pn:probable atp-dependent helicase homolog:atp-dependent helicase:hepa) (gn:hepa) (gtcfc:10.2) (ec:) (hepa_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0616 HI0616 Haemophilus influenzae 727 10019161

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881488	14594	36750	243	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881496	14595	36751	465	154

Description

6500733383 nusg:hi0717 transcription antitermination protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0717 HI0717 Haemophilus influenzae 727 -11537241 87244 nusg:hi0717 (de:transcription antitermination protein nusg) (db:swissprot) NUSG_HAEIN P43916 HAEMOPHILUS INFLUENZAE 727 -11537241 154358 transcription antitermination factor nusg:transcription elongation factor nusg (cl:transcription antitermination factor nusg) (db:pir2.dat) G64088 G64088 Haemophilus influenzae 727 -11537241 7500887017 hi0717 transcription antitermination protein nusg (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to sp:p16921 pid:147801 pid:396321) (le:8167) (re:8724) (di:direct) U32754 U32754 g1573719 Haemophilus influenzae Rd 71421 -11537241 5000694498 (de:(hi0717) (pn:transcription antitermination protein :transcription antitermination protein:nusg) (gn:nusg) (gtcfc:10.2) (ec:) (nusg_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0717 HI0717 Haemophilus influenzae 727 10029395

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881515	14596	36752	1932	643

Description

6500733384 rhlb:hi0892 atp-dependent rna helicase:atp-dependent rna helicase homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0892 HI0892 Haemophilus influenzae 727 -11537242 94274 rhlb:hi0892 (de:atp-dependent rna helicase rhlb homolog) (db:swissprot) RHLB_HAEIN P44922 HAEMOPHILUS INFLUENZAE 727 -11537242 166023 probable atp-dependent rna helicase (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) E64100 E64100 Haemophilus influenzae 727 -11537242 7500889739 hi0892 atp-dependent rna helicase rhlb (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p24229 gb:m83316 pid:146251) (le:2356) (re:3612) (di:direct) U32771 U32771 g1573911 Haemophilus influenzae Rd 71421 -11537242 5000694499 (de:(hi0892) (pn:atp-dependent rna helicase homolog:atp-dependent rna helicase:rhlb) (gn:rhlb) (gtcfc:10.2) (ec:) (rhlb_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0892 HI0892 Haemophilus influenzae 727 10036257

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881532	14597	36753	243	80

Description

6500733385 nusa:hi1283 transcription factor:n utilization substance protein a:protein:l factor (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI1283 HI1283 Haemophilus influenzae 727 -11537243 87228 nusa:hi1283 (de:n utilization substance protein a (nusa protein) (l factor)) (db:swissprot) NUSA_HAEIN P43915 HAEMOPHILUS INFLUENZAE 727 -11537243 7500887008 hi1283 n utilization substance protein a nusa (db:genpept-bct1) (de:haemophilus influenzae rd section 123 of 163 of the completegenome.) (nt:similar to sp:p03003 pid:606109 gb:u00096) (le:1635) (re:3122) (di:direct) U32808 U32808 g1574741 Haemophilus influenzae Rd 71421 -11537243 5000694500 (de:(hi1283) (pn:n utilization substance protein a: protein:l factor:transcription factor:nusa) (gn:nusa) (gtcfc:10.2) (ec:) (nusa_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI1283 HI1283 Haemophilus influenzae 727 10029379

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881533	14598	36754	867	288

Description

6500733386 nusb:hi1304 n utilization substance protein b:n utilization substance protein b homolog:protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI1304 HI1304 Haemophilus influenzae 727 -11537244 87240 nusb:hi1304 (de:n utilization substance protein b homolog (nusb protein)) (db:swissprot) NUSB_HAEIN P45150 HAEMOPHILUS INFLUENZAE 727 -11537244 154415 nusb transcription termination factor nusb:n utilization substance protein b (cl:nusb protein) (db:pir2.dat) D64115 D64115 Haemophilus influenzae 727 -11537244 7500887014 hi1304 n utilization substance protein b nusb (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to gb:m26839 sp:p04381 gb:x00681 gb:x64395) (le:2174) (re:2608) (di:direct) U32810 U32810 g1574763 Haemophilus influenzae Rd 71421 -11537244 5000694501 (de:(hi1304) (pn:n utilization substance protein b homolog: protein:n utilization substance protein b:nusb) (gn:nusb) (gtcfc:10.2) (ec:) (nusb_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI1304 HI1304 Haemophilus influenzae 727 10029391

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881549	14599	36755	1293	430

Description

6500733387 grea:hi1331 transcription elongation factor:transcript cleavage factor grea (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI1331 HI1331 Haemophilus influenzae 727 -11537245 74476 grea:hi1331 (de:grea)) (db:swissprot) GREA_HAEIN P43881 HAEMOPHILUS INFLUENZAE 727 -11537245 167200 grea transcription elongation factor grea (cl:transcription elongation factor greb) (db:pir2.dat) B64117 B64117 Haemophilus influenzae 727 -11537245 7500882722 hi1331 transcription elongation factor grea (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:similar to sp:p21346 gb:u01376 gb:x54718 pid:41611) (le:6462) (re:6938) (di:direct) U32812 U32812 g1574790 Haemophilus influenzae Rd 71421 -11537245 5000694502 (de:(hi1331) (pn:transcription elongation factor :transcript cleavage factor grea:transcription elongation factor:grea) (gn:grea) (gtcfc:10.2) (ec:) (grea_haein) (keggfc:11.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI1331 HI1331 Haemophilus influenzae 727 10016992

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881555	14600	36756	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881566	14601	36757	387	128

Description

5000694503 sigma factor:algu:probable rna polymerase sigma factor hi1459 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI1459 HI1459 Haemophilus influenzae 727 -11537246 111434 hi1459 (de:probable rna polymerase sigma factor hi1459) (db:swissprot) YE59_HAEIN P45215 HAEMOPHILUS INFLUENZAE 727 -11537246 167161 transcription initiation factor sigma homolog hi1459 (cl:transcription initiation factor sigma e) (db:pir2.dat) G64124 G64124 Haemophilus influenzae 727 -11537246 7500922715 hi1459 sigma factor:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 139 of 163 of the completegenome.) (nt:similar to gb:al009126 percent ident: 26.75;) (le:698) (re:1282) (di:complement) U32824 U32824 g1574301 Haemophilus influenzae Rd 71421 -11537246 6500733388 sigma factor:algu:probable rna polymerase sigma factor hi1459 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI1459 HI1459 Haemophilus influenzae 727 -11537246

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881572	14602	36758	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881583	14603	36759	900	299

Description

6500733389 rimi:hi0010 ribosomal-protein-alanine acetyltransferase:acetylating enzyme for n-terminal of ribosomal protein s18 (gtcfc:10.4) (ec:2.3.1.128) (keggfc:14.1) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0010 HI0010 Haemophilus influenzae 727 -11537247 94358 rimi:hi0010 (ec:2.3.1.128) (de:(acetylating enzyme for n-terminal of ribosomal protein s18)) (db:swissprot) RIMI_HAEIN P44305 HAEMOPHILUS INFLUENZAE 727 -11537247 7500889787 hi0010 ribosomal-protein-alanine acetyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to sp:p09453 gb:l05387 gb:x06117 pid:409555) (le:11414) (re:11854) (di:complement) U32686 U32686 g1572953 Haemophilus influenzae Rd 71421 -11537247 5000694504 (de:(hi0010) (pn:acetylating enzyme for n-terminal of ribosomal protein s18:ribosomal-protein-alanine acetyltransferase:rimi) (gn:rimi) (gtcfc:10.4) (ec:2.3.1.128) (rimi_haein) (keggfc:11.1) (tigrfc:12.5) (db:gtc-haemophilus inf) HI0010 HI0010 Haemophilus influenzae 727 10036338

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881585	14604	36760	207	68

Description

5000694505 rpmf:rpl32:hi0158 ribosomal protein l32:rpl32:50s ribosomal protein l32 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0158 HI0158 Haemophilus influenzae 727 -11537248 149036 rpmf:rpl32 ribosomal protein l32 (cl:escherichia coli ribosomal protein l32) (db:pir1.dat) G64051 G64051 Haemophilus influenzae 727 -11537248 7500954960 hi0158 ribosomal protein l32 rpl32 (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:similar to gb:m29698 sp:p02435 pid:147712 gb:u00096) (le:9029) (re:9199) (di:complement) U32701 U32701 g1573115 Haemophilus influenzae Rd 71421 -11537248 6500733390 rpmf:rpl32 ribosomal protein l32:rpl32:50s ribosomal protein l32 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0158 HI0158 Haemophilus influenzae 727 -11537248

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881586	14605	36761	309	102

Description

5000694506 rpls:rpl19:hi0201 ribosomal protein l19:rpl19:50s ribosomal protein l19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0201 HI0201 Haemophilus influenzae 727 -11537249 148931 ribosomal protein l19 (cl:escherichia coli ribosomal protein l19) (db:pir2.dat) B64054 B64054 Haemophilus influenzae 727 -11537249 7500954938 hi0201 ribosomal protein l19 rpl19 (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:similar to gb:x01818 sp:p02420 pid:43145 gb:u00096) (le:3928) (re:4278) (di:complement) U32705 U32705 g1573161 Haemophilus influenzae Rd 71421 -11537249 6500733391 rpls:rpl19 ribosomal protein l19:rpl19:50s ribosomal protein l19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0201 HI0201 Haemophilus influenzae 727 -11537249

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881593	14606	36762	210	69

Description

6500733392 rpsp:rps16:hi0204 ribosomal protein s16:rps16:30s ribosomal protein s16 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0204 HI0204 Haemophilus influenzae 727 -11537250 97057 rpsp:rps16:hi0204 (de:30s ribosomal protein s16) (db:swissprot) RS16_HAEIN P44382 HAEMOPHILUS INFLUENZAE 727 -11537250 148580 ribosomal protein s16 (cl:escherichia coli ribosomal protein s16) (db:pir2.dat) D64054 D64054 Haemophilus influenzae 727 -11537250 7500890922 hi0204 ribosomal protein s16 rps16 (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:similar to sp:p02372 pid:43143 gb:u00096) (le:5665) (re:5913) (di:complement) U32705 U32705 g1573164 Haemophilus influenzae Rd 71421 -11537250 5000694507 (de:(hi0204) (pn:30s ribosomal protein s16:ribosomal protein s16:rps16) (gn:rprps16) (gtcfc:10.4) (ec:) (rs16_haein) (keggfc:11.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae)) HI0204 HI0204 Haemophilus influenzae 727 10038979

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881596	14607	36763	675	224

Description

GTC ORF with score 201 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1700.) (nt:similar to saccharomyces cerevisiae p8283.8 gene) (le:<1) (re:1169) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881600	14608	36764	504	168

Description

5000694508 rpla:rpl1:hi0516 ribosomal protein l1:rpl1:50s ribosomal protein l1 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0516 HI0516 Haemophilus influenzae 727 -11537251 148665 ribosomal protein l1 (cl:escherichia coli ribosomal protein l1) (db:pir2.dat) I64073 I64073 Haemophilus influenzae 727 -11537251 7500954875 hi0516 ribosomal protein l1 rpl1 (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to pid:2267574 percent ident: 94.32;) (le:222) (re:911) (di:complement) U32734 U32734 g1573499 Haemophilus influenzae Rd 71421 -11537251 6500733393 rpla:rpl1 ribosomal protein l1:rpl1:50s ribosomal protein l1 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0516 HI0516 Haemophilus influenzae 727 -11537251

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881639	14609	36765	780	260

Description

5000694509 rplk:rpl11:hi0517 ribosomal protein l11:rpl11:50s ribosomal protein l11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0517 HI0517 Haemophilus influenzae 727 -11537252 148861 ribosomal protein l11 (cl:escherichia coli ribosomal protein l11) (db:pir2.dat) A64074 A64074 Haemophilus influenzae 727 -11537252 7500954918 hi0517 ribosomal protein l11 rpl11 (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to gb:u00006 sp:p02409 gb:v00339 pid:396322) (le:916) (re:1344) (di:complement) U32734 U32734 g1573500 Haemophilus influenzae Rd 71421 -11537252 6500733394 rplk:rpl11 ribosomal protein l11:rpl11:50s ribosomal protein l11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0517 HI0517 Haemophilus influenzae 727 -11537252

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881640	14610	36766	267	88

Description

GTC ORF with score 112 to: (sr:saccharomyces cerevisiae (library: yep13) dna) (db:genpept-pln1) (ec:1.5.1.5) (de:saccharomyces cerevisiae (clone yep13-3) methylenetetrahydrofolatedehydrogenase gene, complete cds.) (le:387) (re:1349) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881642	14611	36767	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881643	14612	36768	600	199

Description

GTC ORF with score 534 to: (sr:saccharomyces cerevisiae (library: yep13) dna) (db:genpept-pln1) (ec:1.5.1.5) (de:saccharomyces cerevisiae (clone yep13-3) methylenetetrahydrofolatedehydrogenase gene, complete cds.) (le:387) (re:1349) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881647	14613	36769	408	135

Description

5000694510 rpsu:rps21:hi0531 ribosomal protein s21:rps21:30s ribosomal protein s21 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0531 HI0531 Haemophilus influenzae 727 -11537253 148639 ribosomal protein s21 (cl:escherichia coli ribosomal protein s21) (db:pir2.dat) I64074 I64074 Haemophilus influenzae 727 -11537253 7500954869 hi0531 ribosomal protein s21 rps21 (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:similar to gb:j01687 sp:p02379 gb:v00346 pid:147754) (le:4486) (re:4701) (di:direct) U32735 U32735 g1573515 Haemophilus influenzae Rd 71421 -11537253 6500733395 rpsu:rps21 ribosomal protein s21:rps21:30s ribosomal protein s21 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0531 HI0531 Haemophilus influenzae 727 -11537253

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881648	14614	36770	321	106

Description

5000694511 rpli:rpl9:hi0544 ribosomal protein l9:rpl9:50s ribosomal protein l9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0544 HI0544 Haemophilus influenzae 727 -11537254 95496 rpli:rpl9:hi0544 (de:50s ribosomal protein l9) (db:swissprot) RL9_HAEIN P44349 HAEMOPHILUS INFLUENZAE 727 -11537254 148916 ribosomal protein l9 (cl:escherichia coli ribosomal protein l9) (db:pir2.dat) D64076 D64076 Haemophilus influenzae 727 -11537254 7500890363 hi0544 ribosomal protein l9 rpl9 (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to sp:p02418 gb:x04022 pid:42848 pid:537044) (le:7845) (re:8294) (di:complement) U32736 U32736 g1573529 Haemophilus influenzae Rd 71421 -11537254 6500733396 rpli:rpl9 ribosomal protein l9:rpl9:50s ribosomal protein l9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0544 HI0544 Haemophilus influenzae 727 -11537254

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881649	14615	36771	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881652	14616	36772	267	88

Description

5000694512 rpsr:rps18:hi0545 ribosomal protein s18:rps18:30s ribosomal protein s18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0545 HI0545 Haemophilus influenzae 727 -11537255 148603 ribosomal protein s18 (cl:escherichia coli ribosomal protein s18) (db:pir2.dat) E64076 E64076 Haemophilus influenzae 727 -11537255 7500954852 hi0545 ribosomal protein s18 rps18 (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p02374 gb:x04022 pid:42847) (le:8311) (re:8538) (di:complement) U32736 U32736 g1573530 Haemophilus influenzae Rd 71421 -11537255 6500733397 rpsr:rps18 ribosomal protein s18:rps18:30s ribosomal protein s18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0545 HI0545 Haemophilus influenzae 727 -11537255

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881657	14617	36773	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881660	14618	36774	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881665	14619	36775	318	105

Description

5000694513 rpsf:rps6:hi0547 ribosomal protein s6:rps6:30s ribosomal protein s6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0547 HI0547 Haemophilus influenzae 727 -11537256 97362 rpsf:rps6:hi0547 (de:30s ribosomal protein s6) (db:swissprot) RS6_HAEIN P44375 HAEMOPHILUS INFLUENZAE 727 -11537256 148391 ribosomal protein s6 (cl:escherichia coli ribosomal protein s6) (db:pir2.dat) G64076 G64076 Haemophilus influenzae 727 -11537256 7500891085 hi0547 ribosomal protein s6 rps6 (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to sp:p02358 gb:x04022 pid:42845 pid:537041) (le:8864) (re:9241) (di:complement) U32736 U32736 g1573532 Haemophilus influenzae Rd 71421 -11537256 6500733398 rpsf:rps6 ribosomal protein s6:rps6:30s ribosomal protein s6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0547 HI0547 Haemophilus influenzae 727 -11537256

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881666	14620	36776	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881669	14621	36777	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881674	14622	36778	1119	372

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881677	14623	36779	351	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881694	14624	36780	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881701	14625	36781	291	96

Description

5000694514 rpsg:rps7:hi0580 ribosomal protein s7:rps7:30s ribosomal protein s7 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0580 HI0580 Haemophilus influenzae 727 -11537257 148415 ribosomal protein s7 (cl:escherichia coli ribosomal protein s7) (db:pir2.dat) G64078 G64078 Haemophilus influenzae 727 -11537257 7500954804 hi0580 ribosomal protein s7 rps7 (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to sp:p02359 gb:j01689 gb:v00355 gb:v00356) (le:7301) (re:7771) (di:complement) U32739 U32739 g1573568 Haemophilus influenzae Rd 71421 -11537257 6500733399 rpsg:rps7 ribosomal protein s7:rps7:30s ribosomal protein s7 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0580 HI0580 Haemophilus influenzae 727 -11537257

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881712	14626	36782	423	140

Description

5000694515 rpsl:rps12:stra:hi0581 stra:30s ribosomal protein s12:streptomycin resistance protein (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0581 HI0581 Haemophilus influenzae 727 -11537258 148538 stra ribosomal protein s12:streptomycin resistance protein (cl:escherichia coli ribosomal protein s12) (db:pir2.dat) A42939 B42939 Haemophilus influenzae 727 -11537258 241334 stra (sr:haemophilus influenzae (strain rd) dna) (db:genpept-bct1) (de:haemophilus influenzae streptomycin resistance (stra) gene,complete cds.) (le:47) (re:421) (di:direct) HEASTRA M86701 g148985 Haemophilus influenzae 727 -11537258 7500954827 hi0581 ribosomal protein s12 rps12 (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to gb:d14640 gb:d14641 gb:j01688 sp:p02367) (le:7928) (re:8302) (di:complement) U32739 U32739 g1573569 Haemophilus influenzae Rd 71421 -11537258 6500733400 rpsl:rps12:stra stra:30s ribosomal protein s12:streptomycin resistance protein (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0581 HI0581 Haemophilus influenzae 727 -11537258

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881718	14627	36783	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881728	14628	36784	651	216

Description

5000694516 rplj:rpl10:hi0640 ribosomal protein l10:rpl10:50s ribosomal protein l10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0640 HI0640 Haemophilus influenzae 727 -11537259 148851 ribosomal protein l10 (cl:escherichia coli ribosomal protein l10) (db:pir2.dat) E64083 E64083 Haemophilus influenzae 727 -11537259 7500954915 hi0640 ribosomal protein l10 rpl10 (db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the complete genome.) (nt:similar to gb:x17216 sp:p17352 pid:47914 pid:47916) (le:2377) (re:2868) (di:direct) U32747 U32747 g1573638 Haemophilus influenzae Rd 71421 -11537259 6500733401 rplj:rpl10 ribosomal protein l10:rpl10:50s ribosomal protein l10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0640 HI0640 Haemophilus influenzae 727 -11537259

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881730	14629	36785	336	111

Description

6500733402 rpll:hi0641 ribosomal protein l7/l12:rpl7/l12:50s ribosomal protein l7/l12 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0641 HI0641 Haemophilus influenzae 727 -11537260 148785 ribosomal protein l12 (cl:escherichia coli ribosomal protein l12) (db:pir2.dat) F64083 F64083 Haemophilus influenzae 727 -11537260 7500954905 hi0641 ribosomal protein l7/l12 rpl7/l12 (db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the complete genome.) (nt:similar to gb:u00006 sp:p02392 gb:m38301 gb:v00339) (le:2923) (re:3294) (di:direct) U32747 U32747 g1573639 Haemophilus influenzae Rd 71421 -11537260 5000694517 (de:(hi0641) (pn:50s ribosomal protein l7:ribosomal protein l7) (gn:rpll) (gtcfc:10.4) (ec:) (rl7_haein) (keggfc:11.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae)) HI0641 HI0641 Haemophilus influenzae 727 10077826

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881743	14630	36786	1851	616

Description

5000694518 rpme:rpl31:hi0758 ribosomal protein l31:rpl31:50s ribosomal protein l31 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0758 HI0758 Haemophilus influenzae 727 -11537261 95147 rpme:rpl31:hi0758 (de:50s ribosomal protein l31) (db:swissprot) RL31_HAEIN P44367 HAEMOPHILUS INFLUENZAE 727 -11537261 129152 rpl31 ribosomal protein l31 (cl:escherichia coli ribosomal protein l31) (db:pir1.dat) B64091 B64091 Haemophilus influenzae 727 -11537261 7500890188 hi0758 ribosomal protein l31 rpl31 (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to sp:q59450 pid:1388150 pid:2198845) (le:2273) (re:2485) (di:complement) U32760 U32760 g1573767 Haemophilus influenzae Rd 71421 -11537261 6500733403 rpme:rpl31 ribosomal protein l31:rpl31:50s ribosomal protein l31 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0758 HI0758 Haemophilus influenzae 727 -11537261

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881748	14631	36787	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881754	14632	36788	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881767	14633	36789	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881770	14634	36790	2514	837

Description

5000694519 rpsj:rps10:hi0776 ribosomal protein s10:rps10:30s ribosomal protein s10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0776 HI0776 Haemophilus influenzae 727 -11537262 96893 rpsj:rps10:hi0776 (de:30s ribosomal protein s10) (db:swissprot) RS10_HAEIN P44378 HAEMOPHILUS INFLUENZAE 727 -11537262 148463 ribosomal protein s10 (cl:escherichia coli ribosomal protein s10) (db:pir2.dat) D64092 D64092 Haemophilus influenzae 727 -11537262 7500890842 hi0776 ribosomal protein s10 rps10 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p02364 gb:v00344 pid:42826 pid:42857) (le:5293) (re:5649) (di:direct) U32761 U32761 g1573786 Haemophilus influenzae Rd 71421 -11537262 6500733404 rpsj:rps10 ribosomal protein s10:rps10:30s ribosomal protein s10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0776 HI0776 Haemophilus influenzae 727 -11537262

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881778	14635	36791	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881794	14636	36792	405	134

Description

5000694520 rplc:rpl3:hi0777 ribosomal protein l3:rpl3:50s ribosomal protein l3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0777 HI0777 Haemophilus influenzae 727 -11537263 95292 rplc:rpl3:hi0777 (de:50s ribosomal protein l3) (db:swissprot) RL3_HAEIN P44344 HAEMOPHILUS INFLUENZAE 727 -11537263 148679 ribosomal protein l3 (cl:escherichia coli ribosomal protein l3) (db:pir2.dat) E64092 E64092 Haemophilus influenzae 727 -11537263 7500890270 hi0777 ribosomal protein l3 rpl3 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p02386 gb:v00344 pid:42827 pid:42858) (le:5666) (re:6292) (di:direct) U32761 U32761 g1573787 Haemophilus influenzae Rd 71421 -11537263 6500733405 rplc:rpl3 ribosomal protein l3:rpl3:50s ribosomal protein l3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0777 HI0777 Haemophilus influenzae 727 -11537263

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881795	14637	36793	516	171

Description

5000694521 rpld:rpl4:hi0778 ribosomal protein l4:rpl4:50s ribosomal protein l4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0778 HI0778 Haemophilus influenzae 727 -11537264 95362 rpld:rpl4:hi0778 (de:50s ribosomal protein l4) (db:swissprot) RL4_HAEIN P44345 HAEMOPHILUS INFLUENZAE 727 -11537264 148704 ribosomal protein l4 (cl:escherichia coli ribosomal protein l4) (db:pir2.dat) F64092 F64092 Haemophilus influenzae 727 -11537264 7500890310 hi0778 ribosomal protein l4 rpl4 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p55836 pid:1841323 percent ident:) (le:6308) (re:6910) (di:direct) U32761 U32761 g1573788 Haemophilus influenzae Rd 71421 -11537264 6500733406 rpld:rpl4 ribosomal protein l4:rpl4:50s ribosomal protein l4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0778 HI0778 Haemophilus influenzae 727 -11537264

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881801	14638	36794	1158	385

Description

5000694522 rplw:rpl23:hi0779 ribosomal protein l23:rpl23:50s ribosomal protein l23 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0779 HI0779 Haemophilus influenzae 727 -11537265 94997 rplw:rpl23:hi0779 (de:50s ribosomal protein l23) (db:swissprot) RL23_HAEIN P44361 HAEMOPHILUS INFLUENZAE 727 -11537265 148972 ribosomal protein l23 (cl:escherichia coli ribosomal protein l23) (db:pir1.dat) G64092 G64092 Haemophilus influenzae 727 -11537265 7500890088 hi0779 ribosomal protein l23 rpl23 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p55839 pid:1841324 pid:2337781) (le:6907) (re:7206) (di:direct) U32761 U32761 g1573789 Haemophilus influenzae Rd 71421 -11537265 6500733407 rplw:rpl23 ribosomal protein l23:rpl23:50s ribosomal protein l23 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0779 HI0779 Haemophilus influenzae 727 -11537265

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881808	14639	36795	993	330

Description

GTC ORF with score 933 to: (fn:catalyzes the conversion of glucose 6-phosphate) (db:genpept-pln2) (ec:5.5.1.4) (de:pichia pastoris inositol 1-phosphate synthase (ino1) gene, completecds.) (nt:first enzyme in inositol biosynthetic pathway) (le:61) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881809	14640	36796	1152	383

Description

5000694523 rplb:rpl2:hi0780 ribosomal protein l2:rpl2:50s ribosomal protein l2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0780 HI0780 Haemophilus influenzae 727 -11537266 148692 ribosomal protein l2 (cl:escherichia coli ribosomal protein l2) (db:pir2.dat) H64092 H64092 Haemophilus influenzae 727 -11537266 7500954881 hi0780 ribosomal protein l2 rpl2 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p55835 pid:1841325 percent ident:) (le:7224) (re:8045) (di:direct) U32761 U32761 g1573790 Haemophilus influenzae Rd 71421 -11537266 6500733408 rplb:rpl2 ribosomal protein l2:rpl2:50s ribosomal protein l2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0780 HI0780 Haemophilus influenzae 727 -11537266

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881810	14641	36797	834	277

Description

5000694524 rpss:rps19:hi0781 ribosomal protein s19:rps19:30s ribosomal protein s19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0781 HI0781 Haemophilus influenzae 727 -11537267 148629 ribosomal protein s19 (cl:escherichia coli ribosomal protein s19) (db:pir2.dat) I64092 I64092 Haemophilus influenzae 727 -11537267 301485 rpss ribosomal protein s19 (sr:actinobacillus actinomycetemcomitans (strain:y4) dna) (db:genpept-bct1) (de:actinobacillus actinomycetemcomitans dna for ribosomal proteins,partial and complete cds.) (le:2151) (re:2426) (di:direct) D64071 D64071 g1841326 Actinobacillus actinomycetemcomitans 714 -11537267 7500954860 hi0781 ribosomal protein s19 rps19 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to gb:x02613 sp:p02375 pid:42830 pid:606250) (le:8071) (re:8346) (di:direct) U32761 U32761 g1573791 Haemophilus influenzae Rd 71421 -11537267 6500733409 rpss:rps19 ribosomal protein s19:rps19:30s ribosomal protein s19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0781 HI0781 Haemophilus influenzae 727 -11537267

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881829	14642	36798	312	103

Description

GTC ORF with score 178 to: (sr:yeast (s.cerevisiae, strain dby939, derived from strain s288c) dna) (db:genpept-pln1) (de:yeast (s.cerevisiae) heat shock protein (sti1) gene, complete cds.) (nt:heat shock protein sti1) (le:361) (re:2130) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881831	14643	36799	1083	360

Description

5000694525 rplv:rpl22:hi0782 ribosomal protein l22:rpl22:50s ribosomal protein l22 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0782 HI0782 Haemophilus influenzae 727 -11537268 94978 rplv:rpl22:hi0782 (de:50s ribosomal protein l22) (db:swissprot) RL22_HAEIN P44360 HAEMOPHILUS INFLUENZAE 727 -11537268 148964 ribosomal protein l22 (cl:escherichia coli ribosomal protein l22) (db:pir2.dat) A64093 A64093 Haemophilus influenzae 727 -11537268 7500890066 hi0782 ribosomal protein l22 rpl22 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p55838 pid:1841327 percent ident:) (le:8358) (re:8690) (di:direct) U32761 U32761 g1573792 Haemophilus influenzae Rd 71421 -11537268 6500733410 rplv:rpl22 ribosomal protein l22:rpl22:50s ribosomal protein l22 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0782 HI0782 Haemophilus influenzae 727 -11537268

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881832	14644	36800	672	223

Description

GTC ORF with score 587 to: (sr:yeast (s.cerevisiae, strain dby939, derived from strain s288c) dna) (db:genpept-pln1) (de:yeast (s.cerevisiae) heat shock protein (sti1) gene, complete cds.) (nt:heat shock protein sti1) (le:361) (re:2130) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881837	14645	36801	450	149

Description

5000694526 rpsc:rps3:hi0783 ribosomal protein s3:rps3:30s ribosomal protein s3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0783 HI0783 Haemophilus influenzae 727 -11537269 148347 ribosomal protein s3 (cl:escherichia coli ribosomal protein s3) (db:pir2.dat) B64093 B64093 Haemophilus influenzae 727 -11537269 7500954792 hi0783 ribosomal protein s3 rps3 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p55827 pid:1841328 percent ident:) (le:8708) (re:9415) (di:direct) U32761 U32761 g1573793 Haemophilus influenzae Rd 71421 -11537269 6500733411 rpsc:rps3 ribosomal protein s3:rps3:30s ribosomal protein s3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0783 HI0783 Haemophilus influenzae 727 -11537269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881845	14646	36802	1272	423

Description

5000694527 rplp:rpl16:hi0784 ribosomal protein l16:rpl16:50s ribosomal protein l16 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0784 HI0784 Haemophilus influenzae 727 -11537270 94838 rplp:rpl16:hi0784 (de:50s ribosomal protein l16) (db:swissprot) RL16_HAEIN P44354 HAEMOPHILUS INFLUENZAE 727 -11537270 148907 ribosomal protein l16 (cl:escherichia coli ribosomal protein l16) (db:pir2.dat) C64093 C64093 Haemophilus influenzae 727 -11537270 7500889978 hi0784 ribosomal protein l16 rpl16 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p55837 pid:1841329 percent ident:) (le:9429) (re:9839) (di:direct) U32761 U32761 g1573794 Haemophilus influenzae Rd 71421 -11537270 6500733412 rplp:rpl16 ribosomal protein l16:rpl16:50s ribosomal protein l16 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0784 HI0784 Haemophilus influenzae 727 -11537270

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881858	14647	36803	954	317

Description

5000694528 rpmc:rpl29:hi0785 ribosomal protein l29:rpl29:50s ribosomal protein l29 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0785 HI0785 Haemophilus influenzae 727 -11537271 95077 rpmc:rpl29:hi0785 (de:50s ribosomal protein l29) (db:swissprot) RL29_HAEIN P44365 HAEMOPHILUS INFLUENZAE 727 -11537271 149005 ribosomal protein l29 (cl:escherichia coli ribosomal protein l29) (db:pir2.dat) D64093 D64093 Haemophilus influenzae 727 -11537271 7500890145 hi0785 ribosomal protein l29 rpl29 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p55840 pid:1841330 percent ident:) (le:9839) (re:10030) (di:direct) U32761 U32761 g1573795 Haemophilus influenzae Rd 71421 -11537271 6500733413 rpmc:rpl29 ribosomal protein l29:rpl29:50s ribosomal protein l29 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0785 HI0785 Haemophilus influenzae 727 -11537271

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881866	14648	36804	693	230

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881870	14649	36805	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881891	14650	36806	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881900	14651	36807	993	330

Description

5000694529 rpsq:rps17:hi0786 ribosomal protein s17:rps17:30s ribosomal protein s17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0786 HI0786 Haemophilus influenzae 727 -11537272 148594 ribosomal protein s17 (cl:escherichia coli ribosomal protein s17) (db:pir2.dat) E64093 E64093 Haemophilus influenzae 727 -11537272 7500954848 hi0786 ribosomal protein s17 rps17 (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to sp:p55829 pid:1841331 percent ident:) (le:10030) (re:10287) (di:direct) U32761 U32761 g1573796 Haemophilus influenzae Rd 71421 -11537272 6500733414 rpsq:rps17 ribosomal protein s17:rps17:30s ribosomal protein s17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0786 HI0786 Haemophilus influenzae 727 -11537272

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881903	14652	36808	684	227

Description

5000694530 rpln:rpl14:hi0788 ribosomal protein l14:rpl14:50s ribosomal protein l14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0788 HI0788 Haemophilus influenzae 727 -11537273 94793 rpln:rpl14:hi0788 (de:50s ribosomal protein l14) (db:swissprot) RL14_HAEIN P44352 HAEMOPHILUS INFLUENZAE 727 -11537273 148875 ribosomal protein l14 (cl:escherichia coli ribosomal protein l14) (db:pir2.dat) F64093 F64093 Haemophilus influenzae 727 -11537273 7500889940 hi0788 ribosomal protein l14 rpl14 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to sp:p02411 pid:42979 pid:606244 gb:u00096) (le:1112) (re:1483) (di:direct) U32762 U32762 g1573798 Haemophilus influenzae Rd 71421 -11537273 6500733415 rpln:rpl14 ribosomal protein l14:rpl14:50s ribosomal protein l14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0788 HI0788 Haemophilus influenzae 727 -11537273

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881909	14653	36809	492	163

Description

5000694531 rplx:rpl24:hi0789 ribosomal protein l24:rpl24:50s ribosomal protein l24 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0789 HI0789 Haemophilus influenzae 727 -11537274 95017 rplx:rpl24:hi0789 (de:50s ribosomal protein l24) (db:swissprot) RL24_HAEIN P44362 HAEMOPHILUS INFLUENZAE 727 -11537274 148981 ribosomal protein l24 (cl:escherichia coli ribosomal protein l24) (db:pir2.dat) G64093 G64093 Haemophilus influenzae 727 -11537274 7500890103 hi0789 ribosomal protein l24 rpl24 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x01563 sp:p02425 pid:42980 pid:606243) (le:1494) (re:1805) (di:direct) U32762 U32762 g1573799 Haemophilus influenzae Rd 71421 -11537274 6500733416 rplx:rpl24 ribosomal protein l24:rpl24:50s ribosomal protein l24 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0789 HI0789 Haemophilus influenzae 727 -11537274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881924	14654	36810	912	303

Description

5000694532 rple:rpl5:hi0790 ribosomal protein l5:rpl5:50s ribosomal protein l5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0790 HI0790 Haemophilus influenzae 727 -11537275 148738 ribosomal protein l5 (cl:escherichia coli ribosomal protein l5) (db:pir2.dat) H64093 H64093 Haemophilus influenzae 727 -11537275 7500954897 hi0790 ribosomal protein l5 rpl5 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x01563 sp:p02389 pid:42981 pid:606242) (le:1823) (re:2362) (di:direct) U32762 U32762 g1573800 Haemophilus influenzae Rd 71421 -11537275 6500733417 rple:rpl5 ribosomal protein l5:rpl5:50s ribosomal protein l5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0790 HI0790 Haemophilus influenzae 727 -11537275

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881947	14655	36811	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881951	14656	36812	504	167

Description

5000694533 rpsn:rps14:hi0791 ribosomal protein s14:rps14:30s ribosomal protein s14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0791 HI0791 Haemophilus influenzae 727 -11537276 148572 ribosomal protein s14 (cl:escherichia coli ribosomal protein s14) (db:pir2.dat) I64093 I64093 Haemophilus influenzae 727 -11537276 7500954838 hi0791 ribosomal protein s14 rps14 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x01563 sp:p02370 pid:42982 pid:606241) (le:2374) (re:2679) (di:direct) U32762 U32762 g1573801 Haemophilus influenzae Rd 71421 -11537276 6500733418 rpsn:rps14 ribosomal protein s14:rps14:30s ribosomal protein s14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0791 HI0791 Haemophilus influenzae 727 -11537276

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881952	14657	36813	1491	497

Description

5000694534 rpsh:rps8:hi0792 ribosomal protein s8:rps8:30s ribosomal protein s8 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0792 HI0792 Haemophilus influenzae 727 -11537277 148425 ribosomal protein s8 (cl:escherichia coli ribosomal protein s8) (db:pir2.dat) A64094 A64094 Haemophilus influenzae 727 -11537277 7500954809 hi0792 ribosomal protein s8 rps8 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x01563 sp:p02361 pid:42983 pid:606240) (le:2716) (re:3108) (di:direct) U32762 U32762 g1573802 Haemophilus influenzae Rd 71421 -11537277 6500733419 rpsh:rps8 ribosomal protein s8:rps8:30s ribosomal protein s8 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0792 HI0792 Haemophilus influenzae 727 -11537277

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881969	14658	36814	1224	408

Description

5000694535 rplf:rpl6:hi0793 ribosomal protein l6:rpl6:50s ribosomal protein l6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0793 HI0793 Haemophilus influenzae 727 -11537278 148749 ribosomal protein l6 (cl:escherichia coli ribosomal protein l6) (db:pir2.dat) B64094 B64094 Haemophilus influenzae 727 -11537278 7500954901 hi0793 ribosomal protein l6 rpl6 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x01563 sp:p02390 pid:42984 pid:606239) (le:3124) (re:3657) (di:direct) U32762 U32762 g1573803 Haemophilus influenzae Rd 71421 -11537278 6500733420 rplf:rpl6 ribosomal protein l6:rpl6:50s ribosomal protein l6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0793 HI0793 Haemophilus influenzae 727 -11537278

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881980	14659	36815	690	229

Description

5000694536 rplr:rpl18:hi0794 ribosomal protein l18:rpl18:50s ribosomal protein l18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0794 HI0794 Haemophilus influenzae 727 -11537279 94865 rplr:rpl18:hi0794 (de:50s ribosomal protein l18) (db:swissprot) RL18_HAEIN P44356 HAEMOPHILUS INFLUENZAE 727 -11537279 148922 ribosomal protein l18 (cl:escherichia coli ribosomal protein l18) (db:pir2.dat) C64094 C64094 Haemophilus influenzae 727 -11537279 7500890000 hi0794 ribosomal protein l18 rpl18 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to sp:p02419 pid:42985 pid:606238 gb:u00096) (le:3671) (re:4024) (di:direct) U32762 U32762 g1573804 Haemophilus influenzae Rd 71421 -11537279 6500733421 rplr:rpl18 ribosomal protein l18:rpl18:50s ribosomal protein l18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0794 HI0794 Haemophilus influenzae 727 -11537279

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881992	14660	36816	210	69

Description

5000694537 rpse:rps5:hi0795 ribosomal protein s5:rps5:30s ribosomal protein s5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0795 HI0795 Haemophilus influenzae 727 -11537280 97341 rpse:rps5:hi0795 (de:30s ribosomal protein s5) (db:swissprot) RS5_HAEIN P44374 HAEMOPHILUS INFLUENZAE 727 -11537280 148386 ribosomal protein s5 (cl:escherichia coli ribosomal protein s5) (db:pir2.dat) D64094 D64094 Haemophilus influenzae 727 -11537280 7500891060 hi0795 ribosomal protein s5 rps5 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x01563 sp:p02356 pid:42986 pid:606237) (le:4039) (re:4539) (di:direct) U32762 U32762 g1573805 Haemophilus influenzae Rd 71421 -11537280 6500733422 rpse:rps5 ribosomal protein s5:rps5:30s ribosomal protein s5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0795 HI0795 Haemophilus influenzae 727 -11537280

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501881996	14661	36817	558	186

Description

5000694538 rpmd:rpl30:hi0796 ribosomal protein l30:rpl30:50s ribosomal protein l30 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0796 HI0796 Haemophilus influenzae 727 -11537281 149018 ribosomal protein l30 (cl:escherichia coli ribosomal protein l30) (db:pir2.dat) E64094 E64094 Haemophilus influenzae 727 -11537281 7500954954 hi0796 ribosomal protein l30 rpl30 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x01563 sp:p02430 gb:m24532 pid:42987) (le:4546) (re:4725) (di:direct) U32762 U32762 g1573806 Haemophilus influenzae Rd 71421 -11537281 6500733423 rpmd:rpl30 ribosomal protein l30:rpl30:50s ribosomal protein l30 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0796 HI0796 Haemophilus influenzae 727 -11537281

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882012	14662	36818	1020	339

Description

5000694539 rplo:rpl15:hi0797 ribosomal protein l15:rpl15:50s ribosomal protein l15 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0797 HI0797 Haemophilus influenzae 727 -11537282 94815 rplo:rpl15:hi0797 (de:50s ribosomal protein l15) (db:swissprot) RL15_HAEIN P44353 HAEMOPHILUS INFLUENZAE 727 -11537282 148885 ribosomal protein l15 (cl:escherichia coli ribosomal protein l15) (db:pir2.dat) F64094 F64094 Haemophilus influenzae 727 -11537282 7500889966 hi0797 ribosomal protein l15 rpl15 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to sp:p02413 pid:42988 pid:606235 gb:u00096) (le:4729) (re:5163) (di:direct) U32762 U32762 g1573807 Haemophilus influenzae Rd 71421 -11537282 6500733424 rplo:rpl15 ribosomal protein l15:rpl15:50s ribosomal protein l15 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0797 HI0797 Haemophilus influenzae 727 -11537282

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882022	14663	36819	1560	519

Description

5000694541 rpsm:rps13:hi0799 ribosomal protein s13:rps13:30s ribosomal protein s13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0799 HI0799 Haemophilus influenzae 727 -11537283 7500976262 hi0799 ribosomal protein s13 rps13 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x02543 sp:p02369 gb:m12432 pid:581217) (le:6778) (re:7146) (di:direct) U32762 U32762 g1573810 Haemophilus influenzae Rd 71421 -11537283 6500733425 rpsm:rps13 ribosomal protein s13:rps13:30s ribosomal protein s13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0799 HI0799 Haemophilus influenzae 727 -11537283

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882024	14664	36820	1200	399

Description

5000694542 rpsk:rps11:hi0800 ribosomal protein s11:rps11:30s ribosomal protein s11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0800 HI0800 Haemophilus influenzae 727 -11537284 148481 ribosomal protein s11 (cl:escherichia coli ribosomal protein s11) (db:pir2.dat) I64094 I64094 Haemophilus influenzae 727 -11537284 7500954817 hi0800 ribosomal protein s11 rps11 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x02543 sp:p02366 pid:42797 pid:606232) (le:7149) (re:7538) (di:direct) U32762 U32762 g1573811 Haemophilus influenzae Rd 71421 -11537284 6500733426 rpsk:rps11 ribosomal protein s11:rps11:30s ribosomal protein s11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0800 HI0800 Haemophilus influenzae 727 -11537284

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882047	14665	36821	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882052	14666	36822	555	184

Description

5000694543 rpsd:rps4:hi0801 ribosomal protein s4:rps4:30s ribosomal protein s4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0801 HI0801 Haemophilus influenzae 727 -11537285 148373 ribosomal protein s4 (cl:escherichia coli ribosomal protein s4) (db:pir2.dat) A64095 A64095 Haemophilus influenzae 727 -11537285 7500954797 hi0801 ribosomal protein s4 rps4 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:x02543 sp:p02354 gb:v00353 pid:147714) (le:7566) (re:8186) (di:direct) U32762 U32762 g1573812 Haemophilus influenzae Rd 71421 -11537285 6500733427 rpsd:rps4 ribosomal protein s4:rps4:30s ribosomal protein s4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0801 HI0801 Haemophilus influenzae 727 -11537285

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882057	14667	36823	363	120

Description

5000694544 rplq:rpl17:hi0803 ribosomal protein l17:rplq:50s ribosomal protein l17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0803 HI0803 Haemophilus influenzae 727 -11537286 94852 rplq:rpl17:hi0803 (de:50s ribosomal protein l17) (db:swissprot) RL17_HAEIN P44355 HAEMOPHILUS INFLUENZAE 727 -11537286 148915 ribosomal protein l17 (cl:escherichia coli ribosomal protein l17) (db:pir2.dat) C64095 C64095 Haemophilus influenzae 727 -11537286 7500889992 hi0803 ribosomal protein l17 rplq (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:j01685 sp:p02416 gb:x00766 pid:147716) (le:9245) (re:9631) (di:direct) U32762 U32762 g1573814 Haemophilus influenzae Rd 71421 -11537286 6500733428 rplq:rpl17 ribosomal protein l17:rplq:50s ribosomal protein l17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0803 HI0803 Haemophilus influenzae 727 -11537286

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882081	14668	36824	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882084	14669	36825	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882097	14670	36826	1884	627

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882106	14671	36827	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882111	14672	36828	834	277

Description

5000694545 rpma:rpl27:hi0879 ribosomal protein l27:rpl27:50s ribosomal protein l27 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0879 HI0879 Haemophilus influenzae 727 -11537287 148999 ribosomal protein l27 (cl:escherichia coli ribosomal protein l27:eubacterial ribosomal protein l27 homology) (db:pir2.dat) F64099 F64099 Haemophilus influenzae 727 -11537287 7500954948 hi0879 ribosomal protein l27 rpl27 (db:genpept-bct1) (de:haemophilus influenzae rd section 84 of 163 of the complete genome.) (nt:similar to gb:d13267 sp:p02427 pid:216637) (le:9469) (re:9726) (di:complement) U32769 U32769 g1573896 Haemophilus influenzae Rd 71421 -11537287 6500733429 rpma:rpl27 ribosomal protein l27:rpl27:50s ribosomal protein l27 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0879 HI0879 Haemophilus influenzae 727 -11537287

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882112	14673	36829	573	190

Description

5000694546 rplu:rpl21:hi0880 ribosomal protein l21:rpl21:50s ribosomal protein l21 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0880 HI0880 Haemophilus influenzae 727 -11537288 94959 rplu:rpl21:hi0880 (de:50s ribosomal protein l21) (db:swissprot) RL21_HAEIN P44359 HAEMOPHILUS INFLUENZAE 727 -11537288 148949 ribosomal protein l21 (cl:escherichia coli ribosomal protein l21) (db:pir2.dat) G64099 G64099 Haemophilus influenzae 727 -11537288 7500890054 hi0880 ribosomal protein l21 rpl21 (db:genpept-bct1) (de:haemophilus influenzae rd section 84 of 163 of the complete genome.) (nt:similar to gb:d13267 sp:p02422 pid:216636) (le:9747) (re:10058) (di:complement) U32769 U32769 g1573897 Haemophilus influenzae Rd 71421 -11537288 6500733430 rplu:rpl21 ribosomal protein l21:rpl21:50s ribosomal protein l21 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0880 HI0880 Haemophilus influenzae 727 -11537288

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882114	14674	36830	408	135

Description

5000694547 rpsb:rps2:hi0913 ribosomal protein s2:rps2:30s ribosomal protein s2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0913 HI0913 Haemophilus influenzae 727 -11537289 97233 rpsb:rps2:hi0913 (de:30s ribosomal protein s2) (db:swissprot) RS2_HAEIN P44371 HAEMOPHILUS INFLUENZAE 727 -11537289 148331 ribosomal protein s2 (cl:escherichia coli ribosomal protein s2) (db:pir2.dat) B64102 B64102 Haemophilus influenzae 727 -11537289 7500891024 hi0913 ribosomal protein s2 rps2 (db:genpept-bct1) (de:haemophilus influenzae rd section 88 of 163 of the complete genome.) (nt:similar to gb:d26562 sp:p02351 gb:v00343 pid:42842) (le:990) (re:1745) (di:direct) U32773 U32773 g1573934 Haemophilus influenzae Rd 71421 -11537289 6500733431 rpsb:rps2 ribosomal protein s2:rps2:30s ribosomal protein s2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0913 HI0913 Haemophilus influenzae 727 -11537289

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882129	14675	36831	1287	428

Description

5000694548 rpmg:rpl33:hi0950 ribosomal protein l33:rpl33:50s ribosomal protein l33 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0950 HI0950 Haemophilus influenzae 727 -11537290 95183 rpmg:rpl33:hi0950 (de:50s ribosomal protein l33) (db:swissprot) RL33_HAEIN P44369 HAEMOPHILUS INFLUENZAE 727 -11537290 149041 ribosomal protein l33 (cl:escherichia coli ribosomal protein l33) (db:pir2.dat) D64104 D64104 Haemophilus influenzae 727 -11537290 7500890210 hi0950 ribosomal protein l33 rpl33 (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to gb:j01677 sp:p02436 pid:147709) (le:5160) (re:5330) (di:complement) U32776 U32776 g1573975 Haemophilus influenzae Rd 71421 -11537290 6500733432 rpmg:rpl33 ribosomal protein l33:rpl33:50s ribosomal protein l33 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0950 HI0950 Haemophilus influenzae 727 -11537290

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882158	14676	36832	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882167	14677	36833	708	236

Description

5000694549 rpmb:rpl28:hi0951 ribosomal protein l28:rpl28:50s ribosomal protein l28 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0951 HI0951 Haemophilus influenzae 727 -11537291 149004 ribosomal protein l28 (cl:escherichia coli ribosomal protein l28) (db:pir2.dat) E64104 E64104 Haemophilus influenzae 727 -11537291 7500954953 hi0951 ribosomal protein l28 rpl28 (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to gb:j01677 sp:p02428 pid:147708) (le:5342) (re:5578) (di:complement) U32776 U32776 g1573976 Haemophilus influenzae Rd 71421 -11537291 6500733433 rpmb:rpl28 ribosomal protein l28:rpl28:50s ribosomal protein l28 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0951 HI0951 Haemophilus influenzae 727 -11537291

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882173	14678	36834	447	148

Description

5000694550 rpmh:rpl34:hi0998 ribosomal protein l34:rpl34:50s ribosomal protein l34 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0998 HI0998 Haemophilus influenzae 727 -11537292 95197 rpmh:rpl34:hi0998 (de:50s ribosomal protein l34) (db:swissprot) RL34_HAEIN P44370 HAEMOPHILUS INFLUENZAE 727 -11537292 149058 ribosomal protein l34 (cl:escherichia coli ribosomal protein l34) (db:pir2.dat) E64107 E64107 Haemophilus influenzae 727 -11537292 7500890222 hi0998 ribosomal protein l34 rpl34 (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p02437 gb:j01602 gb:m11056) (le:121) (re:255) (di:direct) U32781 U32781 g1574029 Haemophilus influenzae Rd 71421 -11537292 6500733434 rpmh:rpl34 ribosomal protein l34:rpl34:50s ribosomal protein l34 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0998 HI0998 Haemophilus influenzae 727 -11537292

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882174	14679	36835	1197	398

Description

5000694551 rpmi:rpl35:hi1319 ribosomal protein l35:rpl35:50s ribosomal protein l35 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1319 HI1319 Haemophilus influenzae 727 -11537293 7500976279 hi1319 ribosomal protein l35 rpl35 (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:similar to sp:p07085 gb:u00096 pid:1742796) (le:3114) (re:3383) (di:direct) U32811 U32811 g1574779 Haemophilus influenzae Rd 71421 -11537293 6500733435 rpmi:rpl35 ribosomal protein l35:rpl35:50s ribosomal protein l35 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1319 HI1319 Haemophilus influenzae 727 -11537293

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882177	14680	36836	204	67

Description

5000694552 rplt:rpl20:hi1320 ribosomal protein l20:rpl20:50s ribosomal protein l20 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1320 HI1320 Haemophilus influenzae 727 -11537294 148942 ribosomal protein l20 (cl:escherichia coli ribosomal protein l20) (db:pir2.dat) C64116 C64116 Haemophilus influenzae 727 -11537294 7500954941 hi1320 ribosomal protein l20 rpl20 (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:similar to gb:k02844 sp:p02421 pid:146344 pid:43068) (le:3450) (re:3803) (di:direct) U32811 U32811 g1574780 Haemophilus influenzae Rd 71421 -11537294 6500733436 rplt:rpl20 ribosomal protein l20:rpl20:50s ribosomal protein l20 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1320 HI1320 Haemophilus influenzae 727 -11537294

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882181	14681	36837	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882194	14682	36838	204	67

Description

5000694553 rpso-a:rps15-a:rpso-b:rps15-b:hi1328 ribosomal protein s15:rps15:30s ribosomal protein s15 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1328 HI1328 Haemophilus influenzae 727 -11537295 148575 ribosomal protein s15 (cl:escherichia coli ribosomal protein s15:eubacterial ribosomal protein s15 homology) (db:pir2.dat) H64116 H64116 Haemophilus influenzae 727 -11537295 7500954841 hi1328 ribosomal protein s15 rps15 (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:similar to gb:j02638 sp:p02371 gb:m14425 gb:x00761) (le:3818) (re:4087) (di:direct) U32812 U32812 g1574788 Haemophilus influenzae Rd 71421 -11537295 7500954842 hi1468 ribosomal protein s15 rps15 (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to gb:j02638 sp:p02371 gb:m14425 gb:x00761) (le:3233) (re:3502) (di:complement) U32825 U32825 g1574309 Haemophilus influenzae Rd 71421 -11537295 6500733437 rpso-a:rps15-a:rpso-b:rps15-b ribosomal protein s15:rps15:30s ribosomal protein s15 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1328 HI1328 Haemophilus influenzae 727 -11537295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882216	14683	36839	651	216

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882221	14684	36840	315	104

Description

5000694554 rpsi:rps9:hi1442 ribosomal protein s9:rps9:30s ribosomal protein s9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1442 HI1442 Haemophilus influenzae 727 -11537296 148447 ribosomal protein s9 (cl:escherichia coli ribosomal protein s9) (db:pir2.dat) F64123 F64123 Haemophilus influenzae 727 -11537296 7500954813 hi1442 ribosomal protein s9 rps9 (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:s75161 sp:p31782 pid:241867 percent) (le:121) (re:513) (di:complement) U32823 U32823 g1574282 Haemophilus influenzae Rd 71421 -11537296 6500733438 rpsi:rps9 ribosomal protein s9:rps9:30s ribosomal protein s9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1442 HI1442 Haemophilus influenzae 727 -11537296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882251	14685	36841	1140	379

Description

5000694555 rplm:rpl13:hi1443 ribosomal protein l13:rpl13:50s ribosomal protein l13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1443 HI1443 Haemophilus influenzae 727 -11537297 94775 rplm:rpl13:hi1443 (de:50s ribosomal protein l13) (db:swissprot) RL13_HAEIN P44387 HAEMOPHILUS INFLUENZAE 727 -11537297 148870 ribosomal protein l13 (cl:escherichia coli ribosomal protein l13) (db:pir2.dat) G64123 G64123 Haemophilus influenzae 727 -11537297 7500889930 hi1443 ribosomal protein l13 rpl13 (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to sp:p31781 percent ident: 95.07;) (le:530) (re:958) (di:complement) U32823 U32823 g1574283 Haemophilus influenzae Rd 71421 -11537297 6500733439 rplm:rpl13 ribosomal protein l13:rpl13:50s ribosomal protein l13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1443 HI1443 Haemophilus influenzae 727 -11537297

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882259	14686	36842	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882265	14687	36843	549	182

Description

6500733440 rimk:hi1531 ribosomal protein s6 modification protein:probable ribosomal protein s6 modification protein (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1531 HI1531 Haemophilus influenzae 727 -11537298 94362 rimk:hi1531 (de:probable ribosomal protein s6 modification protein) (db:swissprot) RIMK_HAEIN P45241 HAEMOPHILUS INFLUENZAE 727 -11537298 167145 ribosomal protein s6--glutamic acid ligase::rimk protein homolog (cl:ribosomal protein s6--glutamic acid ligase) (ec:6.3.2.-) (db:pir2.dat) H64127 H64127 Haemophilus influenzae 727 -11537298 7500889790 hi1531 ribosomal protein s6 modification protein (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:similar to sp:p17116 gb:x15859 pid:42747 gb:u00096) (le:13471) (re:14379) (di:complement) U32828 U32828 g1574372 Haemophilus influenzae Rd 71421 -11537298 5000694556 (de:(hi1531) (pn:probable ribosomal protein s6 modification protein:ribosomal protein s6 modification protein:rimk) (gn:rimk) (gtcfc:10.4) (ec:) (rimk_haein) (keggfc:11.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae)) HI1531 HI1531 Haemophilus influenzae 727 10036342

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882279	14688	36844	729	242

Description

5000694557 rply:rpl25:hi1630 ribosomal protein l25:rpl25:50s ribosomal protein l25 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1630 HI1630 Haemophilus influenzae 727 -11537299 95035 rply:rpl25:hi1630 (de:50s ribosomal protein l25) (db:swissprot) RL25_HAEIN P45281 HAEMOPHILUS INFLUENZAE 727 -11537299 148990 ribosomal protein l25 (cl:escherichia coli ribosomal protein l25) (db:pir2.dat) E64133 E64133 Haemophilus influenzae 727 -11537299 7500890121 hi1630 ribosomal protein l25 rpl25 (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:similar to gb:u00008 sp:p02426 gb:d13326 pid:405949) (le:1739) (re:2026) (di:direct) U32836 U32836 g1574477 Haemophilus influenzae Rd 71421 -11537299 6500733441 rply:rpl25 ribosomal protein l25:rpl25:50s ribosomal protein l25 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI1630 HI1630 Haemophilus influenzae 727 -11537299

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882284	14689	36845	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882308	14690	36846	1011	336

Description

GTC ORF with score 136 to: (sr:soybean) (db:genpept-pln1) (ec:2.7.7.6) (de:soybean rpb1-b1 gene for the largest subunit of rna polymerase ii(ec 2.7.7.6).) (nt:largest subunit of rna polymerase ii) (le:<1:2062:2196) (re:1736:2133:2265) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882315	14691	36847	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882327	14692	36848	462	153

Description

5000694579 miaa:trpx:hi0068 trpx:trna delta:2-isopentenylpyrophosphate transferase:ipp transferase (gtcfc:10.6) (ec:2.5.1.8) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0068 HI0068 Haemophilus influenzae 727 -11537300 83701 miaa:trpx:hi0068 (ec:2.5.1.8) (de:(ipp transferase)) (db:swissprot) MIAA_HAEIN P44495 HAEMOPHILUS INFLUENZAE 727 -11537300 167228 delta 2 -isopentenylpyrophosphate transferase (cl:delta(2)-isopentenylpyrophosphate transferase) (ec:2.5.1.-) (db:pir2.dat) F64046 F64046 Haemophilus influenzae 727 -11537300 7500885627 hi0068 trna delta 2 -isopentenylpyrophosphate (db:genpept-bct1) (de:haemophilus influenzae rd section 7 of 163 of the complete genome.) (nt:similar to sp:p16384 gb:d00743 gb:u00005 gb:z11831) (le:3748) (re:4683) (di:direct) U32692 U32692 g1573017 Haemophilus influenzae Rd 71421 -11537300 6500733442 miaa:trpx trpx:trna delta:2-isopentenylpyrophosphate transferase:ipp transferase (gtcfc:10.6) (ec:2.5.1.8) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0068 HI0068 Haemophilus influenzae 727 -11537300

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882338	14693	36849	438	145

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882342	14694	36850	618	205

Description

GTC ORF with score 132 to: (sr:chlamydomonas reinhardtii (strain cc-621) vegetative cdna to mrna) (db:genpept-pln1) (de:chlamydomonas reinhardtii structural wall protein (vsp1) mrna,complete cds.) (le:273) (re:1175) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882346	14695	36851	807	268

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882347	14696	36852	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882367	14697	36853	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882385	14698	36854	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882390	14699	36855	447	148

Description

6500733443 trmd:hi0202
trna:guanine-n1-methyltransferase:m1g-methyltransferase (gtcfc:10.6)
(ec:2.1.1.31) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae)
HI0202 HI0202 Haemophilus influenzae 727 -11537301 102277 trmd:hi0202
(ec:2.1.1.31) (de:methyltransferase) (trna (gm37) methyltransferase))
(db:swissprot) TRMD_HAEIN P43912 HAEMOPHILUS INFLUENZAE 727 -11537301
137759 trna guanine-n1--methyltransferase (cl:trna (guanine-n1)
methyltransferase) (ec:2.1.1.31) (db:pir2.dat) C64054 C64054 Haemophilus
influenzae 727 -11537301 7500893406 hi0202 trna guanine-n1
-methyltransferase trmd (db:genpept-bct1) (de:haemophilus influenzae rd
section 20 of 163 of the complete genome.) (nt:similar to sp:p07020
pid:43144 gb:u00096) (le:4315) (re:5055) (di:complement) U32705 U32705
g1573162 Haemophilus influenzae Rd 71421 -11537301 5000694581 (de:(hi0202)
(pn:m1g-methyltransferase:trna:guanine-n1-methyltransferase:trmd) (gn:trmd)
(gtcfc:10.6) (ec:2.1.1.31) (trmd_haein) (keggfc:11.1) (tigrfc:12.1)
(db:gtc-haemophilus influenzae)) HI0202 HI0202 Haemophilus influenzae 727
10044096

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882393	14700	36856	804	267

Description

6500733444 tgt:hi0244 queuine trna-ribosyltransferase:trna-guanine transglycosylase:guanine insertion enzyme (gtcfc:10.6) (ec:2.4.2.29) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0244 HI0244 Haemophilus influenzae 727 -11537302 101227 tgt:hi0244 (ec:2.4.2.29) (de:transglycosylase) (guanine insertion enzyme)) (db:swissprot) TGT_HAEIN P44594 HAEMOPHILUS INFLUENZAE 727 -11537302 167229 queuine trna-ribosyltransferase (cl:queuine trna-ribosyltransferase) (ec:2.4.2.29) (db:pir2.dat) A64057 A64057 Haemophilus influenzae 727 -11537302 7500893011 hi0244 trna-guanine transglycosylase tgt (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:similar to gb:m63939 sp:p19675 gb:s68715 gb:x56175) (le:6110) (re:7258) (di:complement) U32710 U32710 g1573209 Haemophilus influenzae Rd 71421 -11537302 5000694582 (de:(hi0244) (pn:queuine trna-ribosyltransferase:guanine insertion enzyme:trna-guanine transglycosylase:tgt) (gn:tgt) (gtcfc:10.6) (ec:2.4.2.29) (tgt_haein) (keggfc:11.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0244 HI0244 Haemophilus influenzae 727 10043068

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882403	14701	36857	1491	496

Description

6500733445 quea:hi0245 queuosine biosynthesis protein:s-adenosylmethionine:trna ribosyltransferase-isomerase:queuosine biosynthesis protein quea (gtcfc:10.6) (ec:5.-.-.-) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0245 HI0245 Haemophilus influenzae 727 -11537303 92738 quea:hi0245 (ec:5.-.-.-) (de:(queuosine biosynthesis protein quea)) (db:swissprot) QUEA_HAEIN P44595 HAEMOPHILUS INFLUENZAE 727 -11537303 167129 s-adenosylmethionine:trna ribosyltransferase-isomerase::queuosine biosynthesis protein quea (cl:s-adenosylmethionine:trna ribosyltransferase-isomerase) (ec:5.-.-.-) (db:pir2.dat) B64057 B64057 Haemophilus influenzae 727 -11537303 7500889220 hi0245 queuosine biosynthesis protein quea (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:similar to gb:m37702 sp:p21516 pid:147485 gb:u00096) (le:7602) (re:8693) (di:complement) U32710 U32710 g1573210 Haemophilus influenzae Rd 71421 -11537303 5000694583 (de:(hi0245) (pn:s-adenosylmethionine:trna ribosyltransferase-isomerase:queuosine biosynthesis protein quea:queuosine biosynthesis protein:quea) (gn:quea) (gtcfc:10.6) (ec:5.-.-.-) (quea_haein) (keggfc:11.1) (tigrfc:12.1) (db:gt) HI0245 HI0245 Haemophilus influenzae 727 10034766

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882404	14702	36858	369	122

Description

6500733446 pth:hi0394 pth:peptidyl-trna hydrolase (gtcfc:10.6) (ec:3.1.1.29) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0394 HI0394 Haemophilus influenzae 727 -11537304 92199 pth:hi0394 (ec:3.1.1.29) (de:peptidyl-trna hydrolase, (pth)) (db:swissprot) PTH_HAEIN P44682 HAEMOPHILUS INFLUENZAE 727 -11537304 167081 pth aminoacyl-trna hydrolase (cl:peptidyl-trna hydrolase) (ec:3.1.1.29) (db:pir2.dat) C64065 C64065 Haemophilus influenzae 727 -11537304 7500888966 hi0394 peptidyl-trna hydrolase pth (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to sp:p23932 gb:x61941 pid:581202 gb:u00096) (le:2335) (re:2919) (di:complement) U32723 U32723 g1573366 Haemophilus influenzae Rd 71421 -11537304 5000694584 (de:(hi0394) (pn:peptidyl-trna hydrolase:pth) (gn:pth) (gtcfc:10.6) (ec:3.1.1.29) (_haein) (keggfc:11.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0394 HI0394 Haemophilus influenzae 727 10034232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882407	14703	36859	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882412	14704	36860	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882413	14705	36861	822	273

Description

6500733447 trma:hi0848 uracil-5--methyltransferase:trna:m-5-u54-methyltransferase:rumt (gtcfc:10.6) (ec:2.1.1.35) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0848 HI0848 Haemophilus influenzae 727 -11537305 102273 trma:hi0848 (ec:2.1.1.35) (de:methyltransferase) (rumt)) (db:swissprot) TRMA_HAEIN P31812 HAEMOPHILUS INFLUENZAE 727 -11537305 167227 trna uracil-5--methyltransferase (ec:2.1.1.35) (db:pir2.dat) C64098 C64098 Haemophilus influenzae 727 -11537305 7500893404 hi0848 trna uracil-5--methyltransferase trma (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to sp:p23003 gb:m57568 pid:148051) (le:5494) (re:6585) (di:direct) U32766 U32766 g1573862 Haemophilus influenzae Rd 71421 -11537305 5000694587 (de:(hi0848) (pn:m-5-u54-methyltransferase:rumt:trna:uracil-5--methyltransferase:trma) (gn:trma) (gtcfc:10.6) (ec:2.1.1.35) (trma_haein) (keggfc:11.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0848 HI0848 Haemophilus influenzae 727 10044092

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882414	14706	36862	1020	339

Description

6500733448 cca:hi1606 trna nucleotidyltransferase:trna adenylyltransferase:trna cca-pyrophosphorylase (gtcfc:10.6) (ec:2.7.7.25) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1606 HI1606 Haemophilus influenzae 727 -11537306 63388 cca:hi1606 (ec:2.7.7.25) (de:(trna cca-pyrophosphorylase) (cca-adding enzyme)) (db:swissprot) CCA_HAEIN P45269 HAEMOPHILUS INFLUENZAE 727 -11537306 139275 trna adenylyltransferase (cl:escherichia coli trna adenylyltransferase) (ec:2.7.7.25) (db:pir2.dat) B64132 B64132 Haemophilus influenzae 727 -11537306 7500878338 hi1606 trna nucleotidyltransferase cca (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:similar to gb:m12788 sp:p06961 pid:145468) (le:5515) (re:6765) (di:direct) U32834 U32834 g1574448 Haemophilus influenzae Rd 71421 -11537306 5000694589 (de:(hi1606) (pn:trna adenylyltransferase:trna cca-pyrophosphorylase:trna nucleotidyltransferase:cca) (gn:cca) (gtcfc:10.6) (ec:2.7.7.25) (cca_haein) (keggfc:11.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI1606 HI1606 Haemophilus influenzae 727 10006058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882431	14707	36863	819	272

Description

5000694590 trua:hist:hi1644 hist:pseudouridylate synthase i:pseudouridine synthase i:uracil hydrolyase (gtcfc:10.6) (ec:4.2.1.70) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1644 HI1644 Haemophilus influenzae 727 -11537307 102498 trua:hist:hi1644 (ec:4.2.1.70) (de:i) (pseudouridine synthase i) (uracil hydrolyase)) (db:swissprot) TRUA_HAEIN P45291 HAEMOPHILUS INFLUENZAE 727 -11537307 141938 hist trna-pseudouridine synthase i (cl:trna-pseudouridine synthase i) (ec:5.4.99.12) (db:pir2.dat) F64134 F64134 Haemophilus influenzae 727 -11537307 7500893516 hi1644 pseudouridylate synthase i trua (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p07649 gb:x02743 pid:41718 gb:u00096) (le:6586) (re:7395) (di:complement) U32837 U32837 g1574492 Haemophilus influenzae Rd 71421 -11537307 6500733449 trua:hist hist:pseudouridylate synthase i:pseudouridine synthase i:uracil hydrolyase (gtcfc:10.6) (ec:4.2.1.70) (keggfc:14.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1644 HI1644 Haemophilus influenzae 727 -11537307

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882434	14708	36864	723	240

Description

6500733450 glne:hi0069 glutamate-ammonia-ligase adenylyltransferase:glutamine-synthetase adenylyltransferase:atase (gtcfc:10.7) (ec:2.7.7.42) (keggfc:14.1) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0069 HI0069 Haemophilus influenzae 727 -11537308 73986 glne:hi0069 (ec:2.7.7.42) (de:synthetase adenylyltransferase) (atase)) (db:swissprot) GLNE_HAEIN P44419 HAEMOPHILUS INFLUENZAE 727 -11537308 166159 glutamate-ammonia-ligase adenylyltransferase homolog (db:pir2.dat) G64046 G64046 Haemophilus influenzae 727 -11537308 7500882472 hi0069 glutamate-ammonia-ligase adenylyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 7 of 163 of the complete genome.) (nt:similar to sp:p30870 gb:z21844 pid:49400 gb:u00096) (le:4689) (re:7634) (di:direct) U32692 U32692 g1573018 Haemophilus influenzae Rd 71421 -11537308 5000694558 (de:(hi0069) (pn:glutamine- synthetase adenylyltransferase:atase:glutamate-ammonia-ligase adenylyltransferase:glne) (gn:glne) (gtcfc:10.5) (ec:2.7.7.42) (glne_haein) (keggfc:11.1) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0069 HI0069 Haemophilus influenzae 727 10016516

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882444	14709	36865	555	184

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882447	14710	36866	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882467	14711	36867	1359	452

Description

6500733451 ppib:hi0079 peptidyl-prolyl cis-trans isomerase b:ppiase b:rotamase b (gtcfc:10.7) (ec:5.2.1.8) (keggfc:14.1) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0079 HI0079 Haemophilus influenzae 727 -11537309 67560 ppib:hi0079 (ec:5.2.1.8) (de:(rotamase b)) (db:swissprot) CYPB_HAEIN P44499 HAEMOPHILUS INFLUENZAE 727 -11537309 142105 peptidylprolyl isomerase (cl:peptidylprolyl isomerase) (ec:5.2.1.8) (db:pir2.dat) D64047 D64047 Haemophilus influenzae 727 -11537309 7500879877 hi0079 peptidyl-prolyl cis-trans isomerase b ppib (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:similar to gb:m55430 sp:p23869 gb:x59293 pid:145290) (le:7373) (re:7882) (di:direct) U32693 U32693 g1573027 Haemophilus influenzae Rd 71421 -11537309 5000694559 (de:(hi0079) (pn:ppiase b:rotamase b:peptidyl-prolyl cis-trans isomerase b:ppib) (gn:ppib) (gtcfc:10.5) (ec:5.2.1.8) (cypb_haein) (keggfc:11.1) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0079 HI0079 Haemophilus influenzae 727 10010159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882468	14712	36868	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882469	14713	36869	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882487	14714	36870	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882488	14715	36871	843	280

Description

6500733452 efp:hi0328 elongation factor p:ef-p (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0328 HI0328 Haemophilus influenzae 727 -11537310 167219 translation elongation factor ef-p (cl:translation elongation factor ef-p) (db:pir2.dat) I64061 I64061 Haemophilus influenzae 727 -11537310 7500960742 hi0328 elongation factor p efp (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p33398 gb:x61676 pid:433670) (le:9964) (re:10530) (di:complement) U32717 U32717 g1573295 Haemophilus influenzae Rd 71421 -11537310 5000694560 (de:(hi0328) (pn:ef-p:elongation factor p:efp) (gn:efp) (gtcfc:10.5) (ec:) (efp_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0328 HI0328 Haemophilus influenzae 727 10088312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882489	14716	36872	552	184

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882524	14717	36873	450	149

Description

6500733453 dsbb:hi0428 oxido-reductase:disulfide bond formation protein b (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0428 HI0428 Haemophilus influenzae 727 -11537311 69308 dsbb:hi0428 (de:disulfide bond formation protein b (disulfide oxidoreductase)) (db:swissprot) DSBB_HAEIN P44707 HAEMOPHILUS INFLUENZAE 727 -11537311 167063 probable protein-disulfide oxidoreductase (cl:protein-disulfide oxidoreductase dsbb) (ec:1.8.4.-) (db:pir2.dat) C64067 C64067 Haemophilus influenzae 727 -11537311 7500880669 hi0428 disulfide bond formation protein b dsbb (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:l03721 sp:p30018 pid:398018) (le:3920) (re:4453) (di:direct) U32726 U32726 g1573403 Haemophilus influenzae Rd 71421 -11537311 5000694561 (de:(hi0428) (pn:disulfide bond formation protein b:oxido-reductase:dsbb) (gn:dsbb) (gtcfc:10.5) (ec:) (dsbb_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0428 HI0428 Haemophilus influenzae 727 10011891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882530	14718	36874	3552	1183

Description

6500733454 infa:hi0548 initiation factor if-1 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0548 HI0548 Haemophilus influenzae 727 -11537312 154289 translation initiation factor if-1 (cl:translation initiation factor if-1) (db:pir2.dat) H64076 H64076 Haemophilus influenzae 727 -11537312 7500955438 hi0548 translation initiation factor 1 infa (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to gb:l10383 sp:p02998 gb:y00373 pid:145167) (le:9440) (re:9694) (di:complement) U32736 U32736 g1573533 Haemophilus influenzae Rd 71421 -11537312 5000694562 (de:(hi0548) (pn:initiation factor if-1:infa) (gn:infa) (gtcfc:10.5) (ec:) (if1_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0548 HI0548 Haemophilus influenzae 727 10081495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882544	14719	36875	882	293

Description

6500733455 slyx:hi0573 slyx protein:protein homolog (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0573 HI0573 Haemophilus influenzae 727 -11537313 98642 slyx:hi0573 (de:slyx protein homolog) (db:swissprot) SLYX_HAEIN P44759 HAEMOPHILUS INFLUENZAE 727 -11537313 167167 slyx protein homolog (db:pir2.dat) D64078 D64078 Haemophilus influenzae 727 -11537313 7500891711 hi0573 slyx protein slyx (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to gb:l13261 sp:p30857 pid:290468) (le:905) (re:1126) (di:complement) U32739 U32739 g1573562 Haemophilus influenzae Rd 71421 -11537313 5000694563 (de:(hi0573) (pn:protein homolog:slyx protein:slyx) (gn:slyx) (gtcfc:10.5) (ec:) (slyx_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0573 HI0573 Haemophilus influenzae 727 10040517

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882548	14720	36876	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882571	14721	36877	1797	598

Description

GTC ORF with score 785 to: (fn:required for gamma-tubulin ring function and) (sr:african clawed frog) (db:genpept-vrt) (de:xenopus laevis gamma-tubulin interacting protein mrna, completecds.) (nt:xgrip109) (le:118) (re:2838) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882572	14722	36878	1119	373

Description

5000694564 elongation factor ef-tu:duplicate:tufa:hi0578 and tufb:hi0632:elongation factor tu:ef-tu (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0578 HI0578 Haemophilus influenzae 727 -11537314 154166 translation elongation factor ef-tu (cl:translation elongation factor tu:translation elongation factor tu homology) (db:pir2.dat) E64078 E64078 Haemophilus influenzae 727 -11537314 7500955420 hi0578 elongation factor tu tufa (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to gb:u00006 sp:p02990 gb:j01717 gb:m10459) (le:3866) (re:5050) (di:complement) U32739 U32739 g1573560 Haemophilus influenzae Rd 71421 -11537314 7500955421 hi0632 elongation factor tu tufb (db:genpept-bct1) (de:haemophilus influenzae rd section 61 of 163 of the complete genome.) (nt:similar to gb:u00006 sp:p02990 gb:j01717 gb:m10459) (le:2748) (re:3932) (di:direct) U32746 U32746 g1573634 Haemophilus influenzae Rd 71421 -11537314 6500733456 elongation factor ef-tu:duplicate:tufa:hi0578 and tufb:hi0632:elongation factor tu:ef-tu (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0578 HI0578 Haemophilus influenzae 727 -11537314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882591	14723	36879	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882614	14724	36880	2430	810

Description

5000694565 fusa:fus:hi0579 fusa:elongation factor g:ef-g (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0579 HI0579 Haemophilus influenzae 727 -11537315 154239 translation elongation factor ef-g (cl:translation elongation factor g:translation elongation factor tu homology) (db:pir2.dat) F64078 F64078 Haemophilus influenzae 727 -11537315 7500955429 hi0579 elongation factor g fusa (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to gb:x00415 sp:p02996 gb:j01689 gb:v00356) (le:5115) (re:7217) (di:complement) U32739 U32739 g1573567 Haemophilus influenzae Rd 71421 -11537315 6500733457 fusa:fus fusa:elongation factor g:ef-g (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0579 HI0579 Haemophilus influenzae 727 -11537315

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882619	14725	36881	1239	412

Description

6500733458 slyd:hi0699 rotamase:peptidyl prolyl cis-trans isomerase:probable fkbp-type peptidyl-prolyl cis-trans isomerase:ppiase:rotamase (gtcfc:10.7) (ec:5.2.1.8) (keggfc:14.1) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0699 HI0699 Haemophilus influenzae 727 -11537316 98640 slyd:hi0699 (ec:5.2.1.8) (de:(ppiase) (rotamase)) (db:swissprot) SLYD_HAEIN P44830 HAEMOPHILUS INFLUENZAE 727 -11537316 167152 slyd probable peptidylprolyl isomerase:fkbp-type slyd (ec:5.2.1.8) (db:pir2.dat) D64087 D64087 Haemophilus influenzae 727 -11537316 7500891709 hi0699 peptidyl-prolyl cis-trans isomerase:fkbp-type (db:genpept-bct1) (de:haemophilus influenzae rd section 68 of 163 of the complete genome.) (nt:similar to gb:l13261 sp:p30856 gb:z21496 pid:394720) (le:106) (re:678) (di:complement) U32753 U32753 g1573702 Haemophilus influenzae Rd 71421 -11537316 5000694566 (de:(hi0699) (pn:probable fkbp-type peptidyl-prolyl cis-trans isomerase :ppiase:rotamase:rotamase, peptidyl prolyl cis-trans isomerase:slyd) (gn:slyd) (gtcfc:10.5) (ec:5.2.1.8) (slyd_haein) (keggfc:11.1) (tigrfc:12.4) (db:gtc-ha) HI0699 HI0699 Haemophilus influenzae 727 10040515

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882621	14726	36882	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882623	14727	36883	642	213

Description

6500733459 selb:hi0709 translation factor:probable translation factor (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0709 HI0709 Haemophilus influenzae 727 -11537317 98384 selb:hi0709 (de:selenocysteine-specific elongation factor (selb translation factor)) (db:swissprot) SELB_HAEIN P43927 HAEMOPHILUS INFLUENZAE 727 -11537317 167220 translation elongation factor ef-selb homolog (cl:translation elongation factor selb:translation elongation factor tu homology) (db:pir2.dat) I64087 I64087 Haemophilus influenzae 727 -11537317 7500891516 hi0709 selenocysteine-specific elongation factor (db:genpept-bct1) (de:haemophilus influenzae rd section 68 of 163 of the complete genome.) (nt:similar to sp:p14081 gb:x16644 pid:42937 pid:466728) (le:9434) (re:11293) (di:direct) U32753 U32753 g1573710 Haemophilus influenzae Rd 71421 -11537317 5000694567 (de:(hi0709) (pn:probable translation factor:translation factor:selb) (gn:selb) (gtcfc:10.5) (ec:) (selb_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0709 HI0709 Haemophilus influenzae 727 10040261

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882624	14728	36884	852	283

Description

6500733460 frr:hi0808 ribosome recycling factor:ribosome releasing factor:rrf (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0808 HI0808 Haemophilus influenzae 727 -11537318 96609 frr:hi0808 (de:ribosome recycling factor (ribosome releasing factor) (rrf)) (db:swissprot) RRF_HAEIN P44307 HAEMOPHILUS INFLUENZAE 727 -11537318 167147 frr:rrf ribosome releasing factor:ribosome recycling factor:translation releasing factor (cl:ribosome releasing factor) (db:pir1.dat) D64095 D64095 Haemophilus influenzae 727 -11537318 7500890811 hi0808 ribosome releasing factor rrf (db:genpept-bct1) (de:haemophilus influenzae rd section 78 of 163 of the complete genome.) (nt:similar to gb:d26562 sp:p16174 gb:d13334 gb:j05113) (le:3065) (re:3622) (di:complement) U32763 U32763 g1573820 Haemophilus influenzae Rd 71421 -11537318 5000694568 (de:(hi0808) (pn:ribosome recycling factor:rrf:ribosome releasing factor:frr) (gn:frr) (gtcfc:10.5) (ec:) (rrf_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0808 HI0808 Haemophilus influenzae 727 10038541

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882636	14729	36885	1632	543

Description

5000694569 dsba:por:hi0846 disulfide oxidoreductase:por:thiol:disulfide interchange protein dsba precursor (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0846 HI0846 Haemophilus influenzae 727 -11537319 69304 dsba:por:hi0846 (de:thiol:disulfide interchange protein dsba precursor) (db:swissprot) DSBA_HAEIN P31810 HAEMOPHILUS INFLUENZAE 727 -11537319 142164 por protein disulfide-isomerase:dsba precursor:thiol:disulfide interchange protein dsba (cl:protein disulfide-isomerase dsba:thioredoxin homology) (ec:5.3.4.1) (db:pir2.dat) B46411 B64098 Haemophilus influenzae 727 -11537319 241259 por disulfide oxidoreductase (sr:haemophilus influenzae (strain rd) dna) (db:genpept-bct1) (de:haemophilus influenzae disulfide oxidoreductase (por) gene,complete cds.) (le:621) (re:1238) (di:direct) HEADSFO M94205 g148887 Haemophilus influenzae 727 -11537319 7500880665 hi0846 periplasmic oxidoreductase por (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to gb:m94205 sp:p31810 pid:1573860 percent) (le:4336) (re:4953) (di:direct) U32766 U32766 g1573860 Haemophilus influenzae Rd 71421 -11537319 6500733461 dsba:por disulfide oxidoreductase:por:thiol:disulfide interchange protein dsba precursor (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0846 HI0846 Haemophilus influenzae 727 -11537319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882638	14730	36886	975	324

Description

6500733462 tsf:hi0914 elongation factor ef-ts (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0914 HI0914 Haemophilus influenzae 727 -11537320 154255 translation elongation factor ef-ts (cl:translation elongation factor ef-ts) (db:pir2.dat) C64102 C64102 Haemophilus influenzae 727 -11537320 7500955433 hi0914 elongation factor ts tsf (db:genpept-bct1) (de:haemophilus influenzae rd section 88 of 163 of the complete genome.) (nt:similar to gb:d26562 sp:p02997 gb:d13334 gb:v00343) (le:1878) (re:2729) (di:direct) U32773 U32773 g1573935 Haemophilus influenzae Rd 71421 -11537320 5000694570 (de:(hi0914) (pn:elongation factor ts:ef-ts:elongation factor ef-ts:tsf) (gn:tsf) (gtcfc:10.5) (ec:) (efts_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI0914 HI0914 Haemophilus influenzae 727 10081476

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882650	14731	36887	1296	431

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882676	14732	36888	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882686	14733	36889	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882688	14734	36890	642	213

Description

5000694571 dpra:smf:hi0985 dna processing chain a:dpra (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0985 HI0985 Haemophilus influenzae 727 -11537321 69240 smf:dpra:hi0985 (de:smf protein (dna processing chain a)) (db:swissprot) SMF_HAEIN P43862 HAEMOPHILUS INFLUENZAE 727 -11537321 166107 dpra dpra protein (db:pir2.dat) D64106 D64106 Haemophilus influenzae 727 -11537321 241596 dpra+ dpra (db:genpept-bct1) (de:haemophilus influenzae leua (leua) gene, partial cds, dpra (dpra+),orf272 and orf193 genes, complete cds, and pfka (pfka) gene,partial cds.) (le:783) (re:1904) (di:direct) HIU18657 U18657 g609332 Haemophilus influenzae 727 -11537321 7500880601 hi0985 dna processing chain a dpra (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:similar to gb:l42023 sp:p43862 pid:1006171) (le:3267) (re:4388) (di:complement) U32779 U32779 g1574014 Haemophilus influenzae Rd 71421 -11537321 6500733463 dpra:smf dna processing chain a:dpra (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI0985 HI0985 Haemophilus influenzae 727 -11537321

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882690	14735	36891	729	242

Description

6500733464 pmba:hi1152 maturation of antibiotic mccb17:protein homolog (gtcfc:10.7:13.3) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1152 HI1152 Haemophilus influenzae 727 -11537322 90062 pmba:hi1152 (de:pmba protein homolog) (db:swissprot) PMBA_HAEIN P45077 HAEMOPHILUS INFLUENZAE 727 -11537322 166978 pmba pmba protein (db:pir2.dat) C64186 C64186 Haemophilus influenzae 727 -11537322 7500888187 hi1152 pmba protein pmba (db:genpept-bct1) (de:haemophilus influenzae rd section 110 of 163 of the completegenome.) (nt:similar to sp:p24231 gb:x54152 pid:42440 pid:537077) (le:75) (re:1430) (di:direct) U32795 U32795 g1574709 Haemophilus influenzae Rd 71421 -11537322 5000694572 (de:(hi1152) (pn:protein homolog:maturation of antibiotic mccb17:pmba) (gn:pmba) (gtcfc:10.5) (ec:) (pmba_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI1152 HI1152 Haemophilus influenzae 727 10032182

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882705	14736	36892	390	129

Description

5000694573 dsbc:xpra:hi1213 disulfide interchange protein:dsbc:xpra:thiol:disulfide interchange protein dsbc precursor (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1213 HI1213 Haemophilus influenzae 727 -11537323 69311 dsbc:xpra:hi1213 (de:thiol:disulfide interchange protein dsbc precursor) (db:swissprot) DSBC_HAEIN P45111 HAEMOPHILUS INFLUENZAE 727 -11537323 142169 protein disulfide-isomerase:dsbc precursor:thiol:disulfide interchange protein dsbc (cl:protein disulfide-isomerase dsbc) (ec:5.3.4.1) (db:pir2.dat) E64110 E64110 Haemophilus influenzae 727 -11537323 7500880671 hi1213 th:disulfide interchange protein dsbc (db:genpept-bct1) (de:haemophilus influenzae rd section 115 of 163 of the completegenome.) (nt:similar to gb:m54884 sp:p21892 pid:147549) (le:9550) (re:10239) (di:direct) U32800 U32800 g1574142 Haemophilus influenzae Rd 71421 -11537323 6500733465 dsbc:xpra disulfide interchange protein:dsbc:xpra:thiol:disulfide interchange protein dsbc precursor (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1213 HI1213 Haemophilus influenzae 727 -11537323

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882721	14737	36893	798	265

Description

6500733466 infb:hi1284 initiation factor if-2 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1284 HI1284 Haemophilus influenzae 727 -11537324 78883 infb:hi1284 (de:translation initiation factor if-2) (db:swissprot) IF2_HAEIN P44323 HAEMOPHILUS INFLUENZAE 727 -11537324 154229 translation initiation factor if-2 (cl:translation initiation factor if-2:translation elongation factor tu homology) (db:pir2.dat) E64114 E64114 Haemophilus influenzae 727 -11537324 7500883889 hi1284 translation initiation factor 2 infb (db:genpept-bct1) (de:haemophilus influenzae rd section 123 of 163 of the completegenome.) (nt:similar to sp:p02995 pid:42145 pid:42146 pid:42217) (le:3134) (re:5623) (di:direct) U32808 U32808 g1574742 Haemophilus influenzae Rd 71421 -11537324 5000694574 (de:(hi1284) (pn:initiation factor if-2:infb) (gn:infb) (gtcfc:10.5) (ec:) (if2_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI1284 HI1284 Haemophilus influenzae 727 10021218

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882724	14738	36894	432	143

Description

6500733467 infc:hi1318 initiation factor 3:initiation factor if-3 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1318 HI1318 Haemophilus influenzae 727 -11537325 154295 translation initiation factor if-3 (cl:translation initiation factor if-3) (db:pir2.dat) B64116 B64116 Haemophilus influenzae 727 -11537325 7500955444 hi1318 translation initiation factor 3 infc (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:similar to gb:k02844 sp:p02999 pid:290449 pid:43067) (le:2568) (re:2975) (di:direct) U32811 U32811 g1574778 Haemophilus influenzae Rd 71421 -11537325 5000694575 (de:(hi1318) (pn:initiation factor if-3:initiation factor 3:infc) (gn:infc) (gtcfc:10.5) (ec:) (if3_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI1318 HI1318 Haemophilus influenzae 727 10081499

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882727	14739	36895	648	215

Description

GTC ORF with score 132 to: (sr:human) (db:genpept-pri2) (de:homo sapiens clone lm1955 h105e3 gene, partial cds, completesequence.) (nt:translation in conflict with u47105) (le:<17272:25729:29555:32778) (re:17382:25875:29683:32920) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882765	14740	36896	549	183

Description

6500733468 prfa:hi1561 polypeptide chain release factor 1:peptide chain release factor 1:rf-1 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1561 HI1561 Haemophilus influenzae 727 -11537326 94088 prfa:hi1561 (de:peptide chain release factor 1 (rf-1)) (db:swissprot) RF1_HAEIN P43917 HAEMOPHILUS INFLUENZAE 727 -11537326 154400 prfa:rf-1 translation releasing factor rf-1:peptide chain release factor 1 (cl:translation releasing factor) (db:pir1.dat) I64129 I64129 Haemophilus influenzae 727 -11537326 7500889655 hi1561 peptide chain release factor 1 prfa (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:m11519 sp:p07011 pid:147567) (le:15222) (re:16307) (di:complement) U32830 U32830 g1574404 Haemophilus influenzae Rd 71421 -11537326 5000694576 (de:(hi1561) (pn:peptide chain release factor 1:rf-1:polypeptide chain release factor 1:prfa) (gn:prfa) (gtcfc:10.5) (ec:) (rf1_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI1561 HI1561 Haemophilus influenzae 727 10036071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882771	14741	36897	1281	427

Description

5000694577 map:hi1722 methionine aminopeptidase:map:peptidase m (gtcfc:10.7) (ec:3.4.11.18) (keggfc:14.1) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1722 HI1722 Haemophilus influenzae 727 -11537327 59384 map:hi1722 (ec:3.4.11.18) (de:methionine aminopeptidase, (map) (peptidase m)) (db:swissprot) AMPM_HAEIN P44421 HAEMOPHILUS INFLUENZAE 727 -11537327 140290 methionyl aminopeptidase (cl:escherichia coli methionyl aminopeptidase) (ec:3.4.11.18) (db:pir2.dat) C64138 C64138 Haemophilus influenzae 727 -11537327 7500876847 hi1722 methionine aminopeptidase map (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to gb:d26562 sp:p07906 gb:m15106 pid:146727) (le:1508) (re:2314) (di:complement) U32845 U32845 g1574578 Haemophilus influenzae Rd 71421 -11537327 6500733469 map methionine aminopeptidase:map:peptidase m (gtcfc:10.7) (ec:3.4.11.18) (keggfc:14.1) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1722 HI1722 Haemophilus influenzae 727 -11537327

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882774	14742	36898	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882790	14743	36899	1065	354

Description

6500733470 prfc:hi1735 peptide-chain-release factor 3:peptide chain release factor 3:rf-3 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae) HI1735 HI1735 Haemophilus influenzae 727 -11537328 94102 prfc:hi1735 (de:peptide chain release factor 3 (rf-3)) (db:swissprot) RF3_HAEIN P43928 HAEMOPHILUS INFLUENZAE 727 -11537328 167080 peptide-chain-release factor 3 (cl:translation elongation factor tu homology) (db:pir2.dat) C64139 C64139 Haemophilus influenzae 727 -11537328 7500889662 hi1735 peptide chain release factor 3 prfc (db:genpept-bct1) (de:haemophilus influenzae rd section 161 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p33998 gb:d17724 gb:z26313) (le:7505) (re:9088) (di:direct) U32846 U32846 g1574592 Haemophilus influenzae Rd 71421 -11537328 5000694578 (de:(hi1735) (pn:peptide chain release factor 3:rf-3:peptide-chain-release factor 3:prfc) (gn:prfc) (gtcfc:10.5) (ec:) (rf3_haein) (keggfc:11.2) (tigrfc:12.4) (db:gtc-haemophilus influenzae)) HI1735 HI1735 Haemophilus influenzae 727 10036085

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882794	14744	36900	513	170

Description

6500733471 ung:hi0018 uracil dna glycosylase:uracil-dna glycosylase (gtcfc:10.8) (ec:3.2.2.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0018 HI0018 Haemophilus influenzae 727 -11537329 103717 ung:hi0018 (ec:3.2.2.-) (de:uracil-dna glycosylase, (udg)) (db:swissprot) UNG_HAEIN P43731 HAEMOPHILUS INFLUENZAE 727 -11537329 140264 uracil-dna glycosylase (cl:uracil-dna glycosylase) (ec:3.2.2.-) (db:pir2.dat) A64043 A64043 Haemophilus influenzae 727 -11537329 7500893811 hi0018 uracil dna glycosylase ung (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to gb:d13169 sp:p12295 gb:j03725 pid:148149) (le:6392) (re:7051) (di:direct) U32687 U32687 g1572962 Haemophilus influenzae Rd 71421 -11537329 5000694591 (de:(hi0018) (pn:uracil-dna glycosylase:uracil dna glycosylase:ung) (gn:ung) (gtcfc:10.8) (ec:3.2.2.-) (ung_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0018 HI0018 Haemophilus influenzae 727 10045487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882799	14745	36901	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882801	14746	36902	453	150

Description

5000694592 rec2:rec-2:hi0061 recombination protein:rec2:recombination protein 2 (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0061 HI0061 Haemophilus influenzae 727 -11537330 93711 rec2:rec-2:hi0061 (de:recombination protein 2) (db:swissprot) REC2_HAEIN P44408 HAEMOPHILUS INFLUENZAE 727 -11537330 167133 rec2 recombination protein rec2 (db:pir2.dat) I64045 I64045 Haemophilus influenzae 727 -11537330 7500889523 hi0061 recombination protein rec2 (db:genpept-bct1) (de:haemophilus influenzae rd section 6 of 163 of the complete genome.) (nt:similar to gb:l20805 pid:305386 percent identity:) (le:5620) (re:7986) (di:complement) U32691 U32691 g1573009 Haemophilus influenzae Rd 71421 -11537330 6500733472 rec2:rec-2 recombination protein:rec2:recombination protein 2 (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0061 HI0061 Haemophilus influenzae 727 -11537330

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882802	14747	36903	318	105

Description

5000694593 dksa:dsh-1:hi0062 dosage-dependent dnak suppressor protein:dksa:dnak suppressor protein homolog (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0062 HI0062 Haemophilus influenzae 727 -11537331 68724 dksa:dsh-1:hi0062 (de:dnak suppressor protein homolog) (db:swissprot) DKSA_HAEIN P43758 HAEMOPHILUS INFLUENZAE 727 -11537331 166114 dosage-dependent dnak suppressor protein (db:pir2.dat) A64046 A64046 Haemophilus influenzae 727 -11537331 7500880350 hi0062 dnak suppressor protein dksa (db:genpept-bct1) (de:haemophilus influenzae rd section 6 of 163 of the complete genome.) (nt:similar to gb:d26562 sp:p18274 gb:m34945 gb:m60726) (le:8245) (re:8682) (di:direct) U32691 U32691 g1573010 Haemophilus influenzae Rd 71421 -11537331 6500733473 dksa:dsh-1 dosage-dependent dnak suppressor protein:dksa:dnak suppressor protein homolog (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0062 HI0062 Haemophilus influenzae 727 -11537331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882829	14748	36904	867	288

Description

6500733474 mutl:hi0067 dna mismatch repair protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0067 HI0067 Haemophilus influenzae 727 -11537332 84741 mutl:hi0067 (de:dna mismatch repair protein mutl) (db:swissprot) MUTL_HAEIN P44494 HAEMOPHILUS INFLUENZAE 727 -11537332 166101 mutl mismatch repair protein mutl (db:pir2.dat) E64046 E64046 Haemophilus influenzae 727 -11537332 7500886160 hi0067 dna mismatch repair protein mutl (db:genpept-bct1) (de:haemophilus influenzae rd section 7 of 163 of the complete genome.) (nt:similar to sp:p23367 gb:z11831 pid:42067 pid:537011) (le:1851) (re:3740) (di:direct) U32692 U32692 g1573016 Haemophilus influenzae Rd 71421 -11537332 5000694594 (de:(hi0067) (pn:dna mismatch repair protein :dna mismatch repair protein:mutl) (gn:mutl) (gtcfc:10.8) (ec:) (mutl_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0067 HI0067 Haemophilus influenzae 727 10026932

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882832	14749	36905	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882841	14750	36906	195	64

Description

6500733475 recn:hi0070 dna repair protein:recombination protein n (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0070 HI0070 Haemophilus influenzae 727 -11537333 93817 recn:hi0070 (de:dna repair protein recn (recombination protein n)) (db:swissprot) RECN_HAEIN P44496 HAEMOPHILUS INFLUENZAE 727 -11537333 166110 recn protein homolog (cl:recn protein) (db:pir2.dat) H64046 H64046 Haemophilus influenzae 727 -11537333 7500889580 hi0070 dna repair protein recn (db:genpept-bct1) (de:haemophilus influenzae rd section 7 of 163 of the complete genome.) (nt:similar to sp:p05824 gb:y00357 pid:42693) (le:7719) (re:9395) (di:complement) U32692 U32692 g1573019 Haemophilus influenzae Rd 71421 -11537333 5000694595 (de:(hi0070) (pn:dna repair protein :recombination protein n:dna repair protein:recn) (gn:recn) (gtcfc:10.8) (ec:) (recn_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0070 HI0070 Haemophilus influenzae 727 10035808

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882843	14751	36907	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882852	14752	36908	1392	463

Description

6500733476 seqa:hi0192 negative modulator of initiation of replication:protein homolog (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0192 HI0192 Haemophilus influenzae 727 -11537334 98408 seqa:hi0192 (de:seqa protein homolog) (db:swissprot) SEQA_HAEIN P44564 HAEMOPHILUS INFLUENZAE 727 -11537334 167030 seqa seqa protein (db:pir2.dat) D64053 D64053 Haemophilus influenzae 727 -11537334 7500891524 hi0192 seqa protein seqa (db:genpept-bct1) (de:haemophilus influenzae rd section 19 of 163 of the complete genome.) (nt:similar to sp:p36658 gb:u07651 pid:464013 gb:u00096) (le:6050) (re:6643) (di:direct) U32704 U32704 g1573151 Haemophilus influenzae Rd 71421 -11537334 5000694596 (de:(hi0192) (pn:protein homolog:negative modulator of initiation of replication:seqa) (gn:seqa) (gtcfc:10.8) (ec:) (seqa_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0192 HI0192 Haemophilus influenzae 727 10040285

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882866	14753	36909	498	165

Description

6500733477 dam:hi0209 dna adenine methylase:deoxyadenosyl-methyltransferase (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0209 HI0209 Haemophilus influenzae 727 -11537335 68776 dam:hi0209 (ec:2.1.1.72) (de:dna adenine methylase, (deoxyadenosyl-methyltransferase)) (db:swissprot) DMA_HAEIN P44431 HAEMOPHILUS INFLUENZAE 727 -11537335 137796 site-specific dna-methyltransferase adenine-specific:dam (cl:site-specific methyltransferase (adenine-specific) ecorv) (ec:2.1.1.72) (db:pir2.dat) H64054 H64054 Haemophilus influenzae 727 -11537335 7500880375 hi0209 dna adenine methylase dam (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:similar to gb:j01600 sp:p00475 gb:v00272 gb:z19601) (le:10750) (re:11610) (di:direct) U32705 U32705 g1573168 Haemophilus influenzae Rd 71421 -11537335 5000694597 (de:(hi0209) (pn:deoxyadenosyl-methyltransferase:dna adenine methylase:dam) (gn:dam) (gtcfc:10.8) (ec:2.1.1.72) (dma_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0209 HI0209 Haemophilus influenzae 727 10011361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882870	14754	36910	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882900	14755	36911	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882907	14756	36912	498	165

Description

GTC ORF with score 498 to: (sr:humicola grisea var. thermoidea (sub_species:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea bgl4 gene for beta-glucosidase,complete cds.) (le:289:437) (re:332:1823) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882925	14757	36913	738	245

Description

6500733478 hsdm:hi0215 type i restriction enzyme ecor124/3 i m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0215 HI0215 Haemophilus influenzae 727 -11537336 167234 type i site-specific deoxyribonuclease ecor124/3 chain hsdm homolog hi0215 (db:pir2.dat) D64055 D64055 Haemophilus influenzae 727 -11537336 5000694598 (de:(hi0215) (pn:type i restriction enzyme ecor124) (gn:hsdm) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0215 HI0215 Haemophilus influenzae 727 10088317

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882927	14758	36914	1437	478

Description

6500733479 hsds:hi0216 type i restriction enzyme ecoki specificity protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0216 HI0216 Haemophilus influenzae 727 -11537337 167233 hypothetical protein hi0216 (db:pir2.dat) E64055 E64055 Haemophilus influenzae 727 -11537337 7500960665 hi0216 type i restriction/modification specificity (db:genpept-bct1) (de:haemophilus influenzae rd section 21 of 163 of the complete genome.) (nt:similar to gb:x73984 pid:393411 percent identity:) (le:8307) (re:9464) (di:direct) U32706 U32706 g1573175 Haemophilus influenzae Rd 71421 -11537337 5000694599 (de:(hi0216) (pn:type i restriction enzyme ecoki specificity protein:hsds) (gn:hsds) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0216 HI0216 Haemophilus influenzae 727 10088316

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882928	14759	36915	570	190

Description

6500733480 uvra:hi0249 excinuclease abc subunit a (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0249 HI0249 Haemophilus influenzae 727 -11537338 104033 uvra:hi0249 (de:excinuclease abc subunit a) (db:swissprot) UVRA_HAEIN P44410 HAEMOPHILUS INFLUENZAE 727 -11537338 153095 uvra excinuclease abc chain a:excision endonuclease abc::chain a:uvra protein (cl:excinuclease abc chain a:atp-binding cassette homology) (ec:3.1.-.-) (db:pir2.dat) D64057 D64057 Haemophilus influenzae 727 -11537338 7500893886 hi0249 excinuclease abc:subunit a uvra (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to sp:p07671 gb:m13495 pid:148165) (le:189) (re:3020) (di:complement) U32711 U32711 g1573215 Haemophilus influenzae Rd 71421 -11537338 5000694600 (de:(hi0249) (pn:excinuclease abc subunit a:uvra) (gn:uvra) (gtcfc:10.8) (ec:) (uvra_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0249 HI0249 Haemophilus influenzae 727 10045803

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882930	14760	36916	597	198

Description

GTC ORF with score 191 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882935	14761	36917	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882953	14762	36918	951	316

Description

6500733481 ssb:hi0250 single-stranded dna binding protein:ssb:single-strand binding protein:helix-destabilizing protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0250 HI0250 Haemophilus influenzae 727 -11537339 99529 ssb:hi0250 (de:single-strand binding protein (ssb) (helix-destabilizing protein)) (db:swissprot) SSB_HAEIN P44409 HAEMOPHILUS INFLUENZAE 727 -11537339 148196 single-stranded dna-binding protein:helix-destabilizing protein (cl:bacterial single-stranded dna-binding protein:single-stranded dna-binding protein homology) (db:pir2.dat) E64057 E64057 Haemophilus influenzae 727 -11537339 7500892119 hi0250 single-stranded dna binding protein ssb (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to gb:u04997 percent identity: 95.83;) (le:3174) (re:3680) (di:direct) U32711 U32711 g1573216 Haemophilus influenzae Rd 71421 -11537339 5000694601 (de:(hi0250) (pn:single-strand binding protein:helix-destabilizing protein:single-stranded dna binding protein:ssb) (gn:ssb) (gtcfc:10.8) (ec:) (ssb_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0250 HI0250 Haemophilus influenzae 727 10041387

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882954	14763	36919	213	70

Description

5000694602 xerd:xprb:hi0309 integrase/recombinase:xprb:integrase/recombinase xerd (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0309 HI0309 Haemophilus influenzae 727 -11537340 108097 xerd:xprb:hi0309 (de:integrase/recombinase xerd) (db:swissprot) XERD_HAEIN P44630 HAEMOPHILUS INFLUENZAE 727 -11537340 166922 probable integrase/recombinase (cl:probable site-specific integrase/recombinase xerc) (db:pir2.dat) A64061 A64061 Haemophilus influenzae 727 -11537340 7500894437 hi0309 integrase/recombinase xerd (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to gb:m54884 sp:p21891 pid:147548) (le:8525) (re:9418) (di:direct) U32716 U32716 g1573278 Haemophilus influenzae Rd 71421 -11537340 6500733482 xerd:xprb integrase/recombinase:xprb:integrase/recombinase xerd (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0309 HI0309 Haemophilus influenzae 727 -11537340

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882955	14764	36920	219	72

Description

6500733483 ruvb:hi0312 holliday junction dna helicase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0312 HI0312 Haemophilus influenzae 727 -11537341 97683 ruvb:hi0312 (de:holliday junction dna helicase ruvb) (db:swissprot) RUVB_HAEIN P44631 HAEMOPHILUS INFLUENZAE 727 -11537341 154417 ruvb dna-binding protein ruvb:holliday junction dna helicase (cl:ruvb protein) (db:pir2.dat) B64061 B64061 Haemophilus influenzae 727 -11537341 7500891235 hi0312 holliday junction dna helicase ruvb (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to gb:m21298 sp:p08577 gb:x07091 pid:147783) (le:9930) (re:10937) (di:complement) U32716 U32716 g1573279 Haemophilus influenzae Rd 71421 -11537341 5000694603 (de:(hi0312) (pn:holliday junction dna helicase :holliday junction dna helicase:ruvb) (gn:ruvb) (gtcfc:10.8) (ec:) (ruvb_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0312 HI0312 Haemophilus influenzae 727 10039570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882956	14765	36921	399	132

Description

6500733484 ruva:hi0313 holliday junction dna helicase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0313 HI0313 Haemophilus influenzae 727 -11537342 97680 ruva:hi0313 (de:holliday junction dna helicase ruva) (db:swissprot) RUVA_HAEIN P44632 HAEMOPHILUS INFLUENZAE 727 -11537342 154425 ruva ruva protein:holliday junction dna helicase (cl:holliday junction dna helicase ruva) (db:pir2.dat) C64061 C64061 Haemophilus influenzae 727 -11537342 7500891221 hi0313 holliday junction dna helicase ruva (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to gb:m21298 sp:p08576 gb:x07091 pid:147782) (le:10945) (re:11559) (di:complement) U32716 U32716 g1573280 Haemophilus influenzae Rd 71421 -11537342 5000694604 (de:(hi0313) (pn:holliday junction dna helicase :holliday junction dna helicase:ruva) (gn:ruva) (gtcfc:10.8) (ec:) (ruva_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0313 HI0313 Haemophilus influenzae 727 10039567

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882977	14766	36922	2007	668

Description

6500733485 ruvc:hi0314 crossover junction endodeoxyribonuclease:holliday junction nuclease ruvc:holliday juction resolvase ruvc (gtcfc:10.8) (ec:3.1.22.4) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0314 HI0314 Haemophilus influenzae 727 -11537343 97686 ruvc:hi0314 (ec:3.1.22.4) (de:junction nuclease ruvc) (holliday juction resolvase ruvc)) (db:swissprot) RUVC_HAEIN P44633 HAEMOPHILUS INFLUENZAE 727 -11537343 166065 ruvc dna repair protein ruvc (cl:dna repair protein ruvc) (db:pir2.dat) D64061 D64061 Haemophilus influenzae 727 -11537343 7500891242 hi0314 crossover junction endodeoxyribonuclease ruvc (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:d10165 sp:p24239 pid:216653 pid:42175) (le:62) (re:634) (di:complement) U32717 U32717 g1573284 Haemophilus influenzae Rd 71421 -11537343 5000694605 (de:(hi0314) (pn:crossover junction endodeoxyribonuclease :holliday junction nuclease ruvc:holliday juction resolvase ruvc:crossover junction endodeoxyribonuclease:ruvc) (gn:ruvc) (gtcfc:10.8) (ec:3.1.22.4) (ruvc_haein) (keggfc:1) HI0314 HI0314 Haemophilus influenzae 727 10039573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882983	14767	36923	636	211

Description

6500733486 reco:hi0332 dna repair protein:recombination protein o (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0332 HI0332 Haemophilus influenzae 727 -11537344 93822 reco:hi0332 (de:dna repair protein reco (recombination protein o)) (db:swissprot) RECO_HAEIN P44642 HAEMOPHILUS INFLUENZAE 727 -11537344 154677 reco reco protein:dna repair protein (cl:reco protein) (db:pir2.dat) C64062 C64062 Haemophilus influenzae 727 -11537344 7500889582 hi0332 dna repair protein reco (db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the complete genome.) (nt:similar to gb:m26416 sp:p15027 gb:m27251 gb:m76470) (le:1842) (re:2552) (di:direct) U32718 U32718 g1573301 Haemophilus influenzae Rd 71421 -11537344 5000694606 (de:(hi0332) (pn:dna repair protein :recombination protein o:dna repair protein:reco) (gn:reco) (gtcfc:10.8) (ec:) (reco_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0332 HI0332 Haemophilus influenzae 727 10035813

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501882992	14768	36924	1296	431

Description

6500733487 pria:hi0339 primosomal protein replication factor:primosomal protein n:replication factor y (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0339 HI0339 Haemophilus influenzae 727 -11537345 91021 pria:hi0339 (de:primosomal protein n' (replication factor y)) (db:swissprot) PRIA_HAEIN P44647 HAEMOPHILUS INFLUENZAE 727 -11537345 167102 primosomal replication factor y (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) G64062 G64062 Haemophilus influenzae 727 -11537345 7500888451 hi0339 primosomal protein n pria (db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p17888 gb:d00616 gb:m33293) (le:8651) (re:10843) (di:complement) U32718 U32718 g1573308 Haemophilus influenzae Rd 71421 -11537345 5000694607 (de:(hi0339) (pn:primosomal protein n":replication factor y:primosomal protein replication factor:pria) (gn:pria) (gtcfc:10.8) (ec:) (pria_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0339 HI0339 Haemophilus influenzae 727 10033130

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883022	14769	36925	300	99

Description

6500733488 ding:hi0387 probable atp-dependent helicase:probable atp-dependent helicase homolog (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0387 HI0387 Haemophilus influenzae 727 -11537346 68665 hi0387 (de:probable atp-dependent helicase hi0387) (db:swissprot) YOAA_HAEIN P44680 HAEMOPHILUS INFLUENZAE 727 -11537346 167103 hypothetical protein hi0387 (db:pir2.dat) A64065 A64065 Haemophilus influenzae 727 -11537346 7500952076 hi0387 atp-dependent helicase ding (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1736441 pid:1736447) (le:6606) (re:8528) (di:direct) U32722 U32722 g1573357 Haemophilus influenzae Rd 71421 -11537346 5000694608 (de:(hi0387) (pn:probable atp-dependent helicase homolog:probable atp-dependent helicase:ding) (gn:ding) (gtcfc:10.8) (ec:) (ding_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0387 HI0387 Haemophilus influenzae 727 10011253

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883023	14770	36926	873	290

Description

GTC ORF with score 167 to: (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae transcription/repair factor tfiih subunittfb3 (tfb3) gene, complete cds.) (nt:contains ring finger motif; similar to mammalian) (le:1) (re:816) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883039	14771	36927	1449	482

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883054	14772	36928	276	91

Description

5000694609 ogt:dat1:hi0402 dat1:methylated-dna--protein-cysteine methyltransferase:6-o-methylguanine-dna methyltransferase:o-6-methylguanine-dna-alkyltransferase (gtcfc:10.8) (ec:2.1.1.63) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0402 HI0402 Haemophilus influenzae 727 -11537347 87535 ogt:dat1:hi0402 (ec:2.1.1.63) (de:alkyltransferase)) (db:swissprot) OGT_HAEIN P44687 HAEMOPHILUS INFLUENZAE 727 -11537347 166991 methylated-dna--protein-cysteine s-methyltransferase homolog (cl:methylated-dna--protein-cysteine s-methyltransferase:methylated-dna--protein-cysteine s-methyltransferase homology) (db:pir2.dat) G64065 G64065 Haemophilus influenzae 727 -11537347 7500887119 hi0402 methylated-dna--protein-cysteine (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to sp:p11742 gb:x15659 pid:39876) (le:9611) (re:10183) (di:direct) U32723 U32723 g1573373 Haemophilus influenzae Rd 71421 -11537347 6500733489 ogt:dat1 dat1:methylated-dna--protein-cysteine methyltransferase:6-o-methylguanine-dna methyltransferase:o-6-methylguanine-dna-alkyltransferase (gtcfc:10.8) (ec:2.1.1.63) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0402 HI0402 Haemophilus influenzae 727 -11537347

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883055	14773	36929	708	235

Description

6500733490 muth:hi0403 dna mismatch protein:dna mismatch repair protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0403 HI0403 Haemophilus influenzae 727 -11537348 84737 muth:hi0403 (de:dna mismatch repair protein muth) (db:swissprot) MUTH_HAEIN P44688 HAEMOPHILUS INFLUENZAE 727 -11537348 154678 muth mutator muth:dna mismatch protein (cl:mutator muth) (db:pir2.dat) H64065 H64065 Haemophilus influenzae 727 -11537348 7500886156 hi0403 dna mismatch repair protein muth (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to gb:y00113 sp:p06722 gb:u16361 pid:42065) (le:10180) (re:10851) (di:direct) U32723 U32723 g1573374 Haemophilus influenzae Rd 71421 -11537348 5000694610 (de:(hi0403) (pn:dna mismatch repair protein :dna mismatch protein:muth) (gn:muth) (gtcfc:10.8) (ec:) (muth_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0403 HI0403 Haemophilus influenzae 727 10026928

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883056	14774	36930	468	156

Description

6500733491 recr:hi0443 recombinational dna repair protein:recombination protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0443 HI0443 Haemophilus influenzae 727 -11537349 93832 recr:hi0443 (de:recombination protein recr) (db:swissprot) RECR_HAEIN P44712 HAEMOPHILUS INFLUENZAE 727 -11537349 154672 recr recombination protein recr (cl:recr protein) (db:pir2.dat) F64068 F64068 Haemophilus influenzae 727 -11537349 7500889591 hi0443 recombination protein recr (db:genpept-bct1) (de:haemophilus influenzae rd section 42 of 163 of the complete genome.) (nt:similar to gb:m38777 sp:p12727 gb:x15761 pid:145299) (le:4151) (re:4753) (di:direct) U32727 U32727 g1573419 Haemophilus influenzae Rd 71421 -11537349 5000694611 (de:(hi0443) (pn:recombination protein :recombinational dna repair protein:recr) (gn:recr) (gtcfc:10.8) (ec:) (recr_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0443 HI0443 Haemophilus influenzae 727 10035823

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883061	14775	36931	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883066	14776	36932	402	133

Description

6500733492 topb:hi0444 topoisomerase iii:dna topoisomerase iii (gtcfc:10.8) (ec:5.99.1.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0444 HI0444 Haemophilus influenzae 727 -11537350 101815 topb:hi0444 (ec:5.99.1.2) (de:dna topoisomerase iii,) (db:swissprot) TOP3_HAEIN P43704 HAEMOPHILUS INFLUENZAE 727 -11537350 167193 dna topoisomerase:iii (ec:5.99.1.2) (db:pir2.dat) G64068 G64068 Haemophilus influenzae 727 -11537350 7500893267 hi0444 dna topoisomerase iii topb (db:genpept-bct1) (de:haemophilus influenzae rd section 42 of 163 of the complete genome.) (nt:similar to gb:j05076 sp:p14294 pid:148026 gb:u00096) (le:4769) (re:6724) (di:direct) U32727 U32727 g1573420 Haemophilus influenzae Rd 71421 -11537350 5000694612 (de:(hi0444) (pn:dna topoisomerase iii:topoisomerase iii:topb) (gn:topb) (gtcfc:10.8) (ec:5.99.1.2) (top3_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0444 HI0444 Haemophilus influenzae 727 10043644

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883072	14777	36933	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883075	14778	36934	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883090	14779	36935	516	171

Description

6500733493 gidb:hi0486 glucose-inhibited division protein:glucose inhibited division protein b (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0486 HI0486 Haemophilus influenzae 727 -11537351 73613 gidb:hi0486 (de:glucose inhibited division protein b) (db:swissprot) GIDB_HAEIN P44728 HAEMOPHILUS INFLUENZAE 727 -11537351 154428 gidb gidb protein:glucose-inhibited division protein (cl:gidb protein) (db:pir2.dat) B64072 B64072 Haemophilus influenzae 727 -11537351 7500882349 hi0486 glucose-inhibited division protein gidb (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p17113 gb:x01631 pid:290589) (le:114) (re:725) (di:complement) U32731 U32731 g1573466 Haemophilus influenzae Rd 71421 -11537351 5000694613 (de:(hi0486) (pn:glucose inhibited division protein b:glucose-inhibited division protein:gidb) (gn:gidb) (gtcfc:10.8) (ec:) (gidb_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0486 HI0486 Haemophilus influenzae 727 10016147

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883093	14780	36936	624	207

Description

GTC ORF with score 153 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus glycoprotein m, dnareplication protein, glycoprotein, dna replication protein, fliceinhibitory ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883095	14781	36937	936	311

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883099	14782	36938	723	240

Description

GTC ORF with score 200 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus glycoprotein m, dnareplication protein, glycoprotein, dna replication protein, fliceinhibitory ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883110	14783	36939	417	138

Description

6500733494 hindiir:hi0512 hincii endonuclease:hincii:probable type ii restriction enzyme hindii:endonuclease hindii:r (gtcfc:10.8) (ec:3.1.21.4) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0512 HI0512 Haemophilus influenzae 727 -11537352 166198 type ii site-specific deoxyribonuclease:hincii (ec:3.1.21.4) (db:pir2.dat) E64073 E64073 Haemophilus influenzae 727 -11537352 7500960745 hi0512 type ii restriction endonuclease hindiir (db:genpept-bct1) (de:haemophilus influenzae rd section 48 of 163 of the complete genome.) (nt:similar to gb:x52124 sp:p17743 pid:1573497 percent) (le:139) (re:915) (di:complement) U32733 U32733 g1573497 Haemophilus influenzae Rd 71421 -11537352 5000694614 (de:(hi0512) (pn:probable type ii restriction enzyme hindii:endonuclease hindii:r:hincii endonuclease:hincii) (gn:hindiir) (gtcfc:10.8) (ec:3.1.21.4) (t2hd_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0512 HI0512 Haemophilus influenzae 727 10088103

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883111	14784	36940	231	76

Description

6500733495 hindiim:hi0513 modification methylase hincii:hinciim:probable modification methylase hindii:adenine-specific methyltransferase hindii:m (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0513 HI0513 Haemophilus influenzae 727 -11537353 84542 hindiim:hi0513 (ec:2.1.1.72) (de:methyltransferase hindii) (m.hindii)) (db:swissprot) MTHD_HAEIN P44414 HAEMOPHILUS INFLUENZAE 727 -11537353 166996 site-specific dna-methyltransferase adenine-specific:hincii (cl:site-specific dna-methyltransferase (adenine-specific) hincii) (ec:2.1.1.72) (db:pir2.dat) F64073 F64073 Haemophilus influenzae 727 -11537353 7500886031 hi0513 modification methylase hindiim (db:genpept-bct1) (de:haemophilus influenzae rd section 48 of 163 of the complete genome.) (nt:similar to sp:p17744 percent ident: 98.41;) (le:912) (re:2468) (di:complement) U32733 U32733 g1573494 Haemophilus influenzae Rd 71421 -11537353 5000694615 (de:(hi0513) (pn:probable modification methylase hindii:adenine-specific methyltransferase hindii:m:modification methylase hincii:hinciim) (gn:hindiim) (gtcfc:10.8) (ec:2.1.1.72) (mthd_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-) HI0513 HI0513 Haemophilus influenzae 727 10026738

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883112	14785	36941	285	94

Description

6500733496 gyrb:hi0567 dna gyrase:subunit b:dna gyrase subunit b (gtcfc:10.8) (ec:5.99.1.3) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0567 HI0567 Haemophilus influenzae 727 -11537354 75220 gyrb:hi0567 (ec:5.99.1.3) (de:dna gyrase subunit b,) (db:swissprot) GYRB_HAEIN P43701 HAEMOPHILUS INFLUENZAE 727 -11537354 142222 dna topoisomerase atp-hydrolyzing:chain b (cl:dna topoisomerase (atp-hydrolyzing) chain b) (ec:5.99.1.3) (db:pir2.dat) A64078 A64078 Haemophilus influenzae 727 -11537354 7500882882 hi0567 dna gyrase:subunit b gyrb (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to gb:110328 sp:p06982 pid:290547 pid:41646) (le:3812) (re:6232) (di:complement) U32738 U32738 g1573554 Haemophilus influenzae Rd 71421 -11537354 5000694616 (de:(hi0567) (pn:dna gyrase subunit b:dna gyrase, subunit b:gyrb) (gn:gyrb) (gtcfc:10.8) (ec:5.99.1.3) (gyrb_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0567 HI0567 Haemophilus influenzae 727 10017731

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883122	14786	36942	654	217

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883123	14787	36943	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883126	14788	36944	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883130	14789	36945	1575	524

Description

6500733497 gida:hi0582 glucose inhibited division protein:glucose inhibited division protein a (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0582 HI0582 Haemophilus influenzae 727 -11537355 73607 gida:hi0582 (de:glucose inhibited division protein a) (db:swissprot) GIDA_HAEIN P44763 HAEMOPHILUS INFLUENZAE 727 -11537355 154427 gida gida protein:glucose-inhibited division protein (cl:gida protein) (db:pir2.dat) I64078 I64078 Haemophilus influenzae 727 -11537355 7500882338 hi0582 glucose inhibited division protein gida (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p17112 gb:k00826 gb:x01631) (le:8484) (re:10373) (di:complement) U32739 U32739 g1573570 Haemophilus influenzae Rd 71421 -11537355 5000694617 (de:(hi0582) (pn:glucose inhibited division protein a:glucose inhibited division protein:gida) (gn:gida) (gtcfc:10.8) (ec:) (gida_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0582 HI0582 Haemophilus influenzae 727 10016141

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883135	14790	36946	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883144	14791	36947	234	77

Description

6500733498 recx:hi0599 regulatory protein:putative regulatory protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0599 HI0599 Haemophilus influenzae 727 -11537356 93836 recx:hi0599 (de:putative regulatory protein recx) (db:swissprot) RECX_HAEIN P43706 HAEMOPHILUS INFLUENZAE 727 -11537356 167134 regulatory protein recx homolog (db:pir2.dat) I64079 I64079 Haemophilus influenzae 727 -11537356 7500889602 hi0599 regulatory protein recx (db:genpept-bct1) (de:haemophilus influenzae rd section 56 of 163 of the complete genome.) (nt:similar to sp:p37861 gb:u05680 pid:468036 percent) (le:6073) (re:6453) (di:complement) U32741 U32741 g1573587 Haemophilus influenzae Rd 71421 -11537356 5000694618 (de:(hi0599) (pn:putative regulatory protein :regulatory protein:recx) (gn:recx) (gtcfc:10.8) (ec:) (recx_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0599 HI0599 Haemophilus influenzae 727 10035827

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883147	14792	36948	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883151	14793	36949	1575	525

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883166	14794	36950	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883176	14795	36951	1128	375

Description

5000694619 reca:rec1:rec-1:hi0600 reca:reca protein:recombinase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0600 HI0600 Haemophilus influenzae 727 -11537357 93743 reca:rec1:rec-1:hi0600 (de:reca protein (recombinase)) (db:swissprot) RECA_HAEIN P43705 HAEMOPHILUS INFLUENZAE 727 -11537357 154657 reca reca protein:rec-1 protein (cl:reca protein) (db:pir2.dat) A49929 A49929 Haemophilus influenzae 727 -11537357 7500889540 rec1 recombinase (fn:dna transformation, damage repair,) (sr:haemophilus influenzae (strain rd) dna) (db:genpept-bct2) (de:haemophilus influenzae recombinase (rec1) gene, complete cds.) (le:278) (re:1342) (di:direct) HEAREC L07529 g305382 Haemophilus influenzae 727 -11537357 241322 hi0600 reca protein reca (db:genpept-bct1) (de:haemophilus influenzae rd section 56 of 163 of the complete genome.) (nt:similar to gb:l07529 pid:1573588 percent identity:) (le:6611) (re:7675) (di:complement) U32741 U32741 g1573588 Haemophilus influenzae Rd 71421 -11537357 6500733499 reca:rec1:rec-1 reca:reca protein:recombinase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0600 HI0600 Haemophilus influenzae 727 -11537357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883179	14796	36952	1149	382

Description

5000694620 tag:hi0654 dna-3-methyladenine glycosidase i:tagi:dna-3-methyladenine glycosidase:3-methyladenine-dna glycosylase (gtcfc:10.8) (ec:3.2.2.20) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0654 HI0654 Haemophilus influenzae 727 -11537358 57521 tag:hi0654 (ec:3.2.2.20) (de:glycosylase) (tag)) (db:swissprot) 3MGA_HAEIN P44321 HAEMOPHILUS INFLUENZAE 727 -11537358 140258 3-methyladenine dna glycosylase:i (cl:3-methyladenine dna glycosylase i) (ec:3.2.2.-) (db:pir2.dat) G64084 G64084 Haemophilus influenzae 727 -11537358 7500876107 hi0654 dna-3-methyladenine glycosidase i tagi (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to sp:p05100 gb:j02606 gb:x03845 pid:147920) (le:6773) (re:7330) (di:complement) U32748 U32748 g1573653 Haemophilus influenzae Rd 71421 -11537358 6500733500 tag dna-3-methyladenine glycosidase i:tagi:dna-3-methyladenine glycosidase:3-methyladenine-dna glycosylase (gtcfc:10.8) (ec:3.2.2.20) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0654 HI0654 Haemophilus influenzae 727 -11537358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883181	14797	36953	828	275

Description

6500733501 mioc:hi0669 mioc protein:protein homolog (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0669 HI0669 Haemophilus influenzae 727 -11537359 83737 mioc:hi0669 (de:mioc protein homolog) (db:swissprot) MIOC_HAEIN P44813 HAEMOPHILUS INFLUENZAE 727 -11537359 166994 hypothetical protein hi0669 (cl:mioc protein:flavodoxin homology) (db:pir2.dat) C64085 C64085 Haemophilus influenzae 727 -11537359 7500885650 hi0669 mioc protein mioc (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p03817 gb:k00826 gb:x01631) (le:426) (re:866) (di:direct) U32750 U32750 g1573670 Haemophilus influenzae Rd 71421 -11537359 5000694621 (de:(hi0669) (pn:protein homolog:mioc protein:mioc) (gn:mioc) (gtcfc:10.8) (ec:) (mioc_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0669 HI0669 Haemophilus influenzae 727 10025951

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883197	14798	36954	411	136

Description

6500733502 xerc:hi0676 integrase-recombinase protein:integrase/recombinase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0676 HI0676 Haemophilus influenzae 727 -11537360 108095 xerc:hi0676 (de:integrase/recombinase xerc) (db:swissprot) XERC_HAEIN P44818 HAEMOPHILUS INFLUENZAE 727 -11537360 166921 probable site-specific recombinase xerc (cl:probable site-specific integrase/recombinase xerc) (db:pir2.dat) F64085 F64085 Haemophilus influenzae 727 -11537360 7500894435 hi0676 integrase/recombinase xerc (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p22885 pid:148210) (le:5235) (re:6122) (di:complement) U32750 U32750 g1573676 Haemophilus influenzae Rd 71421 -11537360 5000694622 (de:(hi0676) (pn:integrase:integrase-recombinase protein:xerc) (gn:xerc) (gtcfc:10.8) (ec:) (xerc_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0676 HI0676 Haemophilus influenzae 727 10049827

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883209	14799	36955	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883212	14800	36956	594	197

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883215	14801	36957	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883221	14802	36958	600	199

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883234	14803	36959	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883250	14804	36960	186	61

Description

6500733503 muts:hi0707 dna mismatch repair protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0707 HI0707 Haemophilus influenzae 727 -11537361 84747 muts:hi0707 (de:dna mismatch repair protein muts) (db:swissprot) MUTS_HAEIN P44834 HAEMOPHILUS INFLUENZAE 727 -11537361 166102 muts dna mismatch repair protein muts (cl:dna mismatch repair protein muts) (db:pir2.dat) G64087 G64087 Haemophilus influenzae 727 -11537361 7500886164 hi0707 dna mismatch repair protein muts (db:genpept-bct1) (de:haemophilus influenzae rd section 68 of 163 of the complete genome.) (nt:similar to gb:m64730 sp:p23909 pid:146906) (le:5261) (re:7846) (di:direct) U32753 U32753 g1573708 Haemophilus influenzae Rd 71421 -11537361 5000694623 (de:(hi0707) (pn:dna mismatch repair protein :dna mismatch repair protein:muts) (gn:muts) (gtcfc:10.8) (ec:) (muts_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0707 HI0707 Haemophilus influenzae 727 10026938

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883251	14805	36961	1491	496

Description

6500733504 muty:hi0759 a/g-specific adenine glycosylase (gtcfc:10.8) (ec:3.2.2.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0759 HI0759 Haemophilus influenzae 727 -11537362 84758 muty:hi0759 (ec:3.2.2.-) (de:a/g-specific adenine glycosylase,) (db:swissprot) MUTY_HAEIN P44320 HAEMOPHILUS INFLUENZAE 727 -11537362 165977 adenine glycosylase (db:pir2.dat) C64091 C64091 Haemophilus influenzae 727 -11537362 7500886173 hi0759 a/g-specific adenine glycosylase muty (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to gb:m59471 sp:p17802 gb:x52391 pid:146864) (le:2662) (re:3798) (di:direct) U32760 U32760 g1573768 Haemophilus influenzae Rd 71421 -11537362 5000694624 (de:(hi0759) (pn:a) (gn:muty) (gtcfc:10.8) (ec:3.2.2.-) (muty_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0759 HI0759 Haemophilus influenzae 727 10026949

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883263	14806	36962	297	98

Description

5000694625 mutm:fpg:hi0946 formamidopyrimidine-dna glycosylase:fapy-dna glycosylase (gtcfc:10.8) (ec:3.2.2.23) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0946 HI0946 Haemophilus influenzae 727 -11537363 72261 mutm:fpg:hi0946 (ec:3.2.2.23) (de:glycosylase)) (db:swissprot) FPG_HAEIN P44948 HAEMOPHILUS INFLUENZAE 727 -11537363 140260 formamidopyrimidine-dna glycosidase (cl:formamidopyrimidine dna glycosylase) (ec:3.2.2.23) (db:pir2.dat) A64104 A64104 Haemophilus influenzae 727 -11537363 7500881728 hi0946 formamidopyrimidine-dna glycosylase fpg (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to sp:p05523 gb:m60670 gb:m86305 gb:x06036) (le:67) (re:882) (di:complement) U32776 U32776 g1573970 Haemophilus influenzae Rd 71421 -11537363 6500733505 mutm:fpg formamidopyrimidine-dna glycosylase:fapy-dna glycosylase (gtcfc:10.8) (ec:3.2.2.23) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0946 HI0946 Haemophilus influenzae 727 -11537363

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883277	14807	36963	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883282	14808	36964	264	87

Description

6500733506 fis:hi0980 factor-for-inversion stimulation protein:hin recombinational enhancer binding protein:fis protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0980 HI0980 Haemophilus influenzae 727 -11537364 71717 fis:hi0980 (de:binding protein) (fis protein)) (db:swissprot) FIS_HAEIN P44966 HAEMOPHILUS INFLUENZAE 727 -11537364 148295 fis dna-binding protein fis:recombinational enhancer-binding protein fis (cl:dna-binding protein fis) (db:pir2.dat) A64106 A64106 Haemophilus influenzae 727 -11537364 7500881476 hi0980 hin recombinational enhancer binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:similar to sp:p11028 gb:u03101 pid:424092 percent) (le:10064) (re:10363) (di:direct) U32778 U32778 g1574008 Haemophilus influenzae Rd 71421 -11537364 5000694626 (de:(hi0980) (pn:factor-for-inversion stimulation protein:hin recombinational enhancer binding protein:fis protein:hin recombinational enhancer binding protein:fis) (gn:fis) (gtcfc:10.8) (ec:) (fis_haein) (keggfc:11.2) (tigrfc:1) HI0980 HI0980 Haemophilus influenzae 727 10014274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883283	14809	36965	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883297	14810	36966	1038	345

Description

6500733507 recf:hi0991 dna/atp binding protein:protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0991 HI0991 Haemophilus influenzae 727 -11537365 93799 recf:hi0991 (de:recf protein) (db:swissprot) RECF_HAEIN P43767 HAEMOPHILUS INFLUENZAE 727 -11537365 7500889570 hi0991 dna/atp binding protein recf (db:genpept-bct1) (de:haemophilus influenzae rd section 95 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p03016 gb:k02179 pid:147539) (le:151) (re:1230) (di:complement) U32780 U32780 g1574021 Haemophilus influenzae Rd 71421 -11537365 5000694627 (de:(hi0991) (pn:protein:dna) (gn:recf) (gtcfc:10.8) (ec:) (recf_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0991 HI0991 Haemophilus influenzae 727 10035790

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883308	14811	36967	618	205

Description

6500733508 dnaa:hi0993 chromosomal replication initiator protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0993 HI0993 Haemophilus influenzae 727 -11537366 68828 dnaa:hi0993 (de:chromosomal replication initiator protein dnaa) (db:swissprot) DNAA_HAEIN P43742 HAEMOPHILUS INFLUENZAE 727 -11537366 154418 dnaa replication initiation protein dnaa:chromosomal replication initiator protein (cl:replication initiation protein dnaa) (db:pir2.dat) B64107 B64107 Haemophilus influenzae 727 -11537366 7500880394 hi0993 chromosomal replication initiator protein (db:genpept-bct1) (de:haemophilus influenzae rd section 95 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p03004 gb:j01602 pid:145760) (le:2345) (re:3709) (di:complement) U32780 U32780 g1574023 Haemophilus influenzae Rd 71421 -11537366 5000694628 (de:(hi0993) (pn:chromosomal replication initiator protein :chromosomal replication initiator protein:dnaa) (gn:dnaa) (gtcfc:10.8) (ec:) (dnaa_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0993 HI0993 Haemophilus influenzae 727 10011413

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883318	14812	36968	315	104

Description

6500733509 restriction enzyme:hgidir:probable type ii restriction enzyme hi1040 (gtcfc:10.8) (ec:3.1.21.4) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1040 HI1040 Haemophilus influenzae 727 -11537367 100306 hi1040 (ec:3.1.21.4) (de:probable type ii restriction enzyme hi1040,) (db:swissprot) T2DX_HAEIN P44999 HAEMOPHILUS INFLUENZAE 727 -11537367 167136 type ii site-specific deoxyribonuclease hgidi homolog (db:pir2.dat) B64109 B64109 Haemophilus influenzae 727 -11537367 7500892705 hi1040 type ii restriction enzyme:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to sp:p25261 sp:p24599 pid:43474 percent) (le:7313) (re:8317) (di:direct) U32784 U32784 g1574072 Haemophilus influenzae Rd 71421 -11537367 5000694629 (de:(hi1040) (pn:probable type ii restriction enzyme hi1040:restriction enzyme:hgidir) (gtcfc:10.8) (ec:3.1.21.4) (t2dx_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1040 HI1040 Haemophilus influenzae 727 10042160

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883322	14813	36969	1173	390

Description

6500733510 modification methylase hgidi:mhgidi:probable modification methylase hi1041:cytosine-specific methyltransferase (gtcfc:10.8) (ec:2.1.1.73) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1041 HI1041 Haemophilus influenzae 727 -11537368 84513 hi1041 (ec:2.1.1.73) (de:specific methyltransferase)) (db:swissprot) MTDX_HAEIN P45000 HAEMOPHILUS INFLUENZAE 727 -11537368 166995 site-specific dna-methyltransferase cytosine-specific (ec:2.1.1.73) (db:pir2.dat) C64109 C64109 Haemophilus influenzae 727 -11537368 7500886022 hi1041 modification methylase (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to sp:p24600 sp:p25267 pid:43482 percent) (le:8314) (re:9228) (di:direct) U32784 U32784 g1574073 Haemophilus influenzae Rd 71421 -11537368 5000694630 (de:(hi1041) (pn:probable modification methylase hi1041:cytosine-specific methyltransferase:modification methylase hgidi:mhgidi) (gtcfc:10.8) (ec:2.1.1.73) (mtdx_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1041 HI1041 Haemophilus influenzae 727 10026709

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883325	14814	36970	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883340	14815	36971	429	142

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883344	14816	36972	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883346	14817	36973	207	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883347	14818	36974	375	124

Description

6500733511 mod:hi1056 type iii restriction-modification ecop15 enzyme:type iii restriction-ification ecop15 enzyme (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1056 HI1056 Haemophilus influenzae 727 -11537369 167239 hypothetical protein hi1056 (db:pir2.dat) C64180 C64180 Haemophilus influenzae 727 -11537369 7500960679 hi1056 h. influenzae predicted coding region hi1056 (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4295) (re:6184) (di:complement) U32786 U32786 g1574609 Haemophilus influenzae Rd 71421 -11537369 5000694631 (de:(hi1056) (pn:type iii restriction-ification ecop15 enzyme:type iii restriction-modification ecop15 enzyme:mod) (gn:mod) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1056 HI1056 Haemophilus influenzae 727 10088321

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883348	14819	36975	477	158

Description

6500733512 rnhb:hi1059 ec 31264:ribonuclease hii:rnase hii (gtcfc:10.8) (ec:3.1.26.4) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1059 HI1059 Haemophilus influenzae 727 -11537370 95719 rnhb:hi1059 (ec:3.1.26.4) (de:ribonuclease hii, (rnase hii)) (db:swissprot) RNH2_HAEIN P43808 HAEMOPHILUS INFLUENZAE 727 -11537370 139847 ribonuclease h:ii (cl:ribonuclease hii) (ec:3.1.26.4) (db:pir2.dat) D64180 D64180 Haemophilus influenzae 727 -11537370 7500890448 hi1059 ribonuclease hii rnhb (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to sp:p10442 pid:1208954 gb:u00096) (le:6758) (re:7351) (di:complement) U32786 U32786 g1574610 Haemophilus influenzae Rd 71421 -11537370 5000694632 (de:(hi1059) (pn:ribonuclease hii:rnase hii:ribonuclease hii:ec 31264:rnase hii) (gn:rnhb) (gtcfc:10.8) (ec:3.1.26.4) (rnh2_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1059 HI1059 Haemophilus influenzae 727 10037669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883354	14820	36976	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883360	14821	36977	1308	435

Description

6500733513 lig:hi1100 dna ligase:dna ase:polydeoxyribonucleotide synthase:nad+ (gtcfc:10.8) (ec:6.5.1.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1100 HI1100 Haemophilus influenzae 727 -11537371 69002 lign:lig:hi1100 (ec:6.5.1.2) (de:dna ligase, (polydeoxyribonucleotide synthase (nad+))) (db:swissprot) DNLJ_HAEIN P43813 HAEMOPHILUS INFLUENZAE 727 -11537371 142460 dna ligase nad+ (cl:polydeoxyribonucleotide synthase (nad+)) (ec:6.5.1.2) (db:pir2.dat) D64182 D64182 Haemophilus influenzae 727 -11537371 7500880523 hi1100 dna ligase lig (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to gb:m24278 sp:p15042 gb:m30255 pid:146613) (le:8950) (re:10989) (di:complement) U32789 U32789 g1574651 Haemophilus influenzae Rd 71421 -11537371 5000694633 (de:(hi1100) (pn:dna ase:polydeoxyribonucleotide synthase:nad:dna ligase:lig) (gn:lig) (gtcfc:10.8) (ec:6.5.1.2) (dnlj_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1100 HI1100 Haemophilus influenzae 727 10011586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883383	14822	36978	381	126

Description

6500733514 himd:hi1221 integration host factor beta-subunit:ihf-beta (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1221 HI1221 Haemophilus influenzae 727 -11537372 79052 himd:hi1221 (de:integration host factor beta-subunit (ihf-beta)) (db:swissprot) IHFB_HAEIN P43724 HAEMOPHILUS INFLUENZAE 727 -11537372 148269 himd integration host factor beta chain (cl:bacterial dna-binding protein) (db:pir2.dat) A64111 A64111 Haemophilus influenzae 727 -11537372 7500883986 hi1221 integration host factor:beta-subunit himd (db:genpept-bct1) (de:haemophilus influenzae rd section 117 of 163 of the completegenome.) (nt:similar to sp:p08756 gb:x04864 pid:414749 gb:u00096) (le:92) (re:376) (di:direct) U32802 U32802 g1574152 Haemophilus influenzae Rd 71421 -11537372 5000694634 (de:(hi1221) (pn:integration host factor beta-subunit:ihf-beta:himd) (gn:himd) (gtcfc:10.8) (ec:) (ihfb_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1221 HI1221 Haemophilus influenzae 727 10021384

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883384	14823	36979	462	153

Description

6500733515 uvrb:hi1247 excinuclease abc subunit b (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1247 HI1247 Haemophilus influenzae 727 -11537373 104044 uvrb:hi1247 (de:excinuclease abc subunit b) (db:swissprot) UVRB_HAEIN P45125 HAEMOPHILUS INFLUENZAE 727 -11537373 154708 excinuclease abc chain b:excision endonuclease abc::chain b:uvrb protein (cl:excinuclease abc chain b:dead/h box helicase homology) (ec:3.1.-.-) (db:pir2.dat) G64112 G64112 Haemophilus influenzae 727 -11537373 7500893897 hi1247 excinuclease abc:subunit b uvrb (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the completegenome.) (nt:similar to sp:p07025 gb:x03678 gb:x03722 pid:43284) (le:10195) (re:12234) (di:complement) U32804 U32804 g1574178 Haemophilus influenzae Rd 71421 -11537373 5000694635 (de:(hi1247) (pn:excinuclease abc subunit b:uvrb) (gn:uvrb) (gtcfc:10.8) (ec:) (uvrb_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1247 HI1247 Haemophilus influenzae 727 10045814

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883388	14824	36980	2379	793

Description

6500733516 mfd:hi1258 transcription-repair coupling factor:trcf (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1258 HI1258 Haemophilus influenzae 727 -11537374 83621 mfd:hi1258 (de:transcription-repair coupling factor (trcf)) (db:swissprot) MFD_HAEIN P45128 HAEMOPHILUS INFLUENZAE 727 -11537374 167202 mfd transcription/repair-coupling protein:mutation frequency decline protein (cl:transcription-repair coupling protein:dead/h box helicase homology) (db:pir2.dat) I64112 I64112 Haemophilus influenzae 727 -11537374 7500885577 hi1258 transcription-repair coupling factor mfd (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:similar to sp:p30958 gb:u00096 pid:1651547) (le:7462) (re:10902) (di:direct) U32805 U32805 g1574188 Haemophilus influenzae Rd 71421 -11537374 5000694636 (de:(hi1258) (pn:trcf:transcription-repair coupling factor:trcf:mfd) (gn:mfd) (gtcfc:10.8) (ec:) (mfd_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1258 HI1258 Haemophilus influenzae 727 10025835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883392	14825	36981	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883423	14826	36982	2298	766

Description

GTC ORF with score 139 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883426	14827	36983	1521	506

Description

GTC ORF with score 140 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883440	14828	36984	690	229

Description

6500733517 gyra:hi1264 dna gyrase:subunit a:dna gyrase subunit a (gtcfc:10.8) (ec:5.99.1.3) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1264 HI1264 Haemophilus influenzae 727 -11537375 75197 gyra:hi1264 (ec:5.99.1.3) (de:dna gyrase subunit a,) (db:swissprot) GYRA_HAEIN P43700 HAEMOPHILUS INFLUENZAE 727 -11537375 125863 gyra dna topoisomerase atp-hydrolyzing:chain a:dna gyrase chain a:type ii dna topoisomerase chain a (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (ec:5.99.1.3) (db:pir1.dat) E64113 E64113 Haemophilus influenzae 727 -11537375 7500882874 hi1264 dna gyrase:subunit a gyra (db:genpept-bct1) (de:haemophilus influenzae rd section 121 of 163 of the completegenome.) (nt:similar to gb:y00544 sp:p09097 gb:m15631 gb:x06373) (le:4579) (re:7221) (di:complement) U32806 U32806 g1574722 Haemophilus influenzae Rd 71421 -11537375 5000694637 (de:(hi1264) (pn:dna gyrase subunit a:dna gyrase, subunit a:gyra) (gn:gyra) (gtcfc:10.8) (ec:5.99.1.3) (gyra_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1264 HI1264 Haemophilus influenzae 727 10017708

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883442	14829	36985	222	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883451	14830	36986	483	160

Description

6500733518 hsdr:hi1285 type i restriction enzyme ecor124/3 r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1285 HI1285 Haemophilus influenzae 727 -11537376 167236 hsdr type i site-specific deoxyribonuclease:chain hsdr (cl:dead/h box helicase homology) (ec:3.1.21.3) (db:pir2.dat) F64114 F64114 Haemophilus influenzae 727 -11537376 7500960744 hi1285 type i restriction enzyme hsdr (db:genpept-bct1) (de:haemophilus influenzae rd section 123 of 163 of the completegenome.) (nt:similar to pid:1685100 percent ident: 59.01;) (le:5702) (re:8869) (di:complement) U32808 U32808 g1574743 Haemophilus influenzae Rd 71421 -11537376 5000694638 (de:(hi1285) (pn:type i restriction enzyme ecor124) (gn:hsdr) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1285 HI1285 Haemophilus influenzae 727 10088319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883458	14831	36987	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883469	14832	36988	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883480	14833	36989	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883487	14834	36990	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883495	14835	36991	432	143

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883502	14836	36992	954	317

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883505	14837	36993	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883516	14838	36994	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883520	14839	36995	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883537	14840	36996	888	295

Description

6500733519 hsdm:hi1287 type i restriction enzyme ecor124/3 i m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1287 HI1287 Haemophilus influenzae 727 -11537377 167235 hsdm site-specific dna-methyltransferase adenine-specific:hsdm (ec:2.1.1.72) (db:pir2.dat) G64114 G64114 Haemophilus influenzae 727 -11537377 7500960735 hi1287 type i modification enzyme hsdm (db:genpept-bct1) (de:haemophilus influenzae rd section 123 of 163 of the completegenome.) (nt:similar to pid:1679866 percent ident: 47.72;) (le:10333) (re:11664) (di:complement) U32808 U32808 g1574745 Haemophilus influenzae Rd 71421 -11537377 5000694639 (de:(hi1287) (pn:type i restriction enzyme ecor124) (gn:hsdm) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1287 HI1287 Haemophilus influenzae 727 10088318

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883542	14841	36997	1869	622

Description

6500733520 hima:hi1313 integration host factor alpha-subunit:ihf-alpha (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1313 HI1313 Haemophilus influenzae 727 -11537378 79046 hima:hi1313 (de:integration host factor alpha-subunit (ihf-alpha)) (db:swissprot) IHFA_HAEIN P43723 HAEMOPHILUS INFLUENZAE 727 -11537378 148265 integration host factor alpha chain (cl:bacterial dna-binding protein) (db:pir2.dat) A64116 A64116 Haemophilus influenzae 727 -11537378 7500883980 hi1313 integration host factor:alpha-subunit hima (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to gb:k02844 sp:p06984 pid:146347 pid:43072) (le:10198) (re:10488) (di:direct) U32810 U32810 g1574771 Haemophilus influenzae Rd 71421 -11537378 5000694640 (de:(hi1313) (pn:ihf-alpha:integration host factor alpha-subunit:hima) (gn:hima) (gtcfc:10.8) (ec:) (ihfa_haein) (keggfc:11.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1313 HI1313 Haemophilus influenzae 727 10021378

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883563	14842	36998	498	165

Description

6500733521 topa:hi1365 topoisomerase i:dna topoisomerase i:omega-protein:relaxing enzyme:untwisting enzyme:swivelase (gtcfc:10.8) (ec:5.99.1.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1365 HI1365 Haemophilus influenzae 727 -11537379 142196 topa dna topoisomerase (cl:bacterial type i dna topoisomerase) (ec:5.99.1.2) (db:pir2.dat) G64119 G64119 Haemophilus influenzae 727 -11537379 7500954467 hi1365 dna topoisomerase i topa (db:genpept-bct1) (de:haemophilus influenzae rd section 131 of 163 of the completegenome.) (nt:similar to gb:x04475 sp:p06612 pid:145664) (le:4214) (re:6820) (di:direct) U32816 U32816 g1574197 Haemophilus influenzae Rd 71421 -11537379 5000694641 (de:(hi1365) (pn:dna topoisomerase i:omega-protein:relaxing enzyme:untwisting enzyme:swivelase:topoisomerase i:topa) (gn:topa) (gtcfc:10.8) (ec:5.99.1.2) (topl_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1365 HI1365 Haemophilus influenzae 727 10072815

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883564	14843	36999	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883566	14844	37000	393	130

Description

6500733522 hindiiim:hi1392 hindiii modification methyltransferase:modification methylase hindiii:adenine-specific methyltransferase hindiii:m (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1392 HI1392 Haemophilus influenzae 727 -11537380 7500976284 hi1392 modification methylase hindiiim (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to gb:l15391 pid:1574226 percent ident:) (le:10701) (re:11630) (di:complement) U32819 U32819 g1574226 Haemophilus influenzae Rd 71421 -11537380 5000694642 (de:(hi1392) (pn:modification methylase hindiii:adenine-specific methyltransferase hindiii:m:hindiii modification methyltransferase:hindiiim) (gn:hindiiim) (gtcfc:10.8) (ec:2.1.1.72) (mth3_haein) (keggfc:11.1) (tigrfc:10.2) (db:) HI1392 HI1392 Haemophilus influenzae 727 10126718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883579	14845	37001	864	287

Description

GTC ORF with score 578 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome viii cosmid 9196.) (nt:member of the atp-binding transport protein family) (le:27976) (re:32754) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883580	14846	37002	297	98

Description

6500733523 hindiiir:hi1393 hindiii restriction endonuclease:type ii restriction enzyme hindiii:endonuclease hindiii:r (gtcfc:10.8) (ec:3.1.21.4) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1393 HI1393 Haemophilus influenzae 727 -11537381 166199 type ii site-specific deoxyribonuclease:hindiii (ec:3.1.21.4) (db:pir2.dat) H64121 H64121 Haemophilus influenzae 727 -11537381 7500960746 hi1393 type ii restriction endonuclease hindiiir (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to gb:l15391 pid:1574230 percent ident:) (le:11611) (re:12513) (di:complement) U32819 U32819 g1574230 Haemophilus influenzae Rd 71421 -11537381 5000694643 (de:(hi1393) (pn:type ii restriction enzyme hindiii:endonuclease hindiii:r:hindiii restriction endonuclease:hindiiir) (gn:hindiiir) (gtcfc:10.8) (ec:3.1.21.4) (t2h3_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenz) HI1393 HI1393 Haemophilus influenzae 727 10088104

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883584	14847	37003	630	209

Description

5000694644 shufflon-specific dna recombinase:rci:putative integrase/recombinase hi1414 (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1424 HI1424 Haemophilus influenzae 727 -11537382 111421 hi1424 (de:putative integrase/recombinase hi1414) (db:swissprot) YE24_HAEIN P45198 HAEMOPHILUS INFLUENZAE 727 -11537382 167160 hypothetical protein hi1424 (db:pir2.dat) D64122 D64122 Haemophilus influenzae 727 -11537382 7500922667 hi1424 integrase/recombinase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:similar to sp:p10487 gb:d90039 sp:p16470 gb:x05022) (le:6227) (re:7141) (di:complement) U32821 U32821 g1574258 Haemophilus influenzae Rd 71421 -11537382 6500733524 shufflon-specific dna recombinase:rci:putative integrase/recombinase hi1414 (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1424 HI1424 Haemophilus influenzae 727 -11537382

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883594	14848	37004	489	162

Description

6500733525 pare:hi1528 topoisomerase iv subunit b (gtcfc:10.8) (ec:5.99.1.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1528 HI1528 Haemophilus influenzae 727 -11537383 88650 pare:hi1528 (ec:5.99.1.-) (de:topoisomerase iv subunit b,) (db:swissprot) PARE_HAEIN P43703 HAEMOPHILUS INFLUENZAE 727 -11537383 167195 pare dna topoisomerase iv:chain pare (cl:dna topoisomerase (atp-hydrolyzing) chain b) (ec:5.99.1.-) (db:pir2.dat) E64127 E64127 Haemophilus influenzae 727 -11537383 7500887668 hi1528 topoisomerase iv:subunit b pare (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:similar to sp:p20083 gb:l22026 gb:m58409 pid:147108) (le:7968) (re:9866) (di:direct) U32828 U32828 g1574369 Haemophilus influenzae Rd 71421 -11537383 5000694645 (de:(hi1528) (pn:topoisomerase iv subunit b:pare) (gn:pare) (gtcfc:10.8) (ec:5.99.1.-) (pare_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1528 HI1528 Haemophilus influenzae 727 10030777

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883598	14849	37005	402	134

Description

6500733526 parc:hi1529 topoisomerase iv subunit a (gtcfc:10.8) (ec:5.99.1.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1529 HI1529 Haemophilus influenzae 727 -11537384 88641 parc:hi1529 (ec:5.99.1.-) (de:topoisomerase iv subunit a,) (db:swissprot) PARC_HAEIN P43702 HAEMOPHILUS INFLUENZAE 727 -11537384 167194 parc dna topoisomerase iv:chain parc (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (ec:5.99.1.-) (db:pir2.dat) F64127 F64127 Haemophilus influenzae 727 -11537384 7500887664 hi1529 topoisomerase iv:subunit a parc (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:similar to sp:p20082 gb:m58408 pid:147106) (le:9933) (re:12176) (di:direct) U32828 U32828 g1574370 Haemophilus influenzae Rd 71421 -11537384 5000694646 (de:(hi1529) (pn:topoisomerase iv subunit a:parc) (gn:parc) (gtcfc:10.8) (ec:5.99.1.-) (parc_haein) (keggfc:11.1) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1529 HI1529 Haemophilus influenzae 727 10030768

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883601	14850	37006	738	245

Description

6500733527 rnc:hi0014 ribonuclease iii:rnase iii (gtcfc:10.9) (ec:3.1.26.3) (keggfc:14.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0014 HI0014 Haemophilus influenzae 727 -11537385 95699 rnc:hi0014 (ec:3.1.26.3) (de:ribonuclease iii, (rnase iii)) (db:swissprot) RNC_HAEIN P44441 HAEMOPHILUS INFLUENZAE 727 -11537385 139842 ribonuclease iii (cl:ribonuclease iii:double-stranded rna-binding repeat homology) (ec:3.1.26.3) (db:pir2.dat) G64042 G64042 Haemophilus influenzae 727 -11537385 7500890439 hi0014 ribonuclease iii rnc (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to sp:p05797 gb:x02946 pid:42769 pid:499371) (le:2044) (re:2727) (di:complement) U32687 U32687 g1572958 Haemophilus influenzae Rd 71421 -11537385 5000694647 (de:(hi0014) (pn:rnase iii:ribonuclease iii:rnc) (gn:rnc) (gtcfc:10.9) (ec:3.1.26.3) (rnc_haein) (keggfc:11.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae)) HI0014 HI0014 Haemophilus influenzae 727 10037649

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883608	14851	37007	693	230

Description

5000694648 rnha:rnh:hi0138 rnh:ribonuclease h:rnase h (gtcfc:10.9) (ec:3.1.26.4) (keggfc:14.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0138 HI0138 Haemophilus influenzae 727 -11537386 95727 rnha:rnh:hi0138 (ec:3.1.26.4) (de:ribonuclease h, (rnase h)) (db:swissprot) RNH_HAEIN P43807 HAEMOPHILUS INFLUENZAE 727 -11537386 139844 ribonuclease h (cl:ribonuclease h) (ec:3.1.26.4) (db:pir2.dat) C64050 C64050 Haemophilus influenzae 727 -11537386 7500890450 hi0138 ribonuclease h rnh (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:similar to sp:p00647 pid:1208974 pid:147677) (le:8229) (re:8693) (di:direct) U32699 U32699 g1573091 Haemophilus influenzae Rd 71421 -11537386 6500733528 rnha:rnh rnh:ribonuclease h:rnase h (gtcfc:10.9) (ec:3.1.26.4) (keggfc:14.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0138 HI0138 Haemophilus influenzae 727 -11537386

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883611	14852	37008	456	151

Description

6500733529 prrd:hi0218 anticodon nuclease masking-agent (gtcfc:10.9) (keggfc:14.2) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0218 HI0218 Haemophilus influenzae 727 -11537387 166004 prrd protein homolog (db:pir2.dat) F64055 F64055 Haemophilus influenzae 727 -11537387 5000694649 (de:(hi0218) (pn:anticodon nuclease masking-agent:prrd) (gn:prrd) (gtcfc:10.9) (ec:) (keggfc:11.2) (tigrfc:11.1) (db:gtc-haemophilus influenzae)) HI0218 HI0218 Haemophilus influenzae 727 10088056

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883616	14853	37009	381	126

Description

6500733530 rph:hi0273 ribonuclease ph:rnase ph:trna nucleotidyltransferase (gtcfc:10.9) (ec:2.7.7.56) (keggfc:14.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0273 HI0273 Haemophilus influenzae 727 -11537388 95776 rph:hi0273 (ec:2.7.7.56) (de:nucleotidyltransferase)) (db:swissprot) RNPH_HAEIN P44444 HAEMOPHILUS INFLUENZAE 727 -11537388 157281 trna nucleotidyltransferase::phosphate-dependent exoribonuclease:ribonuclease ph (cl:trna nucleotidyltransferase) (ec:2.7.7.56) (db:pir1.dat) A64059 A64059 Haemophilus influenzae 727 -11537388 7500890473 hi0273 ribonuclease ph rph (db:genpept-bct1) (de:haemophilus influenzae rd section 28 of 163 of the complete genome.) (nt:similar to sp:p03842 gb:x00781 pid:499181) (le:7004) (re:7720) (di:complement) U32713 U32713 g1573239 Haemophilus influenzae Rd 71421 -11537388 5000694650 (de:(hi0273) (pn:rnase ph:trna nucleotidyltransferase:ribonuclease ph:rph) (gn:rph) (gtcfc:10.9) (ec:2.7.7.56) (rnph_haein) (keggfc:11.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae)) HI0273 HI0273 Haemophilus influenzae 727 10037725

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883617	14854	37010	570	189

Description

GTC ORF with score 547 to: (fn:atpase) (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae atpase rca1p (rca1) gene, complete cds.) (nt:mutations in the rca1 gene cause a mitochondrial) (le:208) (re:2685) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883619	14855	37011	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883620	14856	37012	258	85

Description

6500733531 rnt:hi0324 ribonuclease t:exoribonuclease t:rnase t (gtcfc:10.9) (ec:3.1.13.-) (keggfc:14.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0324 HI0324 Haemophilus influenzae 727 -11537389 95844 rnt:hi0324 (ec:3.1.13.-) (de:ribonuclease t, (exoribonuclease t) (rnase t)) (db:swissprot) RNT_HAEIN P44639 HAEMOPHILUS INFLUENZAE 727 -11537389 167149 ribonuclease t (ec:3.1.13.-) (db:pir2.dat) H64061 H64061 Haemophilus influenzae 727 -11537389 7500890481 hi0324 ribonuclease t rnt (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:l01622 sp:p30014 pid:147688 gb:u00096) (le:6639) (re:7328) (di:direct) U32717 U32717 g1573293 Haemophilus influenzae Rd 71421 -11537389 5000694651 (de:(hi0324) (pn:ribonuclease t:exoribonuclease t:rnase t:rnt) (gn:rnt) (gtcfc:10.9) (ec:3.1.13.-) (rnt_haein) (keggfc:11.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae)) HI0324 HI0324 Haemophilus influenzae 727 10037791

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883621	14857	37013	183	60

Description

6500733532 rnd:hi0390 ribonuclease d:rnase d (gtcfc:10.9) (ec:3.1.26.3) (keggfc:14.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0390 HI0390 Haemophilus influenzae 727 -11537390 95703 rnd:hi0390 (ec:3.1.26.3) (de:ribonuclease d, (rnase d)) (db:swissprot) RND_HAEIN P44442 HAEMOPHILUS INFLUENZAE 727 -11537390 167141 ribonuclease iii homolog (db:pir2.dat) B64065 B64065 Haemophilus influenzae 727 -11537390 7500890444 hi0390 ribonuclease d rnd (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to sp:p09155 gb:x07055 gb:x70994 pid:581071) (le:11558) (re:12757) (di:direct) U32722 U32722 g1573361 Haemophilus influenzae Rd 71421 -11537390 5000694652 (de:(hi0390) (pn:rnase d:ribonuclease d:rnd) (gn:rnd) (gtcfc:10.9) (ec:3.1.26.3) (rnd_haein) (keggfc:11.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae)) HI0390 HI0390 Haemophilus influenzae 727 10037653

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883622	14858	37014	243	81

Description

6500733533 rnpa:hi0999 ribonuclease p protein component:protein c5:rnase p (gtcfc:10.9) (ec:3.1.26.5) (keggfc:14.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI0999 HI0999 Haemophilus influenzae 727 -11537391 95761 rnpa:hi0999 (ec:3.1.26.5) (de:ribonuclease p protein component, (protein c5) (rnase p)) (db:swissprot) RNPA_HAEIN P44306 HAEMOPHILUS INFLUENZAE 727 -11537391 7500890464 hi0999 ribonuclease p rnpa (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p06277 gb:m11056 pid:147683) (le:275) (re:634) (di:direct) U32781 U32781 g1574030 Haemophilus influenzae Rd 71421 -11537391 5000694653 (de:(hi0999) (pn:ribonuclease p protein component:protein c5:rnase p:rnpa) (gn:rnpa) (gtcfc:10.9) (ec:3.1.26.5) (rnpa_haein) (keggfc:11.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae)) HI0999 HI0999 Haemophilus influenzae 727 10126703

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883624	14859	37015	381	126

Description

6500733534 rnb:hi1733 rnaseii:exoribonuclease ii:ribonuclease ii:rnase ii (gtcfc:10.9) (ec:3.1.13.1) (keggfc:14.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae) HI1733 HI1733 Haemophilus influenzae 727 -11537392 95692 rnb:hi1733 (ec:3.1.13.1) (de:exoribonuclease ii, (ribonuclease ii) (rnase ii)) (db:swissprot) RNB_HAEIN P44440 HAEMOPHILUS INFLUENZAE 727 -11537392 166123 ribonuclease t2 homolog (cl:exoribonuclease ii) (db:pir2.dat) A64139 A64139 Haemophilus influenzae 727 -11537392 7500890436 hi1733 exoribonuclease ii rnb (db:genpept-bct1) (de:haemophilus influenzae rd section 161 of 163 of the completegenome.) (nt:similar to sp:p30850 gb:x67913 pid:559438 gb:u00096) (le:4476) (re:6455) (di:complement) U32846 U32846 g1574590 Haemophilus influenzae Rd 71421 -11537392 5000694654 (de:(hi1733) (pn:ribonuclease ii:rnase ii:exoribonuclease ii:rnaseii) (gn:rnb) (gtcfc:10.9) (ec:3.1.13.1) (rnb_haein) (keggfc:11.1) (tigrfc:11.1) (db:gtc-haemophilus influenzae)) HI1733 HI1733 Haemophilus influenzae 727 10037642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883628	14860	37016	618	205

Description

6500733535 rlpa:hi0030 rare lipoprotein a (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0030 HI0030 Haemophilus influenzae 727 -11537393 4000708213 hi0030 (de:hypothetical protein hi0030 precursor) (db:swissprot) Y030_HAEIN Q57092 HAEMOPHILUS INFLUENZAE 727 -11537393 167130 rare lipoprotein a homolog (db:pir2.dat) A64044 A64044 Haemophilus influenzae 727 -11537393 7500894558 hi0030 lipoprotein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to gb:m18276 sp:p10100 pid:147660 gb:u00096) (le:7353) (re:8216) (di:complement) U32688 U32688 g1572975 Haemophilus influenzae Rd 71421 -11537393 5000694655 (de:(hi0030) (pn:rare lipoprotein a:rlpa) (gn:rlpa) (gtcfc:11.1) (ec:) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0030 HI0030 Haemophilus influenzae 727 10088289

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883630	14861	37017	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883634	14862	37018	1380	459

Description

6500733536 ompp2:hi0139 outer membrane protein p2 precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0139 HI0139 Haemophilus influenzae 727 -11537394 87604 ompp2:hi0139 (de:outer membrane protein p2 precursor (omp p2)) (db:swissprot) OM21_HAEIN P43839 HAEMOPHILUS INFLUENZAE 727 -11537394 167060 major outer membrane protein p2 (db:pir2.dat) D64050 D64050 Haemophilus influenzae 727 -11537394 7500887167 hi0139 outer membrane protein p2 ompp2 (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:similar to gb:j03359 sp:p20149 percent identity:) (le:8945) (re:10024) (di:direct) U32699 U32699 g1573092 Haemophilus influenzae Rd 71421 -11537394 5000694656 (de:(hi0139) (pn:outer membrane protein p2 precursor:omp p2:outer membrane protein p2:ompp2) (gn:ompp2) (gtcfc:11.1) (ec:) (om21_haein) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0139 HI0139 Haemophilus influenzae 727 10029747

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883637	14863	37019	741	246

Description

5000694657 lipoprotein-34:sp:p21167:hypothetical protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0256 HI0256 Haemophilus influenzae 727 -11537395 109028 hi0256 (de:hypothetical protein hi0256) (db:swissprot) Y256_HAEIN P43973 HAEMOPHILUS INFLUENZAE 727 -11537395 166335 hypothetical protein hi0256 (db:pir2.dat) I64004 I64004 Haemophilus influenzae 727 -11537395 7500894980 hi0256 lipoprotein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to sp:p21167 pid:147409 pid:42126 gb:u00096) (le:7323) (re:7970) (di:direct) U32711 U32711 g1573222 Haemophilus influenzae Rd 71421 -11537395 6500733537 lipoprotein-34:sp:p21167:hypothetical protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0256 HI0256 Haemophilus influenzae 727 -11537395

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883638	14864	37020	900	299

Description

GTC ORF with score 189 to: (sr:fruit fly) (db:genpept-inv) (de:d. melanogaster retrotransposon gypsy gene fragment for reversetranscriptase-like enzyme.) (nt:reverse transcriptase-like enzyme (930 aa)) (le:<1) (re:2790) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883644	14865	37021	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883645	14866	37022	423	140

Description

5000694658 hydrophobic membrane protein:hypothetical protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0360 HI0360 Haemophilus influenzae 727 -11537396 109116 hi0360 (de:hypothetical protein hi0360) (db:swissprot) Y360_HAEIN P44661 HAEMOPHILUS INFLUENZAE 727 -11537396 166211 hypothetical protein hi0360 (cl:conserved hypothetical protein hi0360) (db:pir2.dat) E64063 E64063 Haemophilus influenzae 727 -11537396 7500895189 hi0360 iron chelated abc transporter:permease (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to pid:1245464 sp:q56954 pid:1245466) (le:5515) (re:6363) (di:complement) U32720 U32720 g1573328 Haemophilus influenzae Rd 71421 -11537396 6500733538 hydrophobic membrane protein:hypothetical protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0360 HI0360 Haemophilus influenzae 727 -11537396

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883650	14867	37023	273	90

Description

6500733539 ompp1:hi0401 outer membrane protein precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0401 HI0401 Haemophilus influenzae 727 -11537397 87597 ompp1:hi0401 (de:outer membrane protein p1 precursor (omp p1)) (db:swissprot) OM11_HAEIN P43838 HAEMOPHILUS INFLUENZAE 727 -11537397 153230 outer membrane protein p1 precursor (cl:long-chain fatty acid transport protein fadl) (db:pir2.dat) F64065 F64065 Haemophilus influenzae 727 -11537397 7500887164 hi0401 long-chain fatty acid transport protein fadl (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to gb:m60607 sp:p10384 gb:y00552 pid:145910) (le:8188) (re:9567) (di:direct) U32723 U32723 g1573372 Haemophilus influenzae Rd 71421 -11537397 5000694659 (de:(hi0401) (pn:outer membrane protein p1 precursor:omp p1:outer membrane protein p1:ompp1) (gn:ompp1) (gtcfc:11.1) (ec:) (om11_haein) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0401 HI0401 Haemophilus influenzae 727 10029740

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883661	14868	37024	360	119

Description

5000694660 hydrophobic membrane protein:hypothetical protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0407 HI0407 Haemophilus influenzae 727 -11537398 111490 znub:hi0407 (de:high-affinity zinc uptake system membrane protein znub) (db:swissprot) ZNUB_HAEIN P44691 HAEMOPHILUS INFLUENZAE 727 -11537398 166210 probable membrane protein hi0407 (db:pir2.dat) A64066 A64066 Haemophilus influenzae 727 -11537398 7500922923 hi0407 conserved hypothetical integral membrane (db:genpept-bct1) (de:haemophilus influenzae rd section 39 of 163 of the complete genome.) (nt:similar to pid:1054959 gb:u00096 pid:1788166) (le:1104) (re:1889) (di:complement) U32724 U32724 g1573380 Haemophilus influenzae Rd 71421 -11537398 6500733540 hydrophobic membrane protein:hypothetical protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0407 HI0407 Haemophilus influenzae 727 -11537398

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883662	14869	37025	1794	597

Description

6500733541 hlpa:hi0620 28 kd outer membrane protein precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0620 HI0620 Haemophilus influenzae 727 -11537399 86102 hlpa:hi0620 (de:28 kd outer membrane protein precursor) (db:swissprot) HLPA_HAEIN P31728 HAEMOPHILUS INFLUENZAE 727 -11537399 153431 outer membrane protein:28k (cl:lipoprotein-28) (db:pir2.dat) B64082 B64082 Haemophilus influenzae 727 -11537399 7500883387 hi0620 28 kda outer membrane protein hlpa (db:genpept-bct1) (de:haemophilus influenzae rd section 59 of 163 of the complete genome.) (nt:similar to gb:m59804 sp:p31728 pid:1573614 percent) (le:6205) (re:7026) (di:complement) U32744 U32744 g1573614 Haemophilus influenzae Rd 71421 -11537399 5000694661 (de:(hi0620) (pn:28 kd outer membrane protein precursor:28 kda membrane protein:hlpa) (gn:hlpa) (gtcfc:11.1) (ec:) (nlpa_haein) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0620 HI0620 Haemophilus influenzae 727 10028269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883663	14870	37026	486	161

Description

5000694662 hel:ompp4:hi0693 lipoprotein e precursor:outer membrane protein p4 (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0693 HI0693 Haemophilus influenzae 727 -11537400 76445 hel:ompp4:hi0693 (de:lipoprotein e precursor (outer membrane protein p4) (omp p4)) (db:swissprot) HEL_HAEIN P26093 HAEMOPHILUS INFLUENZAE 727 -11537400 166959 hel outer membrane protein p4 precursor:lipoprotein e (db:pir2.dat) B64087 B64087 Haemophilus influenzae 727 -11537400 7500883129 hi0693 lipoprotein e hel (db:genpept-bct1) (de:haemophilus influenzae rd section 67 of 163 of the complete genome.) (nt:similar to gb:m68502 sp:p26093 pid:1573696 percent) (le:3297) (re:4121) (di:direct) U32752 U32752 g1573696 Haemophilus influenzae Rd 71421 -11537400 6500733542 hel:ompp4 lipoprotein e precursor:outer membrane protein p4 (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0693 HI0693 Haemophilus influenzae 727 -11537400

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883669	14871	37027	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883672	14872	37028	489	162

Description

5000694663 lipoprotein b:lppb:hypothetical 21 (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0703 HI0703 Haemophilus influenzae 727 -11537401 109264 hi0703 (de:hypothetical 21.7 kd protein sure-lppb intergenic region) (db:swissprot) Y703_HAEIN P44832 HAEMOPHILUS INFLUENZAE 727 -11537401 166961 hypothetical protein hi0703 (cl:conserved hypothetical protein mj0201) (db:pir2.dat) E64087 E64087 Haemophilus influenzae 727 -11537401 7500895464 hi0703 lipoprotein b lppb (db:genpept-bct1) (de:haemophilus influenzae rd section 68 of 163 of the complete genome.) (nt:similar to gb:l10653 sp:p36684 pid:148929 percent) (le:3115) (re:3693) (di:direct) U32753 U32753 g1573705 Haemophilus influenzae Rd 71421 -11537401 6500733543 lipoprotein b:lppb:hypothetical 21 (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0703 HI0703 Haemophilus influenzae 727 -11537401

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883673	14873	37029	249	82

Description

6500733544 lppb:nlpd:hi0706 outer membrane antigenic lipoprotein b precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0706 HI0706 Haemophilus influenzae 727 -11537402 82414 lppb:hi0706 (de:outer membrane antigenic lipoprotein b precursor) (db:swissprot) LPPB_HAEIN P44833 HAEMOPHILUS INFLUENZAE 727 -11537402 166960 lipoprotein d homolog (cl:lipoprotein d) (db:pir2.dat) F64087 F64087 Haemophilus influenzae 727 -11537402 7500885130 hi0706 lipoprotein (db:genpept-bct1) (de:haemophilus influenzae rd section 68 of 163 of the complete genome.) (nt:similar to gb:l07869 sp:p33648 pid:404099) (le:3911) (re:5128) (di:direct) U32753 U32753 g1573707 Haemophilus influenzae Rd 71421 -11537402 5000694664 (de:(hi0706) (pn:outer membrane antigenic lipoprotein b precursor:lipoprotein:nlpd) (gn:lppb) (gtcfc:11.1) (ec:) (lppb_haein) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0706 HI0706 Haemophilus influenzae 727 10024638

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883676	14874	37030	351	116

Description

GTC ORF with score 198 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone 1750.) (nt:similar to medicago sativa cdc2 kinase homologue:) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883679	14875	37031	261	86

Description

6500733545 lgtd:hi0868 glycosyl transferase (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0868 HI0868 Haemophilus influenzae 727 -11537403 7500895572 hi0868 (ec:2.-.-.-) (de:putative glycosyl transferase hi0868,) (db:swissprot) Y868_HAEIN Q57022 HAEMOPHILUS INFLUENZAE 727 -11537403 166171 glycosyl transferase homolog hi0868 (db:pir2.dat) A64099 A64099 Haemophilus influenzae 727 -11537403 7500895574 hi0868 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 83 of 163 of the complete genome.) (nt:similar to gb:al009126 percent ident: 35.37;) (le:7778) (re:8530) (di:direct) U32768 U32768 g1573885 Haemophilus influenzae Rd 71421 -11537403 5000694665 (de:(hi0868) (pn:glycosyl transferase:lgtd) (gn:lgtd) (gtcfc:11.1) (ec:) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0868 HI0868 Haemophilus influenzae 727 10088095

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883680	14876	37032	519	172

Description

6500733546 mtrc:hi0894 membrane fusion protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0894 HI0894 Haemophilus influenzae 727 -11537404 4000707970 hi0894 (de:hypothetical protein hi0894) (db:swissprot) Y894_HAEIN Q57500 HAEMOPHILUS INFLUENZAE 727 -11537404 7500895628 hi0894 lipoprotein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to gb:u14993 sp:p43505 pid:438192) (le:4497) (re:5645) (di:direct) U32771 U32771 g1573913 Haemophilus influenzae Rd 71421 -11537404 5000694666 (de:(hi0894) (pn:membrane fusion protein:mtrc) (gn:mtrc) (gtcfc:11.1) (ec:) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0894 HI0894 Haemophilus influenzae 727 10126701

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883681	14877	37033	195	64

Description

6500733547 rlpb:hi0922 rare lipoprotein b (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI0922 HI0922 Haemophilus influenzae 727 -11537405 4000708795 hi0922 (de:hypothetical lipoprotein hi0922 precursor) (db:swissprot) Y922_HAEIN Q57457 HAEMOPHILUS INFLUENZAE 727 -11537405 167131 lipoprotein rlpb homolog hi0922 (db:pir2.dat) I64102 I64102 Haemophilus influenzae 727 -11537405 7500895680 hi0922 rare lipoprotein b:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 89 of 163 of the complete genome.) (nt:similar to gb:m18277 sp:p10101 pid:147663 gb:u00096) (le:2790) (re:3338) (di:direct) U32774 U32774 g1573944 Haemophilus influenzae Rd 71421 -11537405 5000694667 (de:(hi0922) (pn:rare lipoprotein b:rlpb) (gn:rlpb) (gtcfc:11.1) (ec:) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI0922 HI0922 Haemophilus influenzae 727 10088290

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883682	14878	37034	228	75

Description

5000694668 ompa:ompp5:hi1164 outer membrane protein p5 precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI1164 HI1164 Haemophilus influenzae 727 -11537406 87620 ompa:ompp5:hi1164 (de:outer membrane protein p5 precursor (omp p5)) (db:swissprot) OM51_HAEIN P43840 HAEMOPHILUS INFLUENZAE 727 -11537406 167062 outer membrane protein a homolog (cl:outer membrane protein a) (db:pir2.dat) C64187 C64187 Haemophilus influenzae 727 -11537406 7500887171 hi1164 outer membrane protein p5 ompa (db:genpept-bct1) (de:haemophilus influenzae rd section 111 of 163 of the completegenome.) (nt:similar to gb:l20309 sp:p38368 percent ident:) (le:5935) (re:6996) (di:direct) U32796 U32796 g1574091 Haemophilus influenzae Rd 71421 -11537406 6500733548 ompa:ompp5 outer membrane protein p5 precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI1164 HI1164 Haemophilus influenzae 727 -11537406

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883686	14879	37035	252	83

Description

GTC ORF with score 206 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone 1750.) (nt:similar to medicago sativa cdc2 kinase homologue:) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883689	14880	37036	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883704	14881	37037	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883714	14882	37038	249	82

Description

6500733549 iroa:hi1567 iron-regulated outer membrane protein a (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI1567 HI1567 Haemophilus influenzae 727 -11537407 166926 hypothetical protein hi1567 (db:pir2.dat) A64130 A64130 Haemophilus influenzae 727 -11537407 5500686575 hi1567 (de:probable tonb-dependent receptor hi1567 precursor) (db:swissprot) YF67_HAEIN Q57408 HAEMOPHILUS INFLUENZAE 727 -11537407 5000694669 (de:(hi1567) (pn:iron-regulated outer membrane protein a:iroa) (gn:iroa) (gtcfc:11.1) (ec:) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI1567 HI1567 Haemophilus influenzae 727 10088202

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883718	14883	37039	2991	996

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883728	14884	37040	507	168

Description

6500733550 lgtd:hi1578 glycosyl transferase (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI1578 HI1578 Haemophilus influenzae 727 -11537408 7500923294 hi1578 (ec:2.-.-.-) (de:putative glycosyl transferase hi1578,) (db:swissprot) YF78_HAEIN Q57287 HAEMOPHILUS INFLUENZAE 727 -11537408 166172 glycosyl transferase homolog hi1578 (db:pir2.dat) H64130 H64130 Haemophilus influenzae 727 -11537408 7500923296 hi1578 glycosyl transferase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to pid:595813 percent ident: 47.32;) (le:641) (re:1612) (di:direct) U32832 U32832 g1574422 Haemophilus influenzae Rd 71421 -11537408 5000694670 (de:(hi1578) (pn:glycosyl transferase:lgtd) (gn:lgtd) (gtcfc:11.1) (ec:) (keggfc:11.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae)) HI1578 HI1578 Haemophilus influenzae 727 10088096

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883729	14885	37041	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883737	14886	37042	285	95

Description

5000694671 pcp:lpp:hi1579 15 kda peptidoglycan-associated lipoprotein:outer membrane lipoprotein pcp precursor:pal cross-reacting lipoprotein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI1579 HI1579 Haemophilus influenzae 727 -11537409 88834 pcp:lpp:hi1579 (de:cross-reacting lipoprotein)) (db:swissprot) PCP_HAEIN P10325 HAEMOPHILUS INFLUENZAE 727 -11537409 165957 pal cross-reacting lipoprotein precursor (cl:pal cross-reacting lipoprotein) (db:pir2.dat) I64130 I64130 Haemophilus influenzae 727 -11537409 7500887738 hi1579 15 kda peptidoglycan-associated lipoprotein (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to gb:m18877 sp:p10325 percent ident:) (le:1795) (re:2262) (di:complement) U32832 U32832 g1574423 Haemophilus influenzae Rd 71421 -11537409 6500733551 pcp:lpp 15 kda peptidoglycan-associated lipoprotein:outer membrane lipoprotein pcp precursor:pal cross-reacting lipoprotein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-haemophilus influenzae) HI1579 HI1579 Haemophilus influenzae 727 -11537409

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883738	14887	37043	564	187

Description

6500733552 tolb:hi0382 colicin tolerance protein:protein precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae) HI0382 HI0382 Haemophilus influenzae 727 -11537410 101760 tolb:hi0382 (de:tolb protein precursor) (db:swissprot) TOLB_HAEIN P44677 HAEMOPHILUS INFLUENZAE 727 -11537410 166060 tolb tolb protein (db:pir2.dat) F64064 F64064 Haemophilus influenzae 727 -11537410 7500893247 hi0382 colicin tolerance protein tolb (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to pid:1685080 percent identity: 96.96;) (le:2218) (re:3501) (di:complement) U32722 U32722 g1573352 Haemophilus influenzae Rd 71421 -11537410 5000694828 (de:(hi0382) (pn:protein precursor:colicin tolerance protein:tolb) (gn:tolb) (gtcfc:12.14) (ec:) (tolb_haein) (keggfc:11.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae)) HI0382 HI0382 Haemophilus influenzae 727 10043589

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883742	14888	37044	723	240

Description

6500733553 tola:hi0383 outer membrane integrity protein:protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae) HI0383 HI0383 Haemophilus influenzae 727 -11537411 101757 tola:hi0383 (de:tola protein) (db:swissprot) TOLA_HAEIN P44678 HAEMOPHILUS INFLUENZAE 727 -11537411 167056 tola outer membrane integrity protein tola (db:pir2.dat) G64064 G64064 Haemophilus influenzae 727 -11537411 7500893245 hi0383 outer membrane integrity protein tola (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to gb:m28232 sp:p19934 pid:148019 gb:u00096) (le:3543) (re:4661) (di:complement) U32722 U32722 g1573353 Haemophilus influenzae Rd 71421 -11537411 5000694829 (de:(hi0383) (pn:protein:outer membrane integrity protein:tola) (gn:tola) (gtcfc:12.14) (ec:) (tola_haein) (keggfc:11.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae)) HI0383 HI0383 Haemophilus influenzae 727 10043586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883743	14889	37045	2001	666

Description

6500733554 tolr:hi0384 inner membrane protein:protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae) HI0384 HI0384 Haemophilus influenzae 727 -11537412 101768 tolr:hi0384 (de:tolr protein) (db:swissprot) TOLR_HAEIN P43769 HAEMOPHILUS INFLUENZAE 727 -11537412 1500685589 tolr tolr protein (cl:tolr protein) (db:pir2.dat) H64064 H64064 Haemophilus influenzae 727 -11537412 7500893253 hi0384 colicin transport protein tolr (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to sp:p05829 pid:1128980 gb:u00096) (le:4677) (re:5096) (di:complement) U32722 U32722 g1573354 Haemophilus influenzae Rd 71421 -11537412 241624 tolr tolr (db:genpept-bct2) (de:haemophilus influenzae tolqrab gene cluster, inner membrane protein(tolq) gene, partial cds, inner membrane protein (tolr), outermembrane integrity protein (tola) and colicin tolerance protein(tolb) genes, complete cds.) (nt:inner... HIU32470 U32470 g1685078 Haemophilus influenzae 727 -11537412 154839 tolr tolr protein (cl:tolr protein) (db:pir) H64064 H64064 Haemophilus influenzae 727 -11537412 5000694830 (de:(hi0384) (pn:protein:inner membrane protein:tolr) (gn:tolr) (gtcfc:12.14) (ec:) (tolr_haein) (keggfc:11.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae)) HI0384 HI0384 Haemophilus influenzae 727 10043597

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883744	14890	37046	303	100

Description

6500733555 tolq:hi0385 inner membrane protein:protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae) HI0385 HI0385 Haemophilus influenzae 727 -11537413 101765 tolq:hi0385 (de:tolq protein) (db:swissprot) TOLQ_HAEIN P43768 HAEMOPHILUS INFLUENZAE 727 -11537413 154836 tolq biopolymer transport protein tolq (cl:biopolymer transport protein) (db:pir2.dat) I64064 I64064 Haemophilus influenzae 727 -11537413 7500893251 hi0385 colicin transport protein tolq (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to sp:p05828 pid:1128978 gb:u00096) (le:5168) (re:5854) (di:complement) U32722 U32722 g1573355 Haemophilus influenzae Rd 71421 -11537413 5000694831 (de:(hi0385) (pn:protein:inner membrane protein:tolq) (gn:tolq) (gtcfc:12.14) (ec:) (tolq_haein) (keggfc:11.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae)) HI0385 HI0385 Haemophilus influenzae 727 10043594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883751	14891	37047	267	88

Description

6500733556 cvpa:hi1206 colicin v production protein:pur regulon:colicin v production protein homolog (gtcfc:11.1) (keggfc:14.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae) HI1206 HI1206 Haemophilus influenzae 727 -11537414 66870 cvpa:hi1206 (de:colicin v production protein homolog) (db:swissprot) CVPA_HAEIN P45108 HAEMOPHILUS INFLUENZAE 727 -11537414 153867 dede dede protein (cl:dede protein) (db:pir2.dat) H64189 H64189 Haemophilus influenzae 727 -11537414 7500879590 hi1206 colicin v production protein cvpa (db:genpept-bct1) (de:haemophilus influenzae rd section 115 of 163 of the completegenome.) (nt:similar to gb:j01666 sp:p08550 pid:146367) (le:2014) (re:2505) (di:direct) U32800 U32800 g1574136 Haemophilus influenzae Rd 71421 -11537414 5000694832 (de:(hi1206) (pn:colicin v production protein homolog:colicin v production protein:pur regulon:cvpa) (gn:cvpa) (gtcfc:12.14) (ec:) (cvpa_haein) (keggfc:11.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae)) HI1206 HI1206 Haemophilus influenzae 727 10009488

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883758	14892	37048	387	128

Description

6500733557 tola:hi1685 outer membrane integrity protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae) HI1685 HI1685 Haemophilus influenzae 727 -11537415 167055 rnfc protein homolog (db:pir2.dat) E64136 E64136 Haemophilus influenzae 727 -11537415 7500960732 hi1685 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1742688 pid:1742696) (le:7865) (re:10324) (di:direct) U32841 U32841 g1574537 Haemophilus influenzae Rd 71421 -11537415 5000694833 (de:(hi1685) (pn:outer membrane integrity protein:tola) (gn:tola) (gtcfc:12.14) (ec:) (keggfc:11.2) (tigrfc:14.2) (db:gtc-haemophilus influenzae)) HI1685 HI1685 Haemophilus influenzae 727 10088273

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883775	14893	37049	417	138

Description

6500733558 gerc2:hi0095 spore germination and vegetative growth protein (gtcfc:12.15:12.8) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0095 HI0095 Haemophilus influenzae 727 -11537416 5500686244 hi0095 (de:hypothetical protein hi0095) (db:swissprot) Y095_HAEIN Q57060 HAEMOPHILUS INFLUENZAE 727 -11537416 167176 hypothetical protein hi0095 (cl:bioc homology) (db:pir2.dat) B64048 B64048 Haemophilus influenzae 727 -11537416 7500894672 hi0095 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:similar to gp:2104289 percent identity: 34.43;) (le:2069) (re:2824) (di:complement) U32695 U32695 g1573047 Haemophilus influenzae Rd 71421 -11537416 5000695292 (de:(hi0095) (pn:spore germination and vegetative growth protein:gerc2) (gn:gerc2) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0095 HI0095 Haemophilus influenzae 727 10088299

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883781	14894	37050	711	236

Description

6500733559 nifc:hi0129 nitrogenase c (gtcfc:2.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0129 HI0129 Haemophilus influenzae 727 -11537417 167043 afub protein homolog (db:pir2.dat) H64049 H64049 Haemophilus influenzae 727 -11537417 5000695293 (de:(hi0129) (pn:nitrogenase c:nifc) (gn:nifc) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0129 HI0129 Haemophilus influenzae 727 10088269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883787	14895	37051	207	68

Description

6500733560 rnfe:hi0166 nitrogen fixation protein (gtcfc:2.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0166 HI0166 Haemophilus influenzae 727 -11537418 167040 nrqb nadh dehydrogenase ubiquinone:chain nqrb (ec:1.6.5.3) (db:pir2.dat) C64052 C64052 Haemophilus influenzae 727 -11537418 7500960716 hi0166 nadh:ubiquinone oxidoreductase:subunit b (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to pid:663269 pid:663271 percent identity:) (le:4312) (re:5547) (di:direct) U32702 U32702 g1573123 Haemophilus influenzae Rd 71421 -11537418 5000695294 (de:(hi0166) (pn:nitrogen fixation protein:rnfe) (gn:rnfe) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0166 HI0166 Haemophilus influenzae 727 10088266

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883792	14896	37052	183	60

Description

5000695295 phenolhydroxylase component (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0171 HI0171 Haemophilus influenzae 727 -11537419 167086 na+-translocating nadh-ubiquinone oxidoreductase:beta chain (ec:1.-.-.-) (db:pir2.dat) D64052 D64052 Haemophilus influenzae 727 -11537419 7500960718 hi0171 nqr6 subunit of na-translocating nadh-quinone (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to pid:893416 percent identity: 81.23;) (le:7513) (re:8748) (di:direct) U32702 U32702 g1573127 Haemophilus influenzae Rd 71421 -11537419 6500733561 phenolhydroxylase component (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0171 HI0171 Haemophilus influenzae 727 -11537419

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883797	14897	37053	666	221

Description

6500733562 rard:hi0223 chloramphenicol-sensitive protein (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0223 HI0223 Haemophilus influenzae 727 -11537420 166052 rard protein homolog hi0223 (db:pir2.dat) A64056 A64056 Haemophilus influenzae 727 -11537420 108995 y223_haein (de:hypothetical protein hi0223.) P44579 P44579 Haemophilus influenzae 727 -11537420 5000695296 (de:(hi0223) (pn:chloramphenicol-sensitive protein:rard) (gn:rard) (gtcfc:13.7) (ec:) (y223_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0223 HI0223 Haemophilus influenzae 727 10050727

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883816	14898	37054	1179	392

Description

5000695297 thiamine-repressed protein:nmt1:putative thiamine biosynthesis protein (gtcfc:9.1) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) HI0357 HI0357 Haemophilus influenzae 727 -11537421 109112 hi0357 (de:putative thiamine biosynthesis protein hi0357) (db:swissprot) Y357_HAEIN P44658 HAEMOPHILUS INFLUENZAE 727 -11537421 167188 hypothetical protein hi0357 (db:pir2.dat) C64063 C64063 Haemophilus influenzae 727 -11537421 7500895186 hi0357 thiamine biosynthesis protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to sp:p42883 sp:p43534 sp:p47183) (le:3006) (re:3950) (di:direct) U32720 U32720 g1573325 Haemophilus influenzae Rd 71421 -11537421 6500733563 thiamine-repressed protein:nmt1:putative thiamine biosynthesis protein (gtcfc:9.1) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0357 HI0357 Haemophilus influenzae 727 -11537421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883821	14899	37055	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883828	14900	37056	1260	419

Description

6500733564 gcpe:hi0368 protein e:protein homolog (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0368 HI0368 Haemophilus influenzae 727 -11537422 73422 gcpe:hi0368 (de:gcpe protein homolog) (db:swissprot) GCPE_HAEIN P44667 HAEMOPHILUS INFLUENZAE 727 -11537422 167116 gcpe gcpe protein (cl:gcpe protein) (db:pir2.dat) H64063 H64063 Haemophilus influenzae 727 -11537422 7500882261 hi0368 gcpe protein gcpe (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to sp:p27433 gb:x64451 pid:41542 gb:u00096) (le:1613) (re:2719) (di:direct) U32721 U32721 g1573337 Haemophilus influenzae Rd 71421 -11537422 5000695298 (de:(hi0368) (pn:protein homolog:protein e:gpce) (gn:gcpe) (gtcfc:13.7) (ec:) (gcpe_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0368 HI0368 Haemophilus influenzae 727 10015956

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883836	14901	37057	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883843	14902	37058	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883862	14903	37059	1824	607

Description

6500733565 nifu:hi0377 nitrogen fixation protein (gtcfc:2.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0377 HI0377 Haemophilus influenzae 727 -11537423 7500976249 hi0377 iscu protein iscu (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to pid:2271522 percent identity: 80.95;) (le:8789) (re:9169) (di:complement) U32721 U32721 g1573346 Haemophilus influenzae Rd 71421 -11537423 5000695299 (de:(hi0377) (pn:nitrogen fixation protein:nifu) (gn:nifu) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0377 HI0377 Haemophilus influenzae 727 10126685

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883879	14904	37060	285	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883892	14905	37061	813	270

Description

6500733566 nifs:hi0378 nitrogen fixation protein (gtcfc:2.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0378 HI0378 Haemophilus influenzae 727 -11537424 1500685847 hi0378 (de:nifs protein homolog) (db:swissprot) NIFS_HAEIN Q57337 HAEMOPHILUS INFLUENZAE 727 -11537424 167036 nifs protein homolog hi0378 (cl:nitrogen fixation protein nifs) (db:pir2.dat) D64064 D64064 Haemophilus influenzae 727 -11537424 7500886454 hi0378 nifs protein nifs (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p39171 pid:1788879) (le:9229) (re:10449) (di:complement) U32721 U32721 g1573347 Haemophilus influenzae Rd 71421 -11537424 5000695300 (de:(hi0378) (pn:nitrogen fixation protein:nifs) (gn:nifs) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0378 HI0378 Haemophilus influenzae 727 10059273

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883893	14906	37062	1482	494

Description

6500733567 mazg:hi0460 beta-lactamase regulatory homolog:protein homolog (gtcfc:12.13) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0460 HI0460 Haemophilus influenzae 727 -11537425 83080 mazg:hi0460 (de:mazg protein homolog) (db:swissprot) MAZG_HAEIN P44723 HAEMOPHILUS INFLUENZAE 727 -11537425 166027 beta-lactamase regulatory protein homolog (cl:beta-lactamase regulatory protein:beta-lactamase regulatory protein homology) (db:pir2.dat) H64069 H64069 Haemophilus influenzae 727 -11537425 7500885352 hi0460 mazg protein mazg (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to gb:j04039 sp:p33646 pid:416198) (le:8398) (re:9189) (di:direct) U32728 U32728 g1573434 Haemophilus influenzae Rd 71421 -11537425 5000695301 (de:(hi0460) (pn:protein homolog:beta-lactamase regulatory homolog:mazg) (gn:mazg) (gtcfc:13.7) (ec:) (mazg_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0460 HI0460 Haemophilus influenzae 727 10025299

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883901	14907	37063	792	263

Description

6500733568 lapb:hi0461 membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0461 HI0461 Haemophilus influenzae 727 -11537426 5500686323 hi0461 (de:hypothetical protein hi0461) (db:swissprot) Y461_HAEIN Q57144 HAEMOPHILUS INFLUENZAE 727 -11537426 166982 hypothetical protein hi0461 (cl:conserved hypothetical protein hi0461) (db:pir2.dat) I64069 I64069 Haemophilus influenzae 727 -11537426 7500895335 hi0461 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to sp:p32181 percent ident: 35.64;) (le:9239) (re:10114) (di:complement) U32728 U32728 g1573435 Haemophilus influenzae Rd 71421 -11537426 5000695302 (de:(hi0461) (pn:membrane protein:lapb) (gn:lapb) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0461 HI0461 Haemophilus influenzae 727 10088243

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883924	14908	37064	330	109

Description

6500733569 hslv:hi0496 hsluv operon heat shock protein (gtcfc:11.1:12.7) (ec:3.4.99.-) (keggfc:14.1) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0496 HI0496 Haemophilus influenzae 727 -11537427 166206 heat shock protein hi0496 (db:pir2.dat) C64072 C64072 Haemophilus influenzae 727 -11537427 7500960656 hi0496 heat shock protein hslv (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p31059 pid:305035 gb:u00096) (le:5139) (re:5666) (di:direct) U32731 U32731 g1573473 Haemophilus influenzae Rd 71421 -11537427 5000695303 (de:(hi0496) (pn:heat shock protein :hsluv operon heat shock protein:hslv) (gn:hslv) (gtcfc:13.7) (ec:3.4.99.-) (hslv_haein) (keggfc:11.1) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0496 HI0496 Haemophilus influenzae 727 10088108

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883928	14909	37065	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883936	14910	37066	270	89

Description

6500733570 hslu:hi0497 hsluv operon heat shock protein (gtcfc:11.1:12.7) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0497 HI0497 Haemophilus influenzae 727 -11537428 77895 hslu:hi0497 (de:heat shock protein hslu) (db:swissprot) HSLU_HAEIN P43773 HAEMOPHILUS INFLUENZAE 727 -11537428 7500883567 hi0497 heat shock protein hslu (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32168 pid:305034 gb:u00096) (le:5677) (re:7011) (di:direct) U32731 U32731 g1573474 Haemophilus influenzae Rd 71421 -11537428 5000695304 (de:(hi0497) (pn:heat shock protein :hsluv operon heat shock protein:hslu) (gn:hslu) (gtcfc:13.7) (ec:) (hslu_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0497 HI0497 Haemophilus influenzae 727 10020254

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883942	14911	37067	1737	578

Description

6500733571 devb:hi0556 putative glucose-6-phosphate dehydrogenase isozyme (gtcfc:1.1) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0556 HI0556 Haemophilus influenzae 727 -11537429 7000685015 devb:hi0556 (de:devb protein homolog) (db:swissprot) DEVB_HAEIN Q57039 HAEMOPHILUS INFLUENZAE 727 -11537429 167105 sol1 protein homolog (db:pir2.dat) D64077 D64077 Haemophilus influenzae 727 -11537429 7500880187 hi0556 oxidoreductase:putative devb (db:genpept-bct1) (de:haemophilus influenzae rd section 52 of 163 of the complete genome.) (nt:similar to sp:p46016 pid:556607 percent ident:) (le:4482) (re:4973) (di:complement) U32737 U32737 g1573542 Haemophilus influenzae Rd 71421 -11537429 5000695305 (de:(hi0556) (pn:putative glucose-6-phosphate dehydrogenase isozyme:devb) (gn:devb) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0556 HI0556 Haemophilus influenzae 727 10088283

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883968	14912	37068	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883970	14913	37069	1131	376

Description

5000695306 n-carbamyl-l-amino acid amidohydrolase (gtcfc:5.16) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0588 HI0588 Haemophilus influenzae 727 -11537430 4000707554 hi0588 (de:hypothetical protein hi0588) (db:swissprot) Y588_HAEIN Q57051 HAEMOPHILUS INFLUENZAE 727 -11537430 167022 n-carbamyl-l-amino acid amidohydrolase homolog (cl:n-carbamyl-l-amino acid amidohydrolase) (db:pir2.dat) D64079 D64079 Haemophilus influenzae 727 -11537430 7500895419 hi0588 n-carbamyl-l-amino acid amidohydrolase (db:genpept-bct1) (de:haemophilus influenzae rd section 55 of 163 of the complete genome.) (nt:similar to sp:p37113 gb:s67784 gb:x74289 pid:460895) (le:5924) (re:7159) (di:direct) U32740 U32740 g1573578 Haemophilus influenzae Rd 71421 -11537430 6500733572 n-carbamyl-l-amino acid amidohydrolase (gtcfc:5.16) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0588 HI0588 Haemophilus influenzae 727 -11537430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883975	14914	37070	630	209

Description

5000695307 hydrolase:hypothetical protein (gtcfc:14.1) (keggfc:14.1) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0597 HI0597 Haemophilus influenzae 727 -11537431 113293 hi0597 (de:hypothetical protein hi0597) (db:swissprot) YIGL_HAEIN P44771 HAEMOPHILUS INFLUENZAE 727 -11537431 166462 hypothetical protein hi0597 (cl:hypothetical protein hi0597) (db:pir2.dat) D64155 D64155 Haemophilus influenzae 727 -11537431 7500937449 hi0597 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 56 of 163 of the complete genome.) (nt:similar to sp:p27848 percent ident: 41.29;) (le:4873) (re:5691) (di:direct) U32741 U32741 g1573586 Haemophilus influenzae Rd 71421 -11537431 6500733573 hydrolase:hypothetical protein (gtcfc:14.1) (keggfc:14.1) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0597 HI0597 Haemophilus influenzae 727 -11537431

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501883977	14915	37071	1899	632

Description

6500733574 rseb:mucb:hi0630 mucoid status locus protein:sigma-e factor regulatory protein homolog precursor (gtcfc:12.13:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0630 HI0630 Haemophilus influenzae 727 -11537432 97460 rseb:hi0630 (de:sigma-e factor regulatory protein rseb homolog precursor) (db:swissprot) RSEB_HAEIN P44792 HAEMOPHILUS INFLUENZAE 727 -11537432 167010 hypothetical protein hi0630 (cl:conserved hypothetical protein hi0630) (db:pir2.dat) H64082 H64082 Haemophilus influenzae 727 -11537432 7500891147 hi0630 sigma-e factor regulatory protein rseb (db:genpept-bct1) (de:haemophilus influenzae rd section 61 of 163 of the complete genome.) (nt:similar to sp:p46186 pid:1050876 pid:987646) (le:70) (re:1017) (di:direct) U32746 U32746 g1573627 Haemophilus influenzae Rd 71421 -11537432 5000695308 (de:(hi0630) (pn:sigma-e factor regulatory protein homolog precursor:mucoid status locus protein:mucb) (gn:rseb) (gtcfc:13.7) (ec:) (rseb_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0630 HI0630 Haemophilus influenzae 727 10039352

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884004	14916	37072	213	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884011	14917	37073	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884026	14918	37074	879	292

Description

6500733575 cydc:hi0664 transport atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0664 HI0664 Haemophilus influenzae 727 -11537433 4000707502 hi0664 (de:hypothetical abc transporter atp-binding protein hi0664) (db:swissprot) Y664_HAEIN Q57538 HAEMOPHILUS INFLUENZAE 727 -11537433 167221 probable atp-binding transport protein hi0664 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) A64085 A64085 Haemophilus influenzae 727 -11537433 7500895451 hi0664 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 64 of 163 of the complete genome.) (nt:similar to gb:al009126 percent ident: 29.51;) (le:6284) (re:7942) (di:direct) U32749 U32749 g1573663 Haemophilus influenzae Rd 71421 -11537433 5000695309 (de:(hi0664) (pn:transport atp-binding protein:cydc) (gn:cydc) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0664 HI0664 Haemophilus influenzae 727 10088313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884033	14919	37075	660	219

Description

6500733576 glpx:hi0667 glp regulon protein homolog (gtcfc:12.13) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0667 HI0667 Haemophilus influenzae 727 -11537434 74057 glpx:hi0667 (de:glpx protein homolog) (db:swissprot) GLPX_HAEIN P44811 HAEMOPHILUS INFLUENZAE 727 -11537434 166153 glpx glpx protein (db:pir2.dat) B64085 B64085 Haemophilus influenzae 727 -11537434 7500882524 hi0667 glpx protein glpx (db:genpept-bct1) (de:haemophilus influenzae rd section 64 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p28860 gb:z11767 pid:146908) (le:9870) (re:10871) (di:complement) U32749 U32749 g1573665 Haemophilus influenzae Rd 71421 -11537434 5000695310 (de:(hi0667) (pn:protein homolog:glp regulon protein:glpx) (gn:glpx) (gtcfc:13.7) (ec:) (glpx_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0667 HI0667 Haemophilus influenzae 727 10016587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884041	14920	37076	552	183

Description

6500733577 rard:hi0680 chloramphenicol-sensitive protein (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0680 HI0680 Haemophilus influenzae 727 -11537435 5500686338 hi0680 (de:hypothetical protein hi0680) (db:swissprot) Y680_HAEIN Q57389 HAEMOPHILUS INFLUENZAE 727 -11537435 166053 rard protein homolog hi0680 (cl:escherichia coli rard protein) (db:pir2.dat) I64085 I64085 Haemophilus influenzae 727 -11537435 7500895461 hi0680 rard protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to sp:p27844 percent ident: 27.15;) (le:7895) (re:8791) (di:complement) U32750 U32750 g1573680 Haemophilus influenzae Rd 71421 -11537435 5000695311 (de:(hi0680) (pn:chloramphenicol-sensitive protein:rard) (gn:rard) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0680 HI0680 Haemophilus influenzae 727 10088065

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884048	14921	37077	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884050	14922	37078	1803	600

Description

6500733578 tagd:hi0751 toxr regulon (gtcfc:14.2) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0751 HI0751 Haemophilus influenzae 727 -11537436 4000709882 tpx:hi0751 (ec:1.11.1.-) (de:probable thiol peroxidase,) (db:swissprot) TPX_HAEIN Q57549 HAEMOPHILUS INFLUENZAE 727 -11537436 167196 thiol peroxidase (cl:thiol peroxidase) (ec:1.11.1.-) (db:pir2.dat) G64090 G64090 Haemophilus influenzae 727 -11537436 7500893342 hi0751 thiol peroxidase tpx (db:genpept-bct1) (de:haemophilus influenzae rd section 74 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1742169 pid:1742181) (le:1971) (re:2468) (di:complement) U32759 U32759 g1573759 Haemophilus influenzae Rd 71421 -11537436 5000695312 (de:(hi0751) (pn:toxr regulon:tagd) (gn:tagd) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0751 HI0751 Haemophilus influenzae 727 10088305

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884064	14923	37079	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884072	14924	37080	1008	335

Description

6500733579 msga:hi0896 suppressor protein (gtcfc:10.2:12.13) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0896 HI0896 Haemophilus influenzae 727 -11537437 5500686445 hi0896 (de:hypothetical protein hi0896) (db:swissprot) Y896_HAEIN Q57434 HAEMOPHILUS INFLUENZAE 727 -11537437 167181 hypothetical protein hi0896 (db:pir2.dat) I64100 I64100 Haemophilus influenzae 727 -11537437 7500895630 hi0896 cell division protein ftsn (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p29131 gb:l14281 pid:290448) (le:9133) (re:9747) (di:direct) U32771 U32771 g1573915 Haemophilus influenzae Rd 71421 -11537437 5000695313 (de:(hi0896) (pn:suppressor protein:msga) (gn:msga) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0896 HI0896 Haemophilus influenzae 727 10088300

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884074	14925	37081	1422	473

Description

6500733580 skp:hi0916 export factor homolog (gtcfc:12.6:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0916 HI0916 Haemophilus influenzae 727 -11537438 4000708218 hi0916 (de:hypothetical protein hi0916 precursor) (db:swissprot) Y916_HAEIN Q57483 HAEMOPHILUS INFLUENZAE 727 -11537438 166124 skp skp protein (db:pir2.dat) E64102 E64102 Haemophilus influenzae 727 -11537438 7500895668 hi0916 outer membrane protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 88 of 163 of the complete genome.) (nt:similar to pid:1935023 percent ident: 37.58;) (le:3947) (re:4540) (di:complement) U32773 U32773 g1573937 Haemophilus influenzae Rd 71421 -11537438 5000695314 (de:(hi0916) (pn:export factor homolog:skp) (gn:skp) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0916 HI0916 Haemophilus influenzae 727 10088079

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884075	14926	37082	438	145

Description

6500733581 suhb:hi0937 extragenic suppressor protein homolog (gtcfc:14.3:12.13) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0937 HI0937 Haemophilus influenzae 727 -11537439 99829 suhb:hi0937 (de:extragenic suppressor protein suhb homolog) (db:swissprot) SUHB_HAEIN P44333 HAEMOPHILUS INFLUENZAE 727 -11537439 166125 suhb suppressor protein suhb (cl:suppressor protein suhb) (db:pir2.dat) F64103 F64103 Haemophilus influenzae 727 -11537439 7500892241 hi0937 extragenic suppressor suhb (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to gb:m34828 sp:p22783 pid:147899 gb:u00096) (le:8754) (re:9557) (di:complement) U32775 U32775 g1573958 Haemophilus influenzae Rd 71421 -11537439 5000695315 (de:(hi0937) (pn:extragenic suppressor protein homolog:extragenic suppressor:suhb) (gn:suhb) (gtcfc:13.7) (ec:) (suhb_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0937 HI0937 Haemophilus influenzae 727 10041684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884088	14927	37083	399	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884114	14928	37084	441	146

Description

6500733582 smpb:hi0981 small protein b homolog (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0981 HI0981 Haemophilus influenzae 727 -11537440 98687 smpb:hi0981 (de:small protein b homolog) (db:swissprot) SMPB_HAEIN P44967 HAEMOPHILUS INFLUENZAE 727 -11537440 167168 smpb small protein smpb (cl:small protein smpb) (db:pir2.dat) B64106 B64106 Haemophilus influenzae 727 -11537440 7500891746 hi0981 small protein b smpb (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:similar to gb:d12501 sp:p32052 pid:216668) (le:78) (re:563) (di:complement) U32779 U32779 g1574010 Haemophilus influenzae Rd 71421 -11537440 5000695316 (de:(hi0981) (pn:small protein b homolog:small protein:smpb) (gn:smpb) (gtcfc:13.7) (ec:) (smpb_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI0981 HI0981 Haemophilus influenzae 727 10040562

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884124	14929	37085	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884126	14930	37086	885	294

Description

5000695317 glyoxylate-induced protein (gtcfc:2.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1013 HI1013 Haemophilus influenzae 727 -11537441 118318 hi1013 (de:hypothetical protein hi1013) (db:swissprot) YGBM_HAEIN Q57151 HAEMOPHILUS INFLUENZAE 727 -11537441 166173 hypothetical protein hi1013 (cl:conserved hypothetical protein hi1013) (db:pir2.dat) C64108 C64108 Haemophilus influenzae 727 -11537441 7500924037 hi1013 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to pid:882632 gb:u00096 sp:q46891) (le:2891) (re:3667) (di:direct) U32782 U32782 g1574045 Haemophilus influenzae Rd 71421 -11537441 6500733583 glyoxylate-induced protein (gtcfc:2.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1013 HI1013 Haemophilus influenzae 727 -11537441

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884135	14931	37087	1230	409

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884137	14932	37088	978	325

Description

6500733584 gltl:sfpo:hi1078 glutamate/aspartate transport atp-binding protein:surfactin (gtcfc:12.1:13.3) (keggfc:11.1) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1078 HI1078 Haemophilus influenzae 727 -11537442 74127 gltl:hi1078 (de:glutamate/aspartate transport atp-binding protein gltl) (db:swissprot) GLTL_HAEIN P45022 HAEMOPHILUS INFLUENZAE 727 -11537442 153039 abc-type transport protein hi1078:surfactin homolog (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) G64181 G64181 Haemophilus influenzae 727 -11537442 7500882560 hi1078 amino acid abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to sp:p39456 percent ident: 62.90;) (le:2996) (re:3769) (di:complement) U32788 U32788 g1574632 Haemophilus influenzae Rd 71421 -11537442 5000695318 (de:(hi1078) (pn:glutamate:surfactin:sfpo) (gn:gltl) (gtcfc:13.7) (ec:) (gltl_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1078 HI1078 Haemophilus influenzae 727 10016657

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884142	14933	37089	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884143	14934	37090	549	182

Description

5000695319 ilv-related protein:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1117 HI1117 Haemophilus influenzae 727 -11537443 113264 hi1117 (de:hypothetical protein hi1117) (db:swissprot) YIFB_HAEIN P45049 HAEMOPHILUS INFLUENZAE 727 -11537443 166919 conserved hypothetical protein hi1117 (cl:conserved hypothetical protein hi1117) (db:pir2.dat) I64183 I64183 Haemophilus influenzae 727 -11537443 7500937422 hi1117 competence protein comm (db:genpept-bct1) (de:haemophilus influenzae rd section 106 of 163 of the completegenome.) (nt:similar to gb:m37337 sp:p22787 pid:147774) (le:9299) (re:10828) (di:complement) U32791 U32791 g1574671 Haemophilus influenzae Rd 71421 -11537443 6500733585 ilv-related protein:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1117 HI1117 Haemophilus influenzae 727 -11537443

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884144	14935	37091	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884158	14936	37092	2709	902

Description

6500733586 lapb:hi1119 membrane protein (gtcfc:11.1) (keggfc:11.1) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1119 HI1119 Haemophilus influenzae 727 -11537444 5500686474 hi1119 (de:hypothetical protein hi1119) (db:swissprot) YB19_HAEIN Q57273 HAEMOPHILUS INFLUENZAE 727 -11537444 166981 membrane protein lapb homolog hi1119 (cl:conserved hypothetical protein hi0461) (db:pir2.dat) A64184 A64184 Haemophilus influenzae 727 -11537444 7500896329 hi1119 membrane protein lapb (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:similar to sp:p32181 gb:m59210 pid:387858 percent) (le:798) (re:1676) (di:direct) U32792 U32792 g1574674 Haemophilus influenzae Rd 71421 -11537444 5000695320 (de:(hi1119) (pn:membrane protein:lapb) (gn:lapb) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1119 HI1119 Haemophilus influenzae 727 10088242

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884168	14937	37093	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884171	14938	37094	831	276

Description

6500733587 cydc:hi1156 transport atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1156 HI1156 Haemophilus influenzae 727 -11537445 67473 cydc:hi1156 (de:transport atp-binding protein cydc) (db:swissprot) CYDC_HAEIN P45081 HAEMOPHILUS INFLUENZAE 727 -11537445 167222 probable atp-binding transport protein hi1156 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) E64186 E64186 Haemophilus influenzae 727 -11537445 7500879838 hi1156 transport atp-binding protein cydc (db:genpept-bct1) (de:haemophilus influenzae rd section 110 of 163 of the completegenome.) (nt:similar to gb:l10383 sp:p23886 gb:l25859 pid:145165) (le:4623) (re:6353) (di:complement) U32795 U32795 g1574713 Haemophilus influenzae Rd 71421 -11537445 5000695321 (de:(hi1156) (pn:transport atp-binding protein :transport atp-binding protein:cydc) (gn:cydc) (gtcfc:13.7) (ec:) (cydc_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1156 HI1156 Haemophilus influenzae 727 10010072

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884174	14939	37095	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884182	14940	37096	1131	376

Description

5000695322 15 kda protein:p15:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1161 HI1161 Haemophilus influenzae 727 -11537446 110225 hi1161 (de:hypothetical protein hi1161) (db:swissprot) YBDB_HAEIN P45083 HAEMOPHILUS INFLUENZAE 727 -11537446 165958 conserved hypothetical protein hi1161 (db:pir2.dat) A64187 A64187 Haemophilus influenzae 727 -11537446 7500896615 hi1161 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 111 of 163 of the completegenome.) (nt:similar to gb:m24143 sp:p15050 pid:450383) (le:1141) (re:1557) (di:complement) U32796 U32796 g1574088 Haemophilus influenzae Rd 71421 -11537446 6500733588 15 kda protein:p15:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1161 HI1161 Haemophilus influenzae 727 -11537446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884189	14941	37097	1455	484

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884190	14942	37098	1326	441

Description

6500733589 nifs:hi1295 nitrogen fixation protein (gtcfc:2.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1295 HI1295 Haemophilus influenzae 727 -11537447 167038 nifs protein homolog hi1295 (cl:nifs protein) (db:pir2.dat) I64114 I64114 Haemophilus influenzae 727 -11537447 7500960720 hi1295 nifs protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to pid:882705 gb:u00096 pid:1789175 percent) (le:4957) (re:6270) (di:complement) U32809 U32809 g1574753 Haemophilus influenzae Rd 71421 -11537447 5000695323 (de:(hi1295) (pn:nitrogen fixation protein:nifs) (gn:nifs) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1295 HI1295 Haemophilus influenzae 727 10088264

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884210	14943	37099	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884223	14944	37100	273	90

Description

6500733590 parb:hi1296 partitioning system protein (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1296 HI1296 Haemophilus influenzae 727 -11537448 5500686490 hi1296 (de:hypothetical protein hi1296 precursor) (db:swissprot) YC96_HAEIN Q57519 HAEMOPHILUS INFLUENZAE 727 -11537448 167070 parb protein homolog (cl:micrococcal nuclease) (db:pir2.dat) A64115 A64115 Haemophilus influenzae 727 -11537448 7500921529 hi1296 nuclease:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to sp:p29769 percent ident: 46.62;) (le:6104) (re:6640) (di:complement) U32809 U32809 g1574754 Haemophilus influenzae Rd 71421 -11537448 5000695324 (de:(hi1296) (pn:partitioning system protein:parb) (gn:parb) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1296 HI1296 Haemophilus influenzae 727 10088277

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884240	14945	37101	723	240

Description

5000695325 embryonic abundant protein:group 3 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1339 HI1339 Haemophilus influenzae 727 -11537449 166116 embryonic abundant protein group 3 homolog hi1339 (db:pir2.dat) F64117 F64117 Haemophilus influenzae 727 -11537449 7500960652 hi1339 h. influenzae predicted coding region hi1339 (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3043) (re:3432) (di:direct) U32813 U32813 g1574799 Haemophilus influenzae Rd 71421 -11537449 6500733591 embryonic abundant protein:group 3 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1339 HI1339 Haemophilus influenzae 727 -11537449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884245	14946	37102	1191	396

Description

GTC ORF with score 621 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8084.) (nt:weak similarity to nifr3 protein (r. capsulatus,) (le:25218) (re:27047) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884251	14947	37103	447	148

Description

6500733592 nifs:hi1343 nitrogen fixation protein (gtcfc:2.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1343 HI1343 Haemophilus influenzae 727 -11537450 167037 nifs protein homolog hi1343 (db:pir2.dat) G64117 G64117 Haemophilus influenzae 727 -11537450 7500960721 hi1343 h. influenzae predicted coding region hi1343 (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5476) (re:6192) (di:complement) U32813 U32813 g1574801 Haemophilus influenzae Rd 71421 -11537450 5000695326 (de:(hi1343) (pn:nitrogen fixation protein:nifs) (gn:nifs) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1343 HI1343 Haemophilus influenzae 727 10088263

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884265	14948	37104	660	219

Description

6500733593 tran:hi1407 tran protein (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1407 HI1407 Haemophilus influenzae 727 -11537451 167197 hypothetical protein hi1407 (db:pir2.dat) B64122 B64122 Haemophilus influenzae 727 -11537451 7500960686 hi1407 tran-related protein (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:similar to gb:l10330 pid:437700 percent ident:) (le:9045) (re:10388) (di:complement) U32820 U32820 g1574238 Haemophilus influenzae Rd 71421 -11537451 5000695327 (de:(hi1407) (pn:protein:tran protein:tran) (gn:tran) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1407 HI1407 Haemophilus influenzae 727 10088306

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884276	14949	37105	1716	571

Description

6500733594 nifc:hi1475 nitrogenase c (gtcfc:2.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1475 HI1475 Haemophilus influenzae 727 -11537452 167042 nifc protein homolog (cl:nifc protein) (db:pir2.dat) A64126 A64126 Haemophilus influenzae 727 -11537452 7500960719 hi1475 h. influenzae predicted coding region hi1475 (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8176) (re:8535) (di:complement) U32825 U32825 g1574316 Haemophilus influenzae Rd 71421 -11537452 5000695328 (de:(hi1475) (pn:nitrogenase c:nifc) (gn:nifc) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1475 HI1475 Haemophilus influenzae 727 10088268

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884281	14950	37106	603	200

Description

5000695329 heterocyst maturation protein:deva:hypothetical abc transporter atp-binding protein hi1549 (gtcfc:12.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1549 HI1549 Haemophilus influenzae 727 -11537453 110199 hi1549 (de:hypothetical abc transporter atp-binding protein hi1549) (db:swissprot) YBBA_HAEIN P45247 HAEMOPHILUS INFLUENZAE 727 -11537453 166191 probable abc-type transport protein hi1549 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) A64129 A64129 Haemophilus influenzae 727 -11537453 7500896561 hi1549 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75957 pid:1787361 percent) (le:4687) (re:5370) (di:complement) U32830 U32830 g1574394 Haemophilus influenzae Rd 71421 -11537453 6500733595 heterocyst maturation protein:deva:hypothetical abc transporter atp-binding protein hi1549 (gtcfc:12.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1549 HI1549 Haemophilus influenzae 727 -11537453

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884290	14951	37107	1374	457

Description

5000695330 vancomycin resistance protein:vanh:transposon tn1546:putative 2-hydroxyacid dehydrogenase (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1556 HI1556 Haemophilus influenzae 727 -11537454 111776 hi1556 (de:putative 2-hydroxyacid dehydrogenase hi1556) (db:swissprot) YF56_HAEIN P45250 HAEMOPHILUS INFLUENZAE 727 -11537454 167262 probable phosphoglycerate dehydrogenase homolog (db:pir2.dat) F64129 F64129 Haemophilus influenzae 727 -11537454 7500923258 hi1556 2-hydroxyacid dehydrogenase (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:ae000511 pid:2313177 percent) (le:11172) (re:12119) (di:complement) U32830 U32830 g1574400 Haemophilus influenzae Rd 71421 -11537454 6500733596 vancomycin resistance protein:vanh:transposon tn1546:putative 2-hydroxyacid dehydrogenase (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1556 HI1556 Haemophilus influenzae 727 -11537454

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884305	14952	37108	321	106

Description

6500733597 ftsk:spoiiie:hi1592 sporulation protein:cell division protein homolog (gtcfc:12.15:12.8) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1592 HI1592 Haemophilus influenzae 727 -11537455 72457 ftsk:hi1592 (de:cell division protein ftsk homolog) (db:swissprot) FTSK_HAEIN P45264 HAEMOPHILUS INFLUENZAE 727 -11537455 167177 sporulation protein spoiiie (db:pir2.dat) G64131 G64131 Haemophilus influenzae 727 -11537455 7500881839 hi1592 cell division protein ftsk-related protein (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:similar to sp:p46889 pid:1004225 gb:u00096) (le:4317) (re:5906) (di:complement) U32833 U32833 g1574437 Haemophilus influenzae Rd 71421 -11537455 5000695331 (de:(hi1592) (pn:cell division protein homolog:sporulation protein:spoiiie) (gn:ftsk) (gtcfc:13.7) (ec:) (ftsk_haein) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1592 HI1592 Haemophilus influenzae 727 10015008

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884309	14953	37109	735	244

Description

5000695332 membrane associated atpase:cbio:hypothetical abc transporter atp-binding protein hi1618 (gtcfc:11.1:12.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1618 HI1618 Haemophilus influenzae 727 -11537456 112046 hi1618 (de:hypothetical abc transporter atp-binding protein hi1618) (db:swissprot) YG18_HAEIN P45275 HAEMOPHILUS INFLUENZAE 727 -11537456 166979 atp-binding transport protein homolog hi1618 (cl:atp-binding cassette homology) (db:pir2.dat) A64133 A64133 Haemophilus influenzae 727 -11537456 7500923630 hi1618 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:similar to gb:ae000666 percent ident: 39.29;) (le:6044) (re:6697) (di:complement) U32835 U32835 g1574464 Haemophilus influenzae Rd 71421 -11537456 6500733598 membrane associated atpase:cbio:hypothetical abc transporter atp-binding protein hi1618 (gtcfc:11.1:12.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1618 HI1618 Haemophilus influenzae 727 -11537456

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884335	14954	37110	1257	418

Description

GTC ORF with score 735 to: (db:genpept) (de:aureobasidium pullulans multidrug resistance protein 1 (mdr1) gene,promoter region and complete cds.) (nt:atp-binding cassette (abc) transporter protein) (le:542) (re:4450) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884342	14955	37111	3378	1125

Description

6500733599 fino:hi1670 conjugative transfer co-repressor (gtcfc:11.1:12.13) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1670 HI1670 Haemophilus influenzae 727 -11537457 4000708222 hi1670 (de:hypothetical protein hi1670) (db:swissprot) YOBE_HAEIN Q57119 HAEMOPHILUS INFLUENZAE 727 -11537457 166064 hypothetical protein hi1670 (db:pir2.dat) G64135 G64135 Haemophilus influenzae 727 -11537457 7500923962 hi1670 h. influenzae predicted coding region hi1670 (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2340) (re:2813) (di:complement) U32840 U32840 g1574528 Haemophilus influenzae Rd 71421 -11537457 5000695333 (de:(hi1670) (pn:conjugative transfer co-repressor:fino) (gn:fino) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1670 HI1670 Haemophilus influenzae 727 10088068

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884347	14956	37112	537	178

Description

GTC ORF with score 208 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884364	14957	37113	1194	397

Description

6500733600 rnfe:hi1686 nitrogen fixation protein (gtcfc:2.6) (keggfc:14.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI1686 HI1686 Haemophilus influenzae 727 -11537458 5500686525 hi1686 (de:hypothetical protein hi1686) (db:swissprot) YDGO_HAEIN Q57288 HAEMOPHILUS INFLUENZAE 727 -11537458 167041 rnfd protein homolog hi1686 (db:pir2.dat) F64136 F64136 Haemophilus influenzae 727 -11537458 7500922312 hi1686 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p76182 pid:1787917 percent) (le:10329) (re:11405) (di:direct) U32841 U32841 g1574538 Haemophilus influenzae Rd 71421 -11537458 5000695334 (de:(hi1686) (pn:nitrogen fixation protein:rnfe) (gn:rnfe) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.7) (db:gtc-haemophilus influenzae)) HI1686 HI1686 Haemophilus influenzae 727 10088267

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884366	14958	37114	1059	352

Description

6500733601 opsx:hi0261 lipopolysaccharide biosynthesis protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0261 HI0261 Haemophilus influenzae 727 -11537459 166956 saccharide biosynthesis regulatory protein opsx homolog (db:pir2.dat) B64058 B64058 Haemophilus influenzae 727 -11537459 7500960733 hi0261 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 27 of 163 of the complete genome.) (nt:similar to gb:l21026 pid:311045 percent identity:) (le:1470) (re:2513) (di:direct) U32712 U32712 g1573227 Haemophilus influenzae Rd 71421 -11537459 5000694672 (de:(hi0261) (pn:lipopolysaccharide biosynthesis protein:opsx) (gn:opsx) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI0261 HI0261 Haemophilus influenzae 727 10088214

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884367	14959	37115	1104	367

Description

6500733602 lex1:hi0550 lipooligosaccharide biosynthesis protein:lipooligosaccharide biosynthesis protein lex-1 (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0550 HI0550 Haemophilus influenzae 727 -11537460 81973 lex1:lic2a:hi0550 (de:lipooligosaccharide biosynthesis protein lex-1) (db:swissprot) LEX1_HAEIN Q03974 HAEMOPHILUS INFLUENZAE 727 -11537460 166954 lic2a lipopolysaccharide biosynthesis protein lic2a (cl:lipopolysaccharide biosynthesis-associated protein) (db:pir2.dat) A64077 A64077 Haemophilus influenzae 727 -11537460 7500884969 hi0550 lipooligosaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to gb:x56903 gb:l19441 percent ident:) (le:10768) (re:11676) (di:complement) U32736 U32736 g1573535 Haemophilus influenzae Rd 71421 -11537460 5000694673 (de:(hi0550) (pn:lipooligosaccharide biosynthesis protein lex-1:lipooligosaccharide biosynthesis protein) (gn:lex1) (gtcfc:11.2) (ec:) (lex1_haein) (keggfc:11.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI0550 HI0550 Haemophilus influenzae 727 10024207

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884380	14960	37116	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884381	14961	37117	513	170

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884416	14962	37118	2256	751

Description

6500733603 kdtb:hi0651 lipopolysaccharide core biosynthesis protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0651 HI0651 Haemophilus influenzae 727 -11537461 80603 kdtb:hi0651 (de:lipopolysaccharide core biosynthesis protein kdtb) (db:swissprot) KDTB_HAEIN P44805 HAEMOPHILUS INFLUENZAE 727 -11537461 166958 kdtb kdtb protein (cl:lipopolysaccharide core biosynthesis protein kdtb) (db:pir2.dat) E64084 E64084 Haemophilus influenzae 727 -11537461 7500884578 hi0651 lipopolysaccharide core biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to sp:p23875 gb:m60670 gb:m86305 pid:146544) (le:4199) (re:4669) (di:complement) U32748 U32748 g1573650 Haemophilus influenzae Rd 71421 -11537461 5000694674 (de:(hi0651) (pn:lipopolysaccharide core biosynthesis protein :lipopolysaccharide core biosynthesis protein:kdtb) (gn:kdtb) (gtcfc:11.2) (ec:) (kdtb_haein) (keggfc:11.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI0651 HI0651 Haemophilus influenzae 727 10022845

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884418	14963	37119	1392	464

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884445	14964	37120	1536	511

Description

6500733604 kdta:hi0652 3-deoxy-d-manno-octulosonic-acid transferase:kdo transferase (gtcfc:11.2) (ec:2.-.-.-) (keggfc:14.1) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0652 HI0652 Haemophilus influenzae 727 -11537462 80601 kdta:hi0652 (ec:2.-.-.-) (de:transferase)) (db:swissprot) KDTA_HAEIN P44806 HAEMOPHILUS INFLUENZAE 727 -11537462 165966 3-deoxy-d-manno-octulosonic acid transferase (ec:2.-.-.-) (db:pir2.dat) F64084 F64084 Haemophilus influenzae 727 -11537462 7500884576 hi0652 3-deoxy-d-manno-octulosonic-acid transferase (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to sp:p23282 gb:m60670 gb:m86305 pid:146543) (le:4666) (re:5949) (di:complement) U32748 U32748 g1573651 Haemophilus influenzae Rd 71421 -11537462 5000694675 (de:(hi0652) (pn:3-deoxy-d-manno-octulosonic-acid transferase:kdo transferase:3-deoxy-d-manno-octulosonic-acid transferase:kdta) (gn:kdta) (gtcfc:11.2) (ec:2.-.-.-) (kdta_haein) (keggfc:11.1) (tigrfc:3.3) (db:gtc-haemophilus inf) HI0652 HI0652 Haemophilus influenzae 727 10022843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884458	14965	37121	2028	676

Description

GTC ORF with score 542 to: (sr:baker's yeast) (db:genpept-pln1) (de:s.cerevisiae chromosome xi (20.7 kb) dna for hsp70 homologue(a881), nucleoside diphosphate kinase homologue (a153), nuclearpore complex protein nup100 (b959), trna-trp, trna-val, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884464	14966	37122	561	186

Description

5000694676 lipooligosaccharide biosynthesis protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0765 HI0765 Haemophilus influenzae 727 -11537463 5500686381 hi0765 (de:hypothetical protein hi0765) (db:swissprot) Y765_HAEIN Q57125 HAEMOPHILUS INFLUENZAE 727 -11537463 166955 lipopolysaccharide biosynthesis protein lic2b homolog (cl:lipopolysaccharide biosynthesis-associated protein) (db:pir2.dat) F64091 F64091 Haemophilus influenzae 727 -11537463 7500895499 hi0765 lipooligosaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to gb:m37913 gb:l19441 pid:1573535 percent) (le:8570) (re:9418) (di:direct) U32760 U32760 g1573773 Haemophilus influenzae Rd 71421 -11537463 6500733605 lipooligosaccharide biosynthesis protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0765 HI0765 Haemophilus influenzae 727 -11537463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884493	14967	37123	468	155

Description

6500733606 rfbp:hi0872 undecaprenyl-phosphate galactosephosphotransferase (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0872 HI0872 Haemophilus influenzae 727 -11537464 4000708217 hi0872 (ec:2.-.-.-) (de:hypothetical sugar transferase hi0872,) (db:swissprot) Y872_HAEIN Q57491 HAEMOPHILUS INFLUENZAE 727 -11537464 167248 undecaprenyl-phosphate galactosephosphotransferase (ec:2.7.8.6) (db:pir2.dat) B64099 B64099 Haemophilus influenzae 727 -11537464 7500895581 hi0872 undecaprenyl-phosphate (db:genpept-bct1) (de:haemophilus influenzae rd section 84 of 163 of the complete genome.) (nt:similar to sp:p26406 gb:x52093 pid:1335815) (le:1570) (re:2985) (di:direct) U32769 U32769 g1573890 Haemophilus influenzae Rd 71421 -11537464 5000694677 (de:(hi0872) (pn:undecaprenyl-phosphate galactosephosphotransferase:rfbp) (gn:rfbp) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI0872 HI0872 Haemophilus influenzae 727 10088322

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884497	14968	37124	402	134

Description

6500733607 rfaf:hi1105 adp-heptose-lps heptosyltransferase ii:adp-heptose--lps heptosyltransferase ii (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1105 HI1105 Haemophilus influenzae 727 -11537465 94121 rfaf:hi1105 (de:adp-heptose--lps heptosyltransferase ii) (db:swissprot) RFAF_HAEIN P45042 HAEMOPHILUS INFLUENZAE 727 -11537465 165987 adp-heptose--lps heptosyltransferase ii (cl:adp-heptose--lps heptosyltransferase ii) (db:pir2.dat) G64182 G64182 Haemophilus influenzae 727 -11537465 7500889672 hi1105 adp-heptose--lps heptosyltransferase ii rfaf (db:genpept-bct1) (de:haemophilus influenzae rd section 105 of 163 of the completegenome.) (nt:similar to sp:p37692 pid:466758 gb:u00096) (le:5135) (re:6175) (di:complement) U32790 U32790 g1574659 Haemophilus influenzae Rd 71421 -11537465 5000694678 (de:(hi1105) (pn:adp-heptose--lps heptosyltransferase ii:adp-heptose-lps heptosyltransferase ii:rfaf) (gn:rfaf) (gtcfc:11.2) (ec:) (rfaf_haein) (keggfc:11.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI1105 HI1105 Haemophilus influenzae 727 10036104

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884502	14969	37125	255	84

Description

6500733608 lica:hi1537 lic-1 operon protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1537 HI1537 Haemophilus influenzae 727 -11537466 166944 lica lic-1 phase variation protein a (db:pir2.dat) B64128 B64128 Haemophilus influenzae 727 -11537466 7500960707 hi1537 lic-1 operon protein lica (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:m27280 sp:p14181 gb:m37912) (le:4052) (re:4855) (di:direct) U32829 U32829 g1574379 Haemophilus influenzae Rd 71421 -11537466 5000694679 (de:(hi1537) (pn:lic-1 operon protein:lica) (gn:lica) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI1537 HI1537 Haemophilus influenzae 727 10088208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884537	14970	37126	1353	450

Description

6500733609 licb:hi1538 lic-1 operon protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1538 HI1538 Haemophilus influenzae 727 -11537467 5000694680 licb:hi1538 (de:licb protein) (db:swissprot) LICB_HAEIN P14182 HAEMOPHILUS INFLUENZAE 727 -11537467 166945 licb lic-1 protein b (db:pir2.dat) C64128 C64128 Haemophilus influenzae 727 -11537467 7500960708 hi1538 lic-1 operon protein licb (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:m27280 sp:p14182 percent ident:) (le:4855) (re:5733) (di:direct) U32829 U32829 g1574380 Haemophilus influenzae Rd 71421 -11537467

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884545	14971	37127	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884547	14972	37128	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884569	14973	37129	828	275

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884591	14974	37130	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884602	14975	37131	399	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884603	14976	37132	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884611	14977	37133	492	163

Description

6500733610 licc:hi1539 lic-1 operon protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1539 HI1539 Haemophilus influenzae 727 -11537468 166946 licc lic-1 protein c (db:pir2.dat) D64128 D64128 Haemophilus influenzae 727 -11537468 7500960709 hi1539 lic-1 operon protein licc (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:m27280 sp:p14183 percent ident:) (le:5730) (re:6431) (di:direct) U32829 U32829 g1574381 Haemophilus influenzae Rd 71421 -11537468 5000694681 (de:(hi1539) (pn:lic-1 operon protein:licc) (gn:licc) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI1539 HI1539 Haemophilus influenzae 727 10088210

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884617	14978	37134	1698	565

Description

6500733611 licd:hi1540 lic-1 operon protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1540 HI1540 Haemophilus influenzae 727 -11537469 166947 licd lic-1 protein d (db:pir2.dat) E64128 E64128 Haemophilus influenzae 727 -11537469 7500960710 hi1540 lic-1 operon protein licd (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:m27280 sp:p14184 percent ident:) (le:6431) (re:7228) (di:direct) U32829 U32829 g1574382 Haemophilus influenzae Rd 71421 -11537469 5000694682 (de:(hi1540) (pn:lic-1 operon protein:licd) (gn:licd) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI1540 HI1540 Haemophilus influenzae 727 10088211

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884619	14979	37135	312	103

Description

GTC ORF with score 182 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f28j12 (essaiiproject).) (nt:similarity to cdc28p, schizosaccharomyces pombe,) (le:52300:52853:53005:53159) (re:52464:52957:53074:53223) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884623	14980	37136	201	66

Description

5000694683 polysialic acid capsule expression protein:kpsf:hypothetical protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1678 HI1678 Haemophilus influenzae 727 -11537470 116110 hi1678 (de:hypothetical protein hi1678) (db:swissprot) YRBH_HAEIN P45313 HAEMOPHILUS INFLUENZAE 727 -11537470 167097 kpsf protein homolog (cl:probable atp-binding protein gutq) (db:pir2.dat) C64136 C64136 Haemophilus influenzae 727 -11537470 7500952622 hi1678 kpsf protein kpsf (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:l19929 sp:p42502 pid:455424 percent) (le:524) (re:1537) (di:direct) U32841 U32841 g1574530 Haemophilus influenzae Rd 71421 -11537470 6500733612 polysialic acid capsule expression protein:kpsf:hypothetical protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1678 HI1678 Haemophilus influenzae 727 -11537470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884628	14981	37137	1014	337

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884635	14982	37138	960	319

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884647	14983	37139	324	107

Description

5000694684 adhesin b precursor:fima:hypothetical protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0119 HI0119 Haemophilus influenzae 727 -11537471 108777 znua:hi0119 (de:high-affinity zinc uptake system protein znua) (db:swissprot) ZNUA_HAEIN P44526 HAEMOPHILUS INFLUENZAE 727 -11537471 165985 adhesin homolog hi0119 (cl:hypothetical protein hi0119) (db:pir2.dat) D64049 D64049 Haemophilus influenzae 727 -11537471 7500894735 hi0119 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p39172 pid:1736500) (le:2168) (re:3181) (di:direct) U32698 U32698 g1573074 Haemophilus influenzae Rd 71421 -11537471 6500733613 adhesin b precursor:fima:hypothetical protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0119 HI0119 Haemophilus influenzae 727 -11537471

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884653	14984	37140	714	237

Description

5000694685 hofc:hopc:hi0297 xcps protein:xcps:protein transport protein hofc homolog (gtcfc:12.6:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0297 HI0297 Haemophilus influenzae 727 -11537472 77454 hofc:hopc:hi0297 (de:protein transport protein hofc homolog) (db:swissprot) HOFC_HAEIN P44621 HAEMOPHILUS INFLUENZAE 727 -11537472 167270 pilus assembly protein pilg homolog (cl:secretion protein xcps) (db:pir2.dat) D64060 D64060 Haemophilus influenzae 727 -11537472 7500883453 hi0297 protein transport protein (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:m32066 sp:p22609 pid:151066 percent) (le:9993) (re:11213) (di:complement) U32715 U32715 g1573265 Haemophilus influenzae Rd 71421 -11537472 6500733614 hofc:hopc xcps protein:xcps:protein transport protein hofc homolog (gtcfc:12.6:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0297 HI0297 Haemophilus influenzae 727 -11537472

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884667	14985	37141	249	82

Description

5000694686 hofb:hopb:pilb:hi0298 pilin biogenesis protein:protein transport protein hofb homolog (gtcfc:12.6:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0298 HI0298 Haemophilus influenzae 727 -11537473 77452 hofb:hopb:hi0298 (de:protein transport protein hofb homolog) (db:swissprot) HOFB_HAEIN P44622 HAEMOPHILUS INFLUENZAE 727 -11537473 167093 pilb protein homolog (cl:secretion protein xcpr) (db:pir2.dat) E64060 E64060 Haemophilus influenzae 727 -11537473 7500883451 hi0298 protein transport protein (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:m32066 sp:p22608 gb:s43866 pid:151065) (le:11210) (re:12604) (di:complement) U32715 U32715 g1573266 Haemophilus influenzae Rd 71421 -11537473 6500733615 hofb:hopb:pilb pilin biogenesis protein:protein transport protein hofb homolog (gtcfc:12.6:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0298 HI0298 Haemophilus influenzae 727 -11537473

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884671	14986	37142	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884687	14987	37143	543	180

Description

6500733616 oapa:hi0330 cell envelope protein:opacity associated proteins (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0330 HI0330 Haemophilus influenzae 727 -11537474 87368 oapa:hi0330 (de:opacity associated proteins oapa) (db:swissprot) OAPA_HAEIN P44415 HAEMOPHILUS INFLUENZAE 727 -11537474 1500685353 oapa cell envelope protein oapa (db:pir2.dat) A64062 A64062 Haemophilus influenzae 727 -11537474 7500887054 oapa oapa (db:genpept-bct1) (de:haemophilus influenzae opacity associated proteins oapa and oapb(oapa and oapb) genes, complete cds, and dna recombination andrepair protein (reco) gene, partial cds.) (nt:opacity associated protein; cell envelope protein;) (le:20... HIU17037 U17037 g595942 Haemophilus influenzae 727 -11537474 241579 hi0330 opacity associated protein oapa (db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the complete genome.) (nt:similar to gb:l42023 sp:p44415 pid:1003551) (le:80) (re:1375) (di:direct) U32718 U32718 g1573300 Haemophilus influenzae Rd 71421 -11537474 166051 oapa cell envelope protein oapa (db:pir) A64062 A64062 Haemophilus influenzae 727 -11537474 5000694687 (de:(hi0330) (pn:opacity associated proteins :cell envelope protein:oapa) (gn:oapa) (gtcfc:11.3) (ec:) (oapa_haein) (keggfc:11.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae)) HI0330 HI0330 Haemophilus influenzae 727 10029511

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884694	14988	37144	993	330

Description

6500733617 oapb:hi0331 opacity associated protein:opacity associated proteins (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0331 HI0331 Haemophilus influenzae 727 -11537475 87369 oapb:hi0331 (de:opacity associated proteins oapb) (db:swissprot) OAPB_HAEIN P44416 HAEMOPHILUS INFLUENZAE 727 -11537475 167050 oapb opacity-associated protein oapb (db:pir2.dat) B64062 B64062 Haemophilus influenzae 727 -11537475 7500887055 hi0331 opacity associated protein oapb (db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the complete genome.) (nt:similar to gb:l42023 sp:p44416 pid:1003553) (le:1435) (re:1839) (di:direct) U32718 U32718 g1573309 Haemophilus influenzae Rd 71421 -11537475 5000694688 (de:(hi0331) (pn:opacity associated proteins :opacity associated protein:oapb) (gn:oapb) (gtcfc:11.3) (ec:) (oapb_haein) (keggfc:11.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae)) HI0331 HI0331 Haemophilus influenzae 727 10029512

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884695	14989	37145	318	105

Description

6500733618 fima:hi0362 adhesin b precursor (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0362 HI0362 Haemophilus influenzae 727 -11537476 165986 probable mn transport protein (cl:adhesin b) (db:pir2.dat) G64063 G64063 Haemophilus influenzae 727 -11537476 7500960726 hi0362 iron chelated abc transporter (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to pid:1245464 percent identity: 74.91;) (le:7287) (re:8168) (di:complement) U32720 U32720 g1573330 Haemophilus influenzae Rd 71421 -11537476 5000694689 (de:(hi0362) (pn:adhesin b precursor:fima) (gn:fima) (gtcfc:11.3) (ec:) (keggfc:11.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae)) HI0362 HI0362 Haemophilus influenzae 727 10088052

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884697	14990	37146	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884698	14991	37147	1143	380

Description

6500733619 opa66:hi0414 opacity protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0414 HI0414 Haemophilus influenzae 727 -11537477 5500686321 hi0414 (de:hypothetical protein hi0414) (db:swissprot) Y414_HAEIN Q57392 HAEMOPHILUS INFLUENZAE 727 -11537477 154062 probable outer membrane protein hi0414:opacity protein homolog (cl:opacity protein) (db:pir2.dat) F64066 F64066 Haemophilus influenzae 727 -11537477 7500895258 hi0414 h. influenzae predicted coding region hi0414 (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:146) (re:358) (di:direct) U32725 U32725 g1573388 Haemophilus influenzae Rd 71421 -11537477 5000694690 (de:(hi0414) (pn:opacity protein:opa66) (gn:opa66) (gtcfc:11.3) (ec:) (keggfc:11.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae)) HI0414 HI0414 Haemophilus influenzae 727 10081355

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884714	14992	37148	279	92

Description

5000694691 mena:hi0509 menaquinone biosynthesis protein:sp:p32166:1:4-dihydroxy-2-naphthoate octaprenyltransferase (gtcfc:9.12) (ec:2.5.-.-) (keggfc:14.1) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0509 HI0509 Haemophilus influenzae 727 -11537478 83437 mena:hi0509 (ec:2.5.1.-) (de:octaprenyltransferase)) (db:swissprot) MENA_HAEIN P44739 HAEMOPHILUS INFLUENZAE 727 -11537478 166436 hypothetical protein hi0509 (cl:hypothetical protein hi0509) (db:pir2.dat) H64153 H64153 Haemophilus influenzae 727 -11537478 7500885476 hi0509 1:4-dihydroxy-2-naphthoate octaprenyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32166 pid:305033 gb:u00096) (le:8699) (re:9625) (di:complement) U32732 U32732 g1573490 Haemophilus influenzae Rd 71421 -11537478 6500733620 mena menaquinone biosynthesis protein:sp:p32166:1:4-dihydroxy-2-naphthoate octaprenyltransferase (gtcfc:9.12) (ec:2.5.-.-) (keggfc:14.1) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0509 HI0509 Haemophilus influenzae 727 -11537478

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884718	14993	37149	1029	342

Description

5000694692 cynate utilization operon positive regulator:cynr:hypothetical transcriptional regulator hi0775 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0775 HI0775 Haemophilus influenzae 727 -11537479 109279 hi0775 (de:hypothetical transcriptional regulator hi0775) (db:swissprot) Y775_HAEIN P44876 HAEMOPHILUS INFLUENZAE 727 -11537479 166067 hypothetical protein hi0775 (db:pir2.dat) C64092 C64092 Haemophilus influenzae 727 -11537479 7500895504 hi0775 transcriptional regulator (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to gb:x73124 sp:p39592 pid:413948) (le:4155) (re:5102) (di:direct) U32761 U32761 g1573785 Haemophilus influenzae Rd 71421 -11537479 6500733621 cynate utilization operon positive regulator:cynr:hypothetical transcriptional regulator hi0775 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0775 HI0775 Haemophilus influenzae 727 -11537479

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884732	14994	37150	1098	365

Description

5000694693 protective surface antigen d15:protective surface antigen d15 precursor:80 kd d15 antigen:d-15-ag (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0917 HI0917 Haemophilus influenzae 727 -11537480 67775 hi0917 (de:(d-15-ag)) (db:swissprot) D152_HAEIN P44935 HAEMOPHILUS INFLUENZAE 727 -11537480 7500879952 hi0917 protective surface antigen d15 (db:genpept-bct1) (de:haemophilus influenzae rd section 88 of 163 of the complete genome.) (nt:similar to gb:u13961 pid:1573938 pid:2231192) (le:4648) (re:7035) (di:complement) U32773 U32773 g1573938 Haemophilus influenzae Rd 71421 -11537480 6500733622 protective surface antigen d15:protective surface antigen d15 precursor:80 kd d15 antigen:d-15-ag (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI0917 HI0917 Haemophilus influenzae 727 -11537480

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884734	14995	37151	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884735	14996	37152	561	186

Description

GTC ORF with score 135 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884737	14997	37153	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884741	14998	37154	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884781	14999	37155	1500	499

Description

6500733623 opa:hi1174 opacity protein:opa66:protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI1174 HI1174 Haemophilus influenzae 727 -11537481 87729 opa:hi1174 (de:opa protein) (db:swissprot) OPA_HAEIN P45088 HAEMOPHILUS INFLUENZAE 727 -11537481 167051 opacity protein homolog hi1174 (db:pir2.dat) I64187 I64187 Haemophilus influenzae 727 -11537481 7500887185 hi1174 opacity protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to gb:x15780 pid:1333789 percent ident:) (le:4933) (re:5298) (di:direct) U32797 U32797 g1574101 Haemophilus influenzae Rd 71421 -11537481 5000694694 (de:(hi1174) (pn:protein:opacity protein:opa66) (gn:opa) (gtcfc:11.3) (ec:) (opa_haein) (keggfc:11.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae)) HI1174 HI1174 Haemophilus influenzae 727 10029871

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884785	15000	37156	606	201

Description

6500733624 opad:hi1457 opacity protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI1457 HI1457 Haemophilus influenzae 727 -11537482 5500686558 hi1457 (de:hypothetical protein hi1457 precursor) (db:swissprot) YE57_HAEIN Q57201 HAEMOPHILUS INFLUENZAE 727 -11537482 167052 opacity protein homolog hi1457 (db:pir2.dat) F64124 F64124 Haemophilus influenzae 727 -11537482 7500922711 hi1457 opacity protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to pid:2367659 percent ident: 34.32;) (le:10454) (re:10990) (di:complement) U32823 U32823 g1574294 Haemophilus influenzae Rd 71421 -11537482 5000694695 (de:(hi1457) (pn:opacity protein:opad) (gn:opad) (gtcfc:11.3) (ec:) (keggfc:11.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae)) HI1457 HI1457 Haemophilus influenzae 727 10088271

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884792	15001	37157	435	144

Description

6500733625 yopa:hi1460 invasin precursor:outer membrane adhesin (gtcfc:11.3:13.8) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI1460 HI1460 Haemophilus influenzae 727 -11537483 166923 hypothetical protein hi1460 (db:pir2.dat) H64124 H64124 Haemophilus influenzae 727 -11537483 5000694696 (de:(hi1460) (pn:invasin precursor:outer membrane adhesin:yopa) (gn:yopa) (gtcfc:11.3) (ec:) (keggfc:11.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae)) HI1460 HI1460 Haemophilus influenzae 727 10088200

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884794	15002	37158	291	97

Description

6500733626 aida-i:hi1732 adhesin (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae) HI1732 HI1732 Haemophilus influenzae 727 -11537484 165984 adhesin homolog hi1732 (db:pir2.dat) I64138 I64138 Haemophilus influenzae 727 -11537484 5000694697 (de:(hi1732) (pn:adhesin:aida-i) (gn:aida-i) (gtcfc:11.3) (ec:) (keggfc:11.2) (tigrfc:3.4) (db:gtc-haemophilus influenzae)) HI1732 HI1732 Haemophilus influenzae 727 10088051

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884796	15003	37159	801	266

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884801	15004	37160	420	139

Description

6500733627 amib:hi0066 n-acetylmuramoyl-l-alanine amidase:probable n-acetylmuramoyl-l-alanine amidase precursor (gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0066 HI0066 Haemophilus influenzae 727 -11537485 59312 amib:hi0066 (ec:3.5.1.28) (de:(ec 3.5.1.28)) (db:swissprot) AMIB_HAEIN P44493 HAEMOPHILUS INFLUENZAE 727 -11537485 167019 n-acetylmuramoyl-l-alanine amidase homolog (db:pir2.dat) D64046 D64046 Haemophilus influenzae 727 -11537485 7500876799 hi0066 n-acetylmuramoyl-l-alanine amidase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 7 of 163 of the complete genome.) (nt:similar to sp:p26365 gb:z11831 pid:304914 pid:42068) (le:552) (re:1850) (di:direct) U32692 U32692 g1573015 Haemophilus influenzae Rd 71421 -11537485 5000694381 (de:(hi0066) (pn:probable n-acetylmuramoyl-l-alanine amidase precursor:n-acetylmuramoyl-l-alanine amidase:amib) (gn:amib) (gtcfc:7.2) (ec:3.5.1.28) (amib_haein) (keggfc:7.3) (tigrfc:3.2) (db:gtc-haemophilus influenzae)) HI0066 HI0066 Haemophilus influenzae 727 10002050

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884812	15005	37161	750	249

Description

6500733628 mray:hi1135 phospho-n-acetylmuramoyl-pentapeptide-transferas e:phospho-n-acetylmuramoyl-pentapeptide-transferase (gtcfc:11.4) (ec:2.7.8.13) (keggfc:7.3) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1135 HI1135 Haemophilus influenzae 727 -11537486 84203 mray:hi1135 (ec:2.7.8.13) (de:(udp-murnac-pentapeptide phosphotransferase)) (db:swissprot) MRAY_HAEIN P45062 HAEMOPHILUS INFLUENZAE 727 -11537486 167091 mray phospho-n-acetylmuramoyl-pentapeptide-transferase (cl:phospho-n-acetylmuramoyl-pentapeptide-transferase) (ec:2.7.8.13) (db:pir2.dat) A64185 A64185 Haemophilus influenzae 727 -11537486 7500885863 hi1135 phospho-n-acetylmuramoyl-pentapeptide- (db:genpept-bct1) (de:haemophilus influenzae rd section 108 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p15876 gb:x51584 pid:216501) (le:6610) (re:7692) (di:direct) U32793 U32793 g1574690 Haemophilus influenzae Rd 71421 -11537486 5000694384 (de:(hi1135) (pn:phospho-n-acetylmuramoyl-pentapeptide-transferase:phospho-n-acetylmuramo yl-pentapeptide-transferas e:mray) (gn:mray) (gtcfc:7.2) (ec:2.7.8.13) (mray_haein) (keggfc:7.3) (tigrfc:3.2) (db:gtc-haemophilus influenza) HI1135 HI1135 Haemophilus influenzae 727 10026404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884817	15006	37162	717	238

Description

6500733629 daca:hi0029 penicillin-binding protein 5:penicillin-binding protein 5 precursor:d-alanyl-d-alanine carboxypeptidase fraction a:dd-peptidase:dd-carboxypeptidase:pbp-5 (gtcfc:11.4:13.3) (ec:3.4.16.4) (keggfc:14.1) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0029 HI0029 Haemophilus influenzae 727 -11537487 67827 daca:hi0029 (ec:3.4.16.4) (de:(dd-carboxypeptidase) (pbp-5)) (db:swissprot) DACA_HAEIN P44466 HAEMOPHILUS INFLUENZAE 727 -11537487 153163 serine-type d-ala-d-ala carboxypeptidase::penicillin-binding protein 5 (cl:penicillin-binding protein 5) (ec:3.4.16.4) (db:pir2.dat) I64043 I64043 Haemophilus influenzae 727 -11537487 7500879966 hi0029 penicillin-binding protein 5 daca (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to sp:p04287 pid:146620 pid:147661) (le:6156) (re:7337) (di:complement) U32688 U32688 g1572974 Haemophilus influenzae Rd 71421 -11537487 5000694698 (de:(hi0029) (pn:penicillin-binding protein 5 precursor:d-alanyl-d-alanine carboxypeptidase fraction a:dd-peptidase:dd-carboxypeptidase:pbp-5:penicillin-binding protein 5:daca) (gn:daca) (gtcfc:11.4) (ec:3.4.16.4) (daca_haein) (k)) HI0029 HI0029 Haemophilus influenzae 727 10010424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884818	15007	37163	441	146

Description

5000694699 mrdb:roda:hi0031 rod shape-determining protein:mreb:rod shape-determining protein roda (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0031 HI0031 Haemophilus influenzae 727 -11537488 95888 mrdb:roda:hi0031 (de:rod shape-determining protein roda) (db:swissprot) RODA_HAEIN P44468 HAEMOPHILUS INFLUENZAE 727 -11537488 154881 rod shape-determining protein mrdb homolog hi0031 (cl:rod shape-determining protein) (db:pir2.dat) B64044 B64044 Haemophilus influenzae 727 -11537488 7500890490 hi0031 rod shape-determining protein roda (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to gb:m22857 sp:p15035 pid:147695 gb:u00096) (le:8268) (re:9383) (di:complement) U32688 U32688 g1572976 Haemophilus influenzae Rd 71421 -11537488 6500733630 mrdb:roda rod shape-determining protein:mreb:rod shape-determining protein roda (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0031 HI0031 Haemophilus influenzae 727 -11537488

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884831	15008	37164	381	126

Description

5000694700 mrda:pbp2:hi0032 pbp2:penicillin-binding protein 2:pbp-2 (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0032 HI0032 Haemophilus influenzae 727 -11537489 88724 mrda:pbp2:hi0032 (de:penicillin-binding protein 2 (pbp-2)) (db:swissprot) PBP2_HAEIN P44469 HAEMOPHILUS INFLUENZAE 727 -11537489 153139 penicillin-binding protein 2 (cl:penicillin-binding protein 3) (db:pir2.dat) C64044 C64044 Haemophilus influenzae 727 -11537489 7500887694 hi0032 penicillin-binding protein 2 pbp2 (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to sp:p08150 gb:x04516 pid:147694 pid:42316) (le:9373) (re:11328) (di:complement) U32688 U32688 g1572977 Haemophilus influenzae Rd 71421 -11537489 6500733631 mrda:pbp2 pbp2:penicillin-binding protein 2:pbp-2 (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0032 HI0032 Haemophilus influenzae 727 -11537489

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884835	15009	37165	576	192

Description

6500733632 mreb:hi0037 rod shape-determining protein (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0037 HI0037 Haemophilus influenzae 727 -11537490 154885 rod shape-determining protein (cl:rod shape-determining protein envb) (db:pir2.dat) E64044 E64044 Haemophilus influenzae 727 -11537490 7500955516 hi0037 rod shape-determining protein mreb (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to sp:p13519 gb:m22055 pid:606191) (le:3781) (re:4917) (di:direct) U32689 U32689 g1572983 Haemophilus influenzae Rd 71421 -11537490 5000694701 (de:(hi0037) (pn:rod shape-determining protein :rod shape-determining protein:mreb) (gn:mreb) (gtcfc:11.4) (ec:) (mreb_haein) (keggfc:11.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae)) HI0037 HI0037 Haemophilus influenzae 727 10081743

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884837	15010	37166	795	264

Description

6500733633 mrec:hi0038 rod shape-determining protein (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0038 HI0038 Haemophilus influenzae 727 -11537491 84209 mrec:hi0038 (de:rod shape-determining protein mrec) (db:swissprot) MREC_HAEIN P44475 HAEMOPHILUS INFLUENZAE 727 -11537491 167150 rod shape-determining protein mrec homolog (db:pir2.dat) F64044 F64044 Haemophilus influenzae 727 -11537491 7500885865 hi0038 rod shape-determining protein mrec (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to gb:m31792 sp:p16926 gb:m22055 pid:146818) (le:4997) (re:6052) (di:direct) U32689 U32689 g1572984 Haemophilus influenzae Rd 71421 -11537491 5000694702 (de:(hi0038) (pn:rod shape-determining protein :rod shape-determining protein:mrec) (gn:mrec) (gtcfc:11.4) (ec:) (mrec_haein) (keggfc:11.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae)) HI0038 HI0038 Haemophilus influenzae 727 10026410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884838	15011	37167	873	290

Description

6500733634 mred:hi0039 rod shape-determining protein (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0039 HI0039 Haemophilus influenzae 727 -11537492 84212 mred:hi0039 (de:rod shape-determining protein mred) (db:swissprot) MRED_HAEIN P44476 HAEMOPHILUS INFLUENZAE 727 -11537492 167151 rod shape-determining protein mred homolog (db:pir2.dat) G64044 G64044 Haemophilus influenzae 727 -11537492 7500885868 hi0039 rod shape-determining protein mred (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to gb:m31792 sp:p16927 pid:146819) (le:6052) (re:6540) (di:direct) U32689 U32689 g1572985 Haemophilus influenzae Rd 71421 -11537492 5000694703 (de:(hi0039) (pn:rod shape-determining protein :rod shape-determining protein:mred) (gn:mred) (gtcfc:11.4) (ec:) (mred_haein) (keggfc:11.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae)) HI0039 HI0039 Haemophilus influenzae 727 10026413

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884840	15012	37168	297	98

Description

6500733635 mepa:hi0197 penicillin-insensitive murein endopeptidase:penicillin-insensitive murein endopeptidase precursor (gtcfc:11.4) (ec:3.4.99.-) (keggfc:14.1) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0197 HI0197 Haemophilus influenzae 727 -11537493 83460 mepa:hi0197 (ec:3.4.99.-) (de:penicillin-insensitive murein endopeptidase precursor,) (db:swissprot) MEPA_HAEIN P44566 HAEMOPHILUS INFLUENZAE 727 -11537493 167072 murein endopeptidase a homolog (db:pir2.dat) H64053 H64053 Haemophilus influenzae 727 -11537493 7500885501 hi0197 penicillin-insensitive murein endopeptidase (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:similar to sp:p14007 pid:41993 gb:u00096) (le:73) (re:933) (di:direct) U32705 U32705 g1573157 Haemophilus influenzae Rd 71421 -11537493 5000694704 (de:(hi0197) (pn:penicillin-insensitive murein endopeptidase precursor:penicillin-insensitive murein endopeptidase:mepa) (gn:mepa) (gtcfc:11.4) (ec:3.4.99.-) (mepa_haein) (keggfc:11.1) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0197 HI0197 Haemophilus influenzae 727 10025674

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884841	15013	37169	591	196

Description

5000694705 pal:ompp6:hi0381 peptidoglycan-associated outer membrane lipoprotein:outer membrane protein p6 precursor:15 kd peptidoglycan-associated lipoprotein (gtcfc:11.2:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0381 HI0381 Haemophilus influenzae 727 -11537494 7500887635 pal:ompp6:hi0381 (de:associated lipoprotein) (pc protein)) (db:swissprot) PAL_HAEIN P10324 HAEMOPHILUS INFLUENZAE 727 -11537494 153428 peptidoglycan-associated lipoprotein precursor:outer membrane protein p6 precursor:protein ompg (cl:outer membrane protein a) (db:pir2.dat) A28543 A28543 Haemophilus influenzae 727 -11537494 241241 (sr:h.influenzae (strain s2, sub-species rb) dna) (db:genpept-bct1) (de:h.influenzae pc protein (15kd peptidoglycan-associated outermembrane lipoprotein), complete cds.) (nt:pc protein precursor) (le:241) (re:702) (di:direct) HEAA15KLP M18878 g148860 Haemophilus influenzae 727 -11537494 241313 (sr:h.influenzae (isolate 1479) dna, clone pbud5) (db:genpept-bct1) (de:h.influenzae outer membrane protein p6 gene, complete cds.) (nt:outer membrane protein p6 precursor) (le:68) (re:529) (di:direct) HEAOMPP6 M19391 g148961 Haemophilus influenzae 727 -11537494 7502852319 hi0381 peptidoglycan-associated outer membrane (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to sp:p10324 pid:1573351 sp:p10324) (le:1733) (re:2194) (di:complement) U32722 U32722 g1573351 Haemophilus influenzae Rd 71421 -11537494 88559 pal:ompp6:hi0381 (de:associated lipoprotein) (pc protein)) (db:swissprot) PAL_HAEIN P10324 HAEMOPHILUS INFLUENZAE 727 -11537494 6500733636 pal:ompp6 peptidoglycan-associated outer membrane lipoprotein:outer membrane protein p6 precursor:15 kd peptidoglycan-associated lipoprotein (gtcfc:11.2:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0381 HI0381 Haemophilus influenzae 727 -11537494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884851	15014	37170	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884870	15015	37171	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884877	15016	37172	927	309

Description

5000694706 mrca:pona:hi0440 penicillin-binding protein:pona:penicillin-binding protein 1a:pbp-1a:penicillin-binding protein a (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0440 HI0440 Haemophilus influenzae 727 -11537495 153113 penicillin-binding protein 1a:orfi protein (cl:penicillin-binding protein) (db:pir2.dat) JH0438 D64068 Haemophilus influenzae 727 -11537495 241338 (fn:possibly involved in the elongation of the) (sr:haemophilus influenzae rd dna) (db:genpept-bct1) (de:haemophilus influenzae transformation gene cluster dna.) (nt:an insertion in orf i causes a modest deficiency in) (le:1068) (re:3662) (di:complement) HEATRANS M62809 g148992 Haemophilus influenzae 727 -11537495 7500955287 hi0440 penicillin-binding protein 1a pona (db:genpept-bct1) (de:haemophilus influenzae rd section 42 of 163 of the complete genome.) (nt:similar to sp:p02918 gb:x02164 pid:581194) (le:80) (re:2674) (di:direct) U32727 U32727 g1573416 Haemophilus influenzae Rd 71421 -11537495 6500733637 mrca:pona penicillin-binding protein:pona:penicillin-binding protein 1a:pbp-1a:penicillin-binding protein a (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0440 HI0440 Haemophilus influenzae 727 -11537495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884886	15017	37173	384	127

Description

6500733638 dacb:hi1330 d-alanyl-d-ala carboxypeptidase:penicillin-binding protein 4 precursor:pbp-4:d-alanyl-d-alanine carboxypeptidase:dd-peptidase:dd-carboxypeptidase / d-alanyl-d-alanine-endopeptidase:dd-endopeptidase (gtcfc:11.4:13.3) (ec:3.4.16.4) (keggfc:14.1) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1330 HI1330 Haemophilus influenzae 727 -11537496 88735 dacb:hi1330 (ec:3.4.16.4) (de:d-alanyl-d-alanine-endopeptidase (dd-endopeptidase)) (db:swissprot) PBP4_HAEIN P45161 HAEMOPHILUS INFLUENZAE 727 -11537496 166079 serine-type d-ala-d-ala carboxypeptidase homolog (db:pir2.dat) A64117 A64117 Haemophilus influenzae 727 -11537496 7500887697 hi1330 d-alanyl-d-alanine (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:similar to sp:p24228 gb:u01376 gb:x59460 gb:x60038) (le:4859) (re:6298) (di:complement) U32812 U32812 g1574789 Haemophilus influenzae Rd 71421 -11537496 5000694707 (de:(hi1330) (pn:penicillin-binding protein 4 precursor:pbp-4:d-alanyl-d- alanine carboxypeptidase:dd-peptidase:dd-carboxypeptidase :d-alanyl-d-ala carboxypeptidase:dacb) (gn:dacb) (gtcfc:11.4) (ec:3.4.16.4) (pbp4_haein) (keggfc:) HI1330 HI1330 Haemophilus influenzae 727 10030862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884893	15018	37174	927	308

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884902	15019	37175	432	143

Description

5000694708 n-acetylmuramoyl-l-alanine amidase (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1494 HI1494 Haemophilus influenzae 727 -11537497 167020 n-acetylmuramoyl-l-alanine amidase homolog (db:pir2.dat) G64126 G64126 Haemophilus influenzae 727 -11537497 7500960715 hi1494 n-acetylmuramoyl-l-alanine amidase (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:similar to sp:p20331 pid:15695 percent ident:) (le:5187) (re:5537) (di:direct) U32826 U32826 g1574326 Haemophilus influenzae Rd 71421 -11537497 6500733639 n-acetylmuramoyl-l-alanine amidase (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1494 HI1494 Haemophilus influenzae 727 -11537497

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884903	15020	37176	522	173

Description

GTC ORF with score 180 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884904	15021	37177	1599	532

Description

GTC ORF with score 307 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884912	15022	37178	585	194

Description

6500733640 prc:hi1668 carboxy-terminal protease:penicillin-binding protein 3:tail-specific protease precursor:protease re (gtcfc:11.4:13.3) (ec:3.4.21.-) (keggfc:14.1) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1668 HI1668 Haemophilus influenzae 727 -11537498 90982 prc:hi1668 (ec:3.4.21.-) (de:tail-specific protease precursor, (protease re)) (db:swissprot) PRC_HAEIN P45306 HAEMOPHILUS INFLUENZAE 727 -11537498 166040 prc carboxy-terminal proteinase (ec:3.4.21.-) (db:pir2.dat) F64135 F64135 Haemophilus influenzae 727 -11537498 7500888432 hi1668 tail specific protease prc (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to gb:d00674 sp:p23865 gb:m75634 gb:s49803) (le:67) (re:2154) (di:complement) U32840 U32840 g1574519 Haemophilus influenzae Rd 71421 -11537498 5000694709 (de:(hi1668) (pn:tail-specific protease precursor:protease re:carboxy-terminal protease, penicillin-binding protein 3:prc) (gn:prc) (gtcfc:11.4) (ec:3.4.21.-) (prc_haein) (keggfc:11.1) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1668 HI1668 Haemophilus influenzae 727 10033091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884915	15023	37179	471	156

Description

5000694710 mrcb:ponb:hi1725 ponb:penicillin-binding protein 1b:pbp-1b (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1725 HI1725 Haemophilus influenzae 727 -11537499 88747 mrcb:ponb:hi1725 (de:penicillin-binding protein 1b (pbp-1b)) (db:swissprot) PBPB_HAEIN P45345 HAEMOPHILUS INFLUENZAE 727 -11537499 167071 penicillin-binding protein 1b homolog (cl:penicillin-binding protein 1b) (db:pir2.dat) D64138 D64138 Haemophilus influenzae 727 -11537499 7500887704 hi1725 penicillin-binding protein 1b ponb (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to gb:d26562 sp:p02919 gb:m12486 gb:x02163) (le:3156) (re:5501) (di:direct) U32845 U32845 g1574581 Haemophilus influenzae Rd 71421 -11537499 6500733641 mrcb:ponb ponb:penicillin-binding protein 1b:pbp-1b (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1725 HI1725 Haemophilus influenzae 727 -11537499

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884926	15024	37180	519	172

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884936	15025	37181	1575	524

Description

6500733642 lepb:hi0015 signal peptidase i:spase i:leader peptidase i (gtcfc:10.7:11.1:12.10) (ec:3.4.21.89) (keggfc:14.1) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0015 HI0015 Haemophilus influenzae 727 -11537500 81901 lepb:hi0015 (ec:3.4.21.89) (de:signal peptidase i, (spase i) (leader peptidase i)) (db:swissprot) LEP_HAEIN P44454 HAEMOPHILUS INFLUENZAE 727 -11537500 167162 signal peptidase i homolog:lepb protein homolog (db:pir2.dat) H64042 H64042 Haemophilus influenzae 727 -11537500 7500884933 hi0015 signal peptidase i lepb (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to gb:k00426 sp:p00803 pid:146600) (le:2729) (re:3778) (di:complement) U32687 U32687 g1572959 Haemophilus influenzae Rd 71421 -11537500 5000694747 (de:(hi0015) (pn:spase i:leader peptidase i:signal peptidase i:lepb) (gn:lepb) (gtcfc:12.10) (ec:3.4.21.89) (lep_haein) (keggfc:11.1) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0015 HI0015 Haemophilus influenzae 727 10024135

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884939	15026	37182	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884944	15027	37183	642	213

Description

6500733643 lepa:hi0016 gtp-binding membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0016 HI0016 Haemophilus influenzae 727 -11537501 81890 lepa:hi0016 (de:gtp-binding protein lepa) (db:swissprot) LEPA_HAEIN P43729 HAEMOPHILUS INFLUENZAE 727 -11537501 154410 lepa gtp-binding membrane protein lepa (cl:gtp-binding membrane protein lepa:translation elongation factor tu homology) (db:pir2.dat) I64042 I64042 Haemophilus influenzae 727 -11537501 7500884920 hi0016 gtp-binding membrane protein lepa (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788922 percent identity:) (le:3787) (re:5583) (di:complement) U32687 U32687 g1572960 Haemophilus influenzae Rd 71421 -11537501 5000694748 (de:(hi0016) (pn:gtp-binding protein :gtp-binding membrane protein:lepa) (gn:lepa) (gtcfc:12.10) (ec:) (lepa_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0016 HI0016 Haemophilus influenzae 727 10024124

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884953	15028	37184	348	115

Description

6500733644 ffh:hi0106 54 homolog:signal recognition particle protein:fifty-four homolog (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0106 HI0106 Haemophilus influenzae 727 -11537502 99402 ffh:hi0106 (de:signal recognition particle protein (fifty-four homolog)) (db:swissprot) SR54_HAEIN P44518 HAEMOPHILUS INFLUENZAE 727 -11537502 167163 ffh signal recognition particle 54k chain homolog ffh (cl:signal recognition particle 54k protein) (db:pir2.dat) H64048 H64048 Haemophilus influenzae 727 -11537502 7500892040 hi0106 signal recognition particle protein ffh (db:genpept-bct1) (de:haemophilus influenzae rd section 11 of 163 of the complete genome.) (nt:similar to sp:p07019 pid:43142 gb:u00096) (le:1035) (re:2423) (di:complement) U32696 U32696 g1573059 Haemophilus influenzae Rd 71421 -11537502 5000694749 (de:(hi0106) (pn:fifty-four homolog:signal recognition particle protein:54 homolog:ffh) (gn:ffh) (gtcfc:12.10) (ec:) (sr54_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0106 HI0106 Haemophilus influenzae 727 10041261

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884957	15029	37185	270	89

Description

6500733645 secf:hi0239 protein-export membrane protein (gtcfc:12.10:12.6) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0239 HI0239 Haemophilus influenzae 727 -11537503 98322 secf:hi0239 (de:protein-export membrane protein secf) (db:swissprot) SECF_HAEIN P44590 HAEMOPHILUS INFLUENZAE 727 -11537503 167119 protein-export protein secf homolog (cl:escherichia coli preprotein translocase chain secf) (db:pir2.dat) H64056 H64056 Haemophilus influenzae 727 -11537503 7500891483 hi0239 protein-export membrane protein secf (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:similar to sp:p19674 gb:x56175 pid:581231 gb:u00096) (le:2003) (re:2980) (di:complement) U32710 U32710 g1573204 Haemophilus influenzae Rd 71421 -11537503 5000694750 (de:(hi0239) (pn:protein-export membrane protein :protein-export membrane protein:secf) (gn:secf) (gtcfc:12.10) (ec:) (secf_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0239 HI0239 Haemophilus influenzae 727 10040201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884959	15030	37186	504	167

Description

6500733646 secd:hi0240 protein-export membrane protein (gtcfc:12.10:12.6) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0240 HI0240 Haemophilus influenzae 727 -11537504 98306 secd:hi0240 (de:protein-export membrane protein secd) (db:swissprot) SECD_HAEIN P44591 HAEMOPHILUS INFLUENZAE 727 -11537504 167118 secd secretion protein secd (db:pir2.dat) I64056 I64056 Haemophilus influenzae 727 -11537504 7500891472 hi0240 protein-export membrane protein secd (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:similar to sp:p19673 gb:s68715 gb:x56175 pid:581230) (le:2988) (re:4838) (di:complement) U32710 U32710 g1573205 Haemophilus influenzae Rd 71421 -11537504 5000694751 (de:(hi0240) (pn:protein-export membrane protein :protein-export membrane protein:secd) (gn:secd) (gtcfc:12.10) (ec:) (secd_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0240 HI0240 Haemophilus influenzae 727 10040185

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884960	15031	37187	516	172

Description

5000694752 hofd:hopd:hi0296 type 4 prepilin-like protein specific leader peptidase:hopd:putative type 4 prepilin-like protein specific leader peptidase (gtcfc:12.10) (ec:3.4.99.-) (keggfc:14.1) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0296 HI0296 Haemophilus influenzae 727 -11537505 81881 hofd:hopd:hi0296 (ec:3.4.99.-) (de:(ec 3.4.99.-)) (db:swissprot) LEP3_HAEIN P44620 HAEMOPHILUS INFLUENZAE 727 -11537505 167232 hypothetical protein hi0296 (cl:hypothetical protein hi0296) (db:pir2.dat) C64060 C64060 Haemophilus influenzae 727 -11537505 7500884917 hi0296 type 4 prepilin-like protein specific leader (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to sp:p25960 gb:l28106 pid:145410) (le:9304) (re:9996) (di:complement) U32715 U32715 g1573264 Haemophilus influenzae Rd 71421 -11537505 6500733647 hofd:hopd type 4 prepilin-like protein specific leader peptidase:hopd:putative type 4 prepilin-like protein specific leader peptidase (gtcfc:12.10) (ec:3.4.99.-) (keggfc:14.1) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0296 HI0296 Haemophilus influenzae 727 -11537505

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884961	15032	37188	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884968	15033	37189	438	145

Description

6500733648 secg:hi0445 protein translocation protein:low temperature:protein-export membrane protein (gtcfc:12.10:12.6) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0445 HI0445 Haemophilus influenzae 727 -11537506 98325 secg:hi0445 (de:protein-export membrane protein secg) (db:swissprot) SECG_HAEIN P44713 HAEMOPHILUS INFLUENZAE 727 -11537506 167117 secg protein-export protein secg:p12 protein:preprotein translocase (db:pir2.dat) H64068 H64068 Haemophilus influenzae 727 -11537506 7500891485 hi0445 protein-export membrane protein secg (db:genpept-bct1) (de:haemophilus influenzae rd section 42 of 163 of the complete genome.) (nt:similar to gb:d16463 sp:p33582 gb:u01376 pid:431135) (le:6833) (re:7171) (di:direct) U32727 U32727 g1573421 Haemophilus influenzae Rd 71421 -11537506 5000694753 (de:(hi0445) (pn:protein-export membrane protein :protein translocation protein, low temperature:secg) (gn:secg) (gtcfc:12.10) (ec:) (secg_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0445 HI0445 Haemophilus influenzae 727 10040204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884969	15034	37190	504	167

Description

6500733649 sece:hi0716 preprotein translocase:preprotein translocase subunit (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0716 HI0716 Haemophilus influenzae 727 -11537507 98311 sece:hi0716 (de:preprotein translocase sece subunit) (db:swissprot) SECE_HAEIN P43805 HAEMOPHILUS INFLUENZAE 727 -11537507 167101 preprotein translocase sece homolog (cl:protein-export protein sece) (db:pir2.dat) F64088 F64088 Haemophilus influenzae 727 -11537507 7500891475 hi0716 preprotein translocase sece subunit sece (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to sp:p16920 pid:147800 pid:396320) (le:7845) (re:8165) (di:direct) U32754 U32754 g1573718 Haemophilus influenzae Rd 71421 -11537507 5000694754 (de:(hi0716) (pn:preprotein translocase subunit:preprotein translocase:sece) (gn:sece) (gtcfc:12.10) (ec:) (sece_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0716 HI0716 Haemophilus influenzae 727 10040190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884975	15035	37191	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884976	15036	37192	585	194

Description

6500733650 secb:hi0743 protein-export protein (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0743 HI0743 Haemophilus influenzae 727 -11537508 98304 secb:hi0743 (de:protein-export protein secb) (db:swissprot) SECB_HAEIN P44853 HAEMOPHILUS INFLUENZAE 727 -11537508 154815 protein-export protein (cl:protein-export protein secb) (db:pir2.dat) I64089 I64089 Haemophilus influenzae 727 -11537508 7500891470 hi0743 protein-export protein secb (db:genpept-bct1) (de:haemophilus influenzae rd section 73 of 163 of the complete genome.) (nt:similar to sp:p15040 gb:m24489 pid:147797) (le:2249) (re:2758) (di:complement) U32758 U32758 g1573750 Haemophilus influenzae Rd 71421 -11537508 5000694755 (de:(hi0743) (pn:protein-export protein :protein-export protein:secb) (gn:secb) (gtcfc:12.10) (ec:) (secb_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0743 HI0743 Haemophilus influenzae 727 10040183

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884986	15037	37193	288	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884988	15038	37194	468	155

Description

6500733651 secy:hi0798 preprotein translocase subunit:preprotein translocase subunit (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0798 HI0798 Haemophilus influenzae 727 -11537509 98349 secy:hi0798 (de:preprotein translocase secy subunit) (db:swissprot) SECY_HAEIN P43804 HAEMOPHILUS INFLUENZAE 727 -11537509 157290 secy preprotein translocase secy (cl:preprotein translocase secy) (db:pir2.dat) G64094 G64094 Haemophilus influenzae 727 -11537509 7500891492 hi0798 preprotein translocase secy subunit secy (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to sp:p03844 pid:42989 pid:606234 gb:u00096) (le:5171) (re:6496) (di:direct) U32762 U32762 g1573808 Haemophilus influenzae Rd 71421 -11537509 5000694756 (de:(hi0798) (pn:preprotein translocase subunit:preprotein translocase subunit:secy) (gn:secy) (gtcfc:12.10) (ec:) (secy_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0798 HI0798 Haemophilus influenzae 727 10040226

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884990	15039	37195	207	68

Description

6500733652 seca:hi0909 preprotein translocase subunit:preprotein translocase subunit (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI0909 HI0909 Haemophilus influenzae 727 -11537510 98293 seca:hi0909 (de:preprotein translocase seca subunit) (db:swissprot) SECA_HAEIN P43803 HAEMOPHILUS INFLUENZAE 727 -11537510 153235 seca preprotein translocase seca:preprotein translocase subunit (cl:preprotein translocase seca:dead/h box helicase homology) (db:pir2.dat) H64101 H64101 Haemophilus influenzae 727 -11537510 7500891450 hi0909 preprotein translocase seca subunit seca (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p10408 gb:m20791 pid:147794) (le:6322) (re:9027) (di:direct) U32772 U32772 g1573926 Haemophilus influenzae Rd 71421 -11537510 5000694757 (de:(hi0909) (pn:preprotein translocase subunit:preprotein translocase subunit:seca) (gn:seca) (gtcfc:12.10) (ec:) (seca_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI0909 HI0909 Haemophilus influenzae 727 10040172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501884993	15040	37196	2028	676

Description

6500733653 lspa:hi1006 lipoprotein signal peptidase:signal peptidase ii:spase ii (gtcfc:10.7:11.1:12.10) (ec:3.4.23.36) (keggfc:14.1) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI1006 HI1006 Haemophilus influenzae 727 -11537511 82514 lspa:hi1006 (ec:3.4.23.36) (de:peptidase) (signal peptidase ii) (spase ii)) (db:swissprot) LSPA_HAEIN P44975 HAEMOPHILUS INFLUENZAE 727 -11537511 140842 lipoprotein signal peptidase (cl:lipoprotein signal peptidase) (ec:3.4.23.36) (db:pir2.dat) H64107 H64107 Haemophilus influenzae 727 -11537511 7500885171 hi1006 lipoprotein signal peptidase lspa (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p00804 gb:k01990 gb:x00776) (le:7773) (re:8288) (di:direct) U32781 U32781 g1574036 Haemophilus influenzae Rd 71421 -11537511 5000694758 (de:(hi1006) (pn:prolipoprotein signal peptidase:signal peptidase ii:spase ii:lipoprotein signal peptidase:lspa) (gn:lspa) (gtcfc:12.10) (ec:3.4.23.36) (lspa_haein) (keggfc:11.1) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI1006 HI1006 Haemophilus influenzae 727 10024734

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885031	15041	37197	348	115

Description

5000694759 colicin v secretion atp-binding protein:cvab:hypothetical abc transporter atp-binding protein hi1467 (gtcfc:12.10:12.6) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI1467 HI1467 Haemophilus influenzae 727 -11537512 111437 hi1467 (de:hypothetical abc transporter atp-binding protein hi1467) (db:swissprot) YE67_HAEIN P45221 HAEMOPHILUS INFLUENZAE 727 -11537512 166061 hypothetical protein hi1467 (cl:atp-binding cassette homology) (db:pir2.dat) D64125 D64125 Haemophilus influenzae 727 -11537512 7500922729 hi1467 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to sp:q50614 pid:1483552 percent ident:) (le:1326) (re:3095) (di:direct) U32825 U32825 g1574308 Haemophilus influenzae Rd 71421 -11537512 6500733654 colicin v secretion atp-binding protein:cvab:hypothetical abc transporter atp-binding protein hi1467 (gtcfc:12.10:12.6) (keggfc:14.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI1467 HI1467 Haemophilus influenzae 727 -11537512

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885032	15042	37198	1236	412

Description

GTC ORF with score 594 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885033	15043	37199	3291	1096

Description

GTC ORF with score 406 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885040	15044	37200	615	204

Description

6500733655 sapf:hi1642 peptide transport system atp-binding protein (gtcfc:12.10:12.6) (keggfc:11.1) (tigrfc:4.5) (db:gtc-haemophilus influenzae) HI1642 HI1642 Haemophilus influenzae 727 -11537513 97930 sapf:hi1642 (de:peptide transport system atp-binding protein sapf) (db:swissprot) SAPF_HAEIN P45289 HAEMOPHILUS INFLUENZAE 727 -11537513 167078 peptide transport system atp-binding protein hi1642 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) E64134 E64134 Haemophilus influenzae 727 -11537513 7500891314 hi1642 peptide abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p36637 gb:u08190 pid:470683 gb:u00096) (le:4657) (re:5466) (di:direct) U32837 U32837 g1574490 Haemophilus influenzae Rd 71421 -11537513 5000694760 (de:(hi1642) (pn:peptide transport system atp-binding protein :peptide transport system atp-binding protein:sapf) (gn:sapf) (gtcfc:12.10) (ec:) (sapf_haein) (keggfc:11.2) (tigrfc:4.5) (db:gtc-haemophilus influenzae)) HI1642 HI1642 Haemophilus influenzae 727 10039809

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885060	15045	37201	852	283

Description

GTC ORF with score 136 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f59a6.) (nt:similar to glycoproteins) (le:13300:13899:15490:15579) (re:13615:15440:15533:15701) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885068	15046	37202	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885069	15047	37203	597	198

Description

5000694711 oligopeptide binding protein:oppa:putative binding protein precursor (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0213 HI0213 Haemophilus influenzae 727 -11537514 108984 hi0213 (de:putative binding protein hi0213 precursor) (db:swissprot) Y213_HAEIN P44572 HAEMOPHILUS INFLUENZAE 727 -11537514 167049 periplasmic oligopeptide-binding protein homolog (db:pir2.dat) B64055 B64055 Haemophilus influenzae 727 -11537514 7500894887 hi0213 oligopeptide transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 21 of 163 of the complete genome.) (nt:similar to sp:p06202 gb:x05491 gb:x52093 pid:47802) (le:2407) (re:3951) (di:complement) U32706 U32706 g1573173 Haemophilus influenzae Rd 71421 -11537514 6500733656 oligopeptide binding protein:oppa:putative binding protein precursor (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0213 HI0213 Haemophilus influenzae 727 -11537514

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885077	15048	37204	270	89

Description

6500733657 brnq:hi0226 membrane-associated component:branched amino acid transport system (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0226 HI0226 Haemophilus influenzae 727 -11537515 7500877939 brnq:hi0226 (de:chain amino acid uptake carrier)) (db:swissprot) BRNQ_HAEIN P71345 HAEMOPHILUS INFLUENZAE 727 -11537515 166983 branched-chain amino acid transport protein brab homolog (cl:branched-chain amino acid transport system ii carrier protein braz) (db:pir2.dat) D64056 D64056 Haemophilus influenzae 727 -11537515 7500877941 hi0226 branched chain amino acid transport system ii (db:genpept-bct1) (de:haemophilus influenzae rd section 24 of 163 of the complete genome.) (nt:similar to sp:p37011 gb:u00096 pid:1657597) (le:124) (re:1434) (di:direct) U32709 U32709 g1573191 Haemophilus influenzae Rd 71421 -11537515 5000694712 (de:(hi0226) (pn:membrane-associated component, branched amino acid transport system:brnq) (gn:brnq) (gtcfc:12.1) (ec:) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0226 HI0226 Haemophilus influenzae 727 10088244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885100	15049	37205	552	183

Description

6500733658 exbd:hi0252 biopolymer transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0252 HI0252 Haemophilus influenzae 727 -11537516 70791 exbd:hi0252 (de:biopolymer transport exbd protein) (db:swissprot) EXBD_HAEIN P43009 HAEMOPHILUS INFLUENZAE 727 -11537516 166030 biopolymer transport protein homolog hi0252 (cl:tolr protein) (db:pir2.dat) G64057 G64057 Haemophilus influenzae 727 -11537516 7500881233 hi0252 biopolymer transport protein exbd (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to pid:555672 pid:1573218 percent identity:) (le:4680) (re:5123) (di:complement) U32711 U32711 g1573218 Haemophilus influenzae Rd 71421 -11537516 5000694713 (de:(hi0252) (pn:biopolymer transport protein:biopolymer transport protein:exbd) (gn:exbd) (gtcfc:12.1) (ec:) (exbd_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0252 HI0252 Haemophilus influenzae 727 10013366

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885101	15050	37206	285	94

Description

GTC ORF with score 90 to: (sr:aspergillus niger strain a733) (db:genpept-pln1) (de:leu2a=beta-isopropylmalate dehydrogenase (aspergillus niger, straina733, mrna, 1238 nt).) (nt:this sequence comes from fig. 1a.) (le:8) (re:1099) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885102	15051	37207	771	256

Description

GTC ORF with score 872 to: (sr:aspergillus niger strain a733) (db:genpept-pln1) (de:leu2a=beta-isopropylmalate dehydrogenase (aspergillus niger, straina733, mrna, 1238 nt).) (nt:this sequence comes from fig. 1a.) (le:8) (re:1099) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885103	15052	37208	258	85

Description

GTC ORF with score 332 to: (sr:aspergillus niger strain a733) (db:genpept-pln1) (de:leu2a=beta-isopropylmalate dehydrogenase (aspergillus niger, straina733, mrna, 1238 nt).) (nt:this sequence comes from fig. 1a.) (le:8) (re:1099) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885117	15053	37209	207	68

Description

6500733659 exbb:hi0253 biopolymer transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0253 HI0253 Haemophilus influenzae 727 -11537517 70787 exbb:hi0253 (de:biopolymer transport exbb protein) (db:swissprot) EXBB_HAEIN P43008 HAEMOPHILUS INFLUENZAE 727 -11537517 166029 biopolymer transport protein homolog hi0253 (cl:biopolymer transport protein) (db:pir2.dat) H64057 H64057 Haemophilus influenzae 727 -11537517 7500881231 hi0253 biopolymer transport protein exbb (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to pid:555671 percent identity: 96.00;) (le:5127) (re:5579) (di:complement) U32711 U32711 g1573219 Haemophilus influenzae Rd 71421 -11537517 5000694714 (de:(hi0253) (pn:biopolymer transport protein:biopolymer transport protein:exbb) (gn:exbb) (gtcfc:12.1) (ec:) (exbb_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0253 HI0253 Haemophilus influenzae 727 10013362

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885118	15054	37210	678	225

Description

6500733660 mtr:hi0287 tryptophan-specific permease:tryptophan-specific transport protein:tryptophan permease (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0287 HI0287 Haemophilus influenzae 727 -11537518 84593 mtr:hi0287 (de:tryptophan-specific transport protein (tryptophan permease)) (db:swissprot) MTR_HAEIN P44614 HAEMOPHILUS INFLUENZAE 727 -11537518 167231 tnab tryptophan transport protein tnab (db:pir2.dat) F64059 F64059 Haemophilus influenzae 727 -11537518 7500886060 hi0287 tryptophan-specific transport protein mtr (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:m58338 sp:p22306 gb:m59862 pid:146894) (le:89) (re:1345) (di:direct) U32715 U32715 g1573255 Haemophilus influenzae Rd 71421 -11537518 5000694715 (de:(hi0287) (pn:tryptophan-specific transport protein:tryptophan permease:tryptophan-specific permease:mtr) (gn:mtr) (gtcfc:12.1) (ec:) (mtr_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0287 HI0287 Haemophilus influenzae 727 10026789

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885119	15055	37211	894	297

Description

6500733661 sdac:hi0289 serine transporter (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0289 HI0289 Haemophilus influenzae 727 -11537519 98235 sdac:hi0289 (de:serine transporter) (db:swissprot) SDAC_HAEIN P44615 HAEMOPHILUS INFLUENZAE 727 -11537519 154711 probable serine transport protein (cl:threonine-serine permease) (db:pir2.dat) G64059 G64059 Haemophilus influenzae 727 -11537519 7500891414 hi0289 serine transporter sdac (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to sp:p36559 gb:u01233 pid:402256) (le:2856) (re:4094) (di:complement) U32715 U32715 g1573257 Haemophilus influenzae Rd 71421 -11537519 5000694716 (de:(hi0289) (pn:serine transporter:sdac) (gn:sdac) (gtcfc:12.1) (ec:) (sdac_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0289 HI0289 Haemophilus influenzae 727 10040114

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885126	15056	37212	537	178

Description

5000694717 leucine-specific transport protein:livg:hypothetical abc transporter atp-binding protein hi0408 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0408 HI0408 Haemophilus influenzae 727 -11537520 111496 znuc:hi0408 (de:high-affinity zinc uptake system atp-binding protein znuc) (db:swissprot) ZNUC_HAEIN P44692 HAEMOPHILUS INFLUENZAE 727 -11537520 166942 probable abc transport system atp-binding protein hi0408 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64066 B64066 Haemophilus influenzae 727 -11537520 7500922925 hi0408 abc transporter:atp-binding protein yebm (db:genpept-bct1) (de:haemophilus influenzae rd section 39 of 163 of the complete genome.) (nt:similar to sp:p52648 gb:u00096 pid:1736501) (le:1889) (re:2695) (di:complement) U32724 U32724 g1573381 Haemophilus influenzae Rd 71421 -11537520 6500733662 leucine-specific transport protein:livg:hypothetical abc transporter atp-binding protein hi0408 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0408 HI0408 Haemophilus influenzae 727 -11537520

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885127	15057	37213	426	141

Description

6500733663 tyrp-a:hi0477 tyrosine-specific transport protein:tyrp:tyrosine-specific transport protein 1:tyrosine permease 1 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0477 HI0477 Haemophilus influenzae 727 -11537521 102927 tyrp-a:hi0477 (de:tyrosine-specific transport protein 1 (tyrosine permease 1)) (db:swissprot) TYRP_HAEIN P44727 HAEMOPHILUS INFLUENZAE 727 -11537521 167241 tyrosine-specific transport protein homolog hi0477 (db:pir2.dat) B64071 B64071 Haemophilus influenzae 727 -11537521 7500893614 hi0477 tyrosine-specific transport protein tyrp (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to gb:m23240 sp:p18199 pid:148089 gb:u00096) (le:5505) (re:6707) (di:direct) U32730 U32730 g1573455 Haemophilus influenzae Rd 71421 -11537521 5000694718 (de:(hi0477) (pn:tyrosine-specific transport protein 1:tyrosine permease 1:tyrosine-specific transport protein:tyrp) (gn:tyrp-a) (gtcfc:12.1) (ec:) (tyrp_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0477 HI0477 Haemophilus influenzae 727 10044739

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885129	15058	37214	243	80

Description

6500733664 potd-a:hi0498 spermidine/putrescine-binding periplasmic protein 2 precursor:spbp (gtcfc:12.1:13.11) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0498 HI0498 Haemophilus influenzae 727 -11537522 167174 potd:potd-a spermidine/putrescine-binding protein 2 precursor hi0498 (db:pir2.dat) E64072 E64072 Haemophilus influenzae 727 -11537522 7500960738 hi0498 spermidine/putrescine abc transporter (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to gb:m64519 sp:p23861 pid:147329 gb:u00096) (le:7081) (re:8019) (di:complement) U32731 U32731 g1573475 Haemophilus influenzae Rd 71421 -11537522 5000694719 (de:(hi0498) (pn:spermidine) (gn:potd-a) (gtcfc:12.1) (ec:) (pot2_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0498 HI0498 Haemophilus influenzae 727 10088297

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885130	15059	37215	240	79

Description

6500733665 tyrp-b:hi0528 tyrosine-specific transport protein 2:tyrosine permease 2 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0528 HI0528 Haemophilus influenzae 727 -11537523 102928 tyrp-b:hi0528 (de:tyrosine-specific transport protein 2 (tyrosine permease 2)) (db:swissprot) TYRQ_HAEIN P44747 HAEMOPHILUS INFLUENZAE 727 -11537523 167242 tyrosine-specific transport protein homolog hi0528 (db:pir2.dat) F64074 F64074 Haemophilus influenzae 727 -11537523 7500893615 hi0528 tyrosine-specific transport protein tyrp (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:similar to gb:m23240 sp:p18199 pid:148089 gb:u00096) (le:1379) (re:2599) (di:complement) U32735 U32735 g1573512 Haemophilus influenzae Rd 71421 -11537523 5000694720 (de:(hi0528) (pn:tyrosine-specific transport protein 2:tyrosine permease 2:tyrosine-specific transport protein:tyrp) (gn:tyrp-b) (gtcfc:12.1) (ec:) (tyrq_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0528 HI0528 Haemophilus influenzae 727 10044740

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885143	15060	37216	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885164	15061	37217	978	325

Description

6500733666 pote:hi0590 putrescine-ornithine antiporter:putrescine transport protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0590 HI0590 Haemophilus influenzae 727 -11537524 90602 pote:hi0590 (de:putrescine-ornithine antiporter (putrescine transport protein)) (db:swissprot) POTE_HAEIN P44768 HAEMOPHILUS INFLUENZAE 727 -11537524 167125 putrescine/ornithine antiporter (cl:l-lysine transport protein) (db:pir2.dat) E64079 E64079 Haemophilus influenzae 727 -11537524 7500888292 hi0590 putrescine-ornithine antiporter pote (db:genpept-bct1) (de:haemophilus influenzae rd section 55 of 163 of the complete genome.) (nt:similar to gb:m64495 sp:p24170 pid:147332 gb:u00096) (le:7895) (re:9202) (di:complement) U32740 U32740 g1573580 Haemophilus influenzae Rd 71421 -11537524 5000694721 (de:(hi0590) (pn:putrescine-ornithine antiporter:putrescine transport protein:pote) (gn:pote) (gtcfc:12.1) (ec:) (pote_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI0590 HI0590 Haemophilus influenzae 727 10032724

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885165	15062	37218	1134	377

Description

5000694722 d-alanine permease:daga:hypothetical protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0883 HI0883 Haemophilus influenzae 727 -11537525 109306 hi0883 (de:hypothetical protein hi0883) (db:swissprot) Y883_HAEIN P44917 HAEMOPHILUS INFLUENZAE 727 -11537525 166078 probable amino acid transport protein hi0883:sodium-dependent (cl:sodium-dependent d-alanine/glycine transport protein) (db:pir2.dat) H64099 H64099 Haemophilus influenzae 727 -11537525 7500895604 hi0883 amino acid carrier protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 85 of 163 of the complete genome.) (nt:similar to pid:757741 sp:q45068 pid:1405464) (le:1973) (re:3343) (di:complement) U32770 U32770 g1573900 Haemophilus influenzae Rd 71421 -11537525 6500733667 d-alanine permease:daga:hypothetical protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI0883 HI0883 Haemophilus influenzae 727 -11537525

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885173	15063	37219	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885177	15064	37220	294	97

Description

5000694723 glutamine-binding periplasmic protein:glnh:hypothetical amino-acid abc transporter binding protein hi1080 precursor (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1080 HI1080 Haemophilus influenzae 727 -11537526 109450 hi1080 (de:precursor) (db:swissprot) YA80_HAEIN P45024 HAEMOPHILUS INFLUENZAE 727 -11537526 166161 probable amino acid-binding protein:periplasmic (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) I64181 I64181 Haemophilus influenzae 727 -11537526 7500895920 hi1080 amino acid abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to sp:p42199 percent ident: 51.06;) (le:4473) (re:5246) (di:complement) U32788 U32788 g1574634 Haemophilus influenzae Rd 71421 -11537526 6500733668 glutamine-binding periplasmic protein:glnh:hypothetical amino-acid abc transporter binding protein hi1080 precursor (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1080 HI1080 Haemophilus influenzae 727 -11537526

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885180	15065	37221	591	196

Description

GTC ORF with score 148 to: (fn:degradation and synthesis of lactone) (sr:fusarium oxysporum (strain:aku 3702) cdna to mrna) (db:genpept-pln2) (de:fusarium oxysporum mrna for lactonohydrolase, complete cds.) (le:8) (re:1210) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885183	15066	37222	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885186	15067	37223	246	81

Description

GTC ORF with score 123 to: (fn:degradation and synthesis of lactone) (sr:fusarium oxysporum (strain:aku 3702) cdna to mrna) (db:genpept-pln2) (de:fusarium oxysporum mrna for lactonohydrolase, complete cds.) (le:8) (re:1210) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885187	15068	37224	366	121

Description

GTC ORF with score 135 to: (fn:degradation and synthesis of lactone) (sr:fusarium oxysporum (strain:aku 3702) cdna to mrna) (db:genpept-pln2) (de:fusarium oxysporum mrna for lactonohydrolase, complete cds.) (le:8) (re:1210) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885195	15069	37225	276	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885197	15070	37226	1050	349

Description

6500733669 oppf:hi1120 oligopeptide transport atp-binding protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1120 HI1120 Haemophilus influenzae 727 -11537527 87766 oppf:hi1120 (de:oligopeptide transport atp-binding protein oppf) (db:swissprot) OPPF_HAEIN P45051 HAEMOPHILUS INFLUENZAE 727 -11537527 153028 oppf oligopeptide transport atp-binding protein oppf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) B64184 B64184 Haemophilus influenzae 727 -11537527 7500887204 hi1120 oligopeptide abc transporter:atp-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77737 pid:1742036) (le:1716) (re:2714) (di:complement) U32792 U32792 g1574675 Haemophilus influenzae Rd 71421 -11537527 5000694724 (de:(hi1120) (pn:oligopeptide transport atp-binding protein :oligopeptide transport atp-binding protein:oppf) (gn:oppf) (gtcfc:12.1) (ec:) (oppf_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1120 HI1120 Haemophilus influenzae 727 10029907

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885216	15071	37227	288	95

Description

6500733670 oppd:hi1121 oligopeptide transport atp-binding protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1121 HI1121 Haemophilus influenzae 727 -11537528 87760 oppd:hi1121 (de:oligopeptide transport atp-binding protein oppd) (db:swissprot) OPPD_HAEIN P45052 HAEMOPHILUS INFLUENZAE 727 -11537528 153026 oppd oligopeptide transport atp-binding protein oppd (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) C64184 C64184 Haemophilus influenzae 727 -11537528 7500887201 hi1121 oligopeptide abc transporter:atp-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:similar to sp:p04285 gb:x05491 gb:x52093 pid:47805) (le:2711) (re:3682) (di:complement) U32792 U32792 g1574676 Haemophilus influenzae Rd 71421 -11537528 5000694725 (de:(hi1121) (pn:oligopeptide transport atp-binding protein :oligopeptide transport atp-binding protein:oppd) (gn:oppd) (gtcfc:12.1) (ec:) (oppd_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1121 HI1121 Haemophilus influenzae 727 10029901

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885232	15072	37228	540	179

Description

6500733671 oppc:hi1122 oligopeptide transport system permease protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1122 HI1122 Haemophilus influenzae 727 -11537529 87755 oppc:hi1122 (de:oligopeptide transport system permease protein oppc) (db:swissprot) OPPC_HAEIN P45053 HAEMOPHILUS INFLUENZAE 727 -11537529 153011 oppb oligopeptide transport system permease protein oppc (cl:oligopeptide permease protein oppb) (db:pir2.dat) D64184 D64184 Haemophilus influenzae 727 -11537529 7500887197 hi1122 oligopeptide abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:similar to sp:p08006 gb:x05491 gb:x52093 pid:47804) (le:3692) (re:4627) (di:complement) U32792 U32792 g1574677 Haemophilus influenzae Rd 71421 -11537529 5000694726 (de:(hi1122) (pn:oligopeptide transport system permease protein :oligopeptide transport system permease protein:oppcc) (gn:oppc) (gtcfc:12.1) (ec:) (oppc_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1122 HI1122 Haemophilus influenzae 727 10029896

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885236	15073	37229	795	264

Description

6500733672 oppb:dppb:hi1123 dipeptide transport system permease protein:oligopeptide transport system permease protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1123 HI1123 Haemophilus influenzae 727 -11537530 87749 oppb:hi1123 (de:oligopeptide transport system permease protein oppb) (db:swissprot) OPPB_HAEIN P45054 HAEMOPHILUS INFLUENZAE 727 -11537530 153010 oppb oligopeptide transport system permease protein oppb (cl:oligopeptide permease protein oppb) (db:pir2.dat) E64184 E64184 Haemophilus influenzae 727 -11537530 7500887193 hi1123 oligopeptide abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1742033 pid:1787497) (le:4637) (re:5557) (di:complement) U32792 U32792 g1574678 Haemophilus influenzae Rd 71421 -11537530 5000694727 (de:(hi1123) (pn:oligopeptide transport system permease protein :dipeptide transport system permease protein:dppb) (gn:oppb) (gtcfc:12.1) (ec:) (oppb_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1123 HI1123 Haemophilus influenzae 727 10029890

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885240	15074	37230	621	206

Description

5000694728 proton glutamate symport protein:gltp:hypothetical symporter hi1154 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1154 HI1154 Haemophilus influenzae 727 -11537531 110088 hi1154 (de:hypothetical symporter hi1154) (db:swissprot) YB54_HAEIN P45079 HAEMOPHILUS INFLUENZAE 727 -11537531 167120 conserved hypothetical protein hi1154 (cl:bacillus subtilis sodium-glutamate symporter homolog yhcl) (db:pir2.dat) D64186 D64186 Haemophilus influenzae 727 -11537531 7500896408 hi1154 proton glutamate symport protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 110 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1742823 pid:1742828) (le:2486) (re:3808) (di:direct) U32795 U32795 g1574711 Haemophilus influenzae Rd 71421 -11537531 6500733673 proton glutamate symport protein:gltp:hypothetical symporter hi1154 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1154 HI1154 Haemophilus influenzae 727 -11537531

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885290	15075	37231	186	61

Description

6500733674 artm:hi1177 arginine transport system permease protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1177 HI1177 Haemophilus influenzae 727 -11537532 60308 artm:hi1177 (de:arginine transport system permease protein artm) (db:swissprot) ARTM_HAEIN P45089 HAEMOPHILUS INFLUENZAE 727 -11537532 166009 artm arginine transport system permease protein artm (cl:histidine permease protein m) (db:pir2.dat) A64188 A64188 Haemophilus influenzae 727 -11537532 7500877219 hi1177 arginine abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to sp:p30862 gb:x67753 gb:x86160 pid:40933) (le:5915) (re:6598) (di:complement) U32797 U32797 g1574102 Haemophilus influenzae Rd 71421 -11537532 5000694729 (de:(hi1177) (pn:arginine transport system permease protein :arginine transport system permease protein:artm) (gn:artm) (gtcfc:12.1) (ec:) (artm_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1177 HI1177 Haemophilus influenzae 727 10003034

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885294	15076	37232	645	214

Description

6500733675 artq:hi1178 arginine transport system permease protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1178 HI1178 Haemophilus influenzae 727 -11537533 60312 artq:hi1178 (de:arginine transport system permease protein artq) (db:swissprot) ARTQ_HAEIN P45090 HAEMOPHILUS INFLUENZAE 727 -11537533 166010 artq arginine transport system permease protein artq (cl:histidine permease protein m) (db:pir2.dat) B64188 B64188 Haemophilus influenzae 727 -11537533 241590 artq artq (db:genpept-bct1) (de:haemophilus influenzae dppb, dppc, dppd, dppf, isn, artp, arti/j,artq, and artm genes, complete cds, and opa gene, partial cds.) (le:7207) (re:7872) (di:direct) HIU17295 U17295 g972902 Haemophilus influenzae 727 -11537533 7500877223 hi1178 arginine abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to sp:p30861 gb:x67753 gb:x86160 pid:40932) (le:6598) (re:7263) (di:complement) U32797 U32797 g1574103 Haemophilus influenzae Rd 71421 -11537533 5000694730 (de:(hi1178) (pn:arginine transport system permease protein :arginine transport system permease protein:artq) (gn:artq) (gtcfc:12.1) (ec:) (artq_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1178 HI1178 Haemophilus influenzae 727 10003038

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885314	15077	37233	789	262

Description

6500733676 arti:hi1179 periplasmic arginine-binding protein:arginine-binding periplasmic protein precursor (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1179 HI1179 Haemophilus influenzae 727 -11537534 60304 arti:hi1179 (de:arginine-binding periplasmic protein precursor) (db:swissprot) ARTI_HAEIN P45091 HAEMOPHILUS INFLUENZAE 727 -11537534 167082 arginine binding protein arti homolog (db:pir2.dat) C64188 C64188 Haemophilus influenzae 727 -11537534 241589 arti/j arti/j (db:genpept-bct1) (de:haemophilus influenzae dppb, dppc, dppd, dppf, isn, artp, arti/j,artq, and artm genes, complete cds, and opa gene, partial cds.) (le:6484) (re:7203) (di:direct) HIU17295 U17295 g972901 Haemophilus influenzae 727 -11537534 7500877216 hi1179 arginine abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to gb:m59210 sp:p49618 pid:387859 percent) (le:7267) (re:7986) (di:complement) U32797 U32797 g1574104 Haemophilus influenzae Rd 71421 -11537534 5000694731 (de:(hi1179) (pn:arginine-binding periplasmic protein precursor:periplasmic arginine-binding protein:arti) (gn:arti) (gtcfc:12.1) (ec:) (arti_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1179 HI1179 Haemophilus influenzae 727 10003030

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885315	15078	37234	621	206

Description

6500733677 artp:hi1180 arginine transport atp-binding protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1180 HI1180 Haemophilus influenzae 727 -11537535 60310 artp:hi1180 (de:arginine transport atp-binding protein artp) (db:swissprot) ARTP_HAEIN P45092 HAEMOPHILUS INFLUENZAE 727 -11537535 166008 artp arginine transport protein artp (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) D64188 D64188 Haemophilus influenzae 727 -11537535 241588 artp artp (db:genpept-bct1) (de:haemophilus influenzae dppb, dppc, dppd, dppf, isn, artp, arti/j,artq, and artm genes, complete cds, and opa gene, partial cds.) (le:5735) (re:6466) (di:direct) HIU17295 U17295 g972900 Haemophilus influenzae 727 -11537535 7500877221 hi1180 arginine abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to sp:p30858 gb:x86160 pid:769790 gb:u00096) (le:8004) (re:8735) (di:complement) U32797 U32797 g1574105 Haemophilus influenzae Rd 71421 -11537535 5000694732 (de:(hi1180) (pn:arginine transport atp-binding protein :arginine transport atp-binding protein:artp) (gn:artp) (gtcfc:12.1) (ec:) (artp_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1180 HI1180 Haemophilus influenzae 727 10003036

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885322	15079	37235	1671	556

Description

6500733678 dppf:hi1184 dipeptide transport atp-binding protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1184 HI1184 Haemophilus influenzae 727 -11537536 69239 dppf:hi1184 (de:dipeptide transport atp-binding protein dppf) (db:swissprot) DPPF_HAEIN P45094 HAEMOPHILUS INFLUENZAE 727 -11537536 166097 dppf dipeptide transport atp-binding protein dppf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) E64188 E64188 Haemophilus influenzae 727 -11537536 241585 dppf dppf (db:genpept-bct1) (de:haemophilus influenzae dppb, dppc, dppd, dppf, isn, artp, arti/j,artq, and artm genes, complete cds, and opa gene, partial cds.) (nt:similar to dipeptide transport atp-binding protein) (le:2999) (re:3982) (di:direct) HIU17295 U17295 g972898 Haemophilus influenzae 727 -11537536 7500880600 hi1184 dipeptide abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to sp:p37313 gb:l08399 pid:466679) (le:271) (re:1254) (di:complement) U32798 U32798 g1574111 Haemophilus influenzae Rd 71421 -11537536 5000694733 (de:(hi1184) (pn:dipeptide transport atp-binding protein :dipeptide transport atp-binding protein:dppf) (gn:dppf) (gtcfc:12.1) (ec:) (dppf_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1184 HI1184 Haemophilus influenzae 727 10011822

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885336	15080	37236	462	153

Description

6500733679 dppd:hi1185 dipeptide transport atp-binding protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1185 HI1185 Haemophilus influenzae 727 -11537537 69236 dppd:hi1185 (de:dipeptide transport atp-binding protein dppd) (db:swissprot) DPPD_HAEIN P45095 HAEMOPHILUS INFLUENZAE 727 -11537537 166096 dppd dipeptide transport atp-binding protein dppd (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F64188 F64188 Haemophilus influenzae 727 -11537537 241584 dppd dppd (db:genpept-bct1) (de:haemophilus influenzae dppb, dppc, dppd, dppf, isn, artp, arti/j,artq, and artm genes, complete cds, and opa gene, partial cds.) (nt:similar to dipeptide transport atp-binding protein) (le:2004) (re:2996) (di:direct) HIU17295 U17295 g972897 Haemophilus influenzae 727 -11537537 7500880598 hi1185 dipeptide abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to sp:p37314 pid:349228 pid:466680) (le:1257) (re:2249) (di:complement) U32798 U32798 g1574112 Haemophilus influenzae Rd 71421 -11537537 5000694734 (de:(hi1185) (pn:dipeptide transport atp-binding protein :dipeptide transport atp-binding protein:dppd) (gn:dppd) (gtcfc:12.1) (ec:) (dppd_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1185 HI1185 Haemophilus influenzae 727 10011819

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885346	15081	37237	228	75

Description

6500733680 dppc:hi1186 dipeptide transport system permease protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1186 HI1186 Haemophilus influenzae 727 -11537538 69233 dppc:hi1186 (de:dipeptide transport system permease protein dppc) (db:swissprot) DPPC_HAEIN P51000 HAEMOPHILUS INFLUENZAE 727 -11537538 241583 dppc dppc (db:genpept-bct1) (de:haemophilus influenzae dppb, dppc, dppd, dppf, isn, artp, arti/j,artq, and artm genes, complete cds, and opa gene, partial cds.) (nt:similar to dipeptide transport system permease dppc) (le:1107) (re:1994) (di:direct) HIU17295 U17295 g972896 Haemophilus influenzae 727 -11537538 7500880595 hi1186 dipeptide abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to sp:p37315 pid:349227 pid:466681) (le:2259) (re:3146) (di:complement) U32798 U32798 g1574113 Haemophilus influenzae Rd 71421 -11537538 5000694735 (de:(hi1186) (pn:dipeptide transport system permease protein :dipeptide transport system permease protein:dppc) (gn:dppc) (gtcfc:12.1) (ec:) (dppc_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1186 HI1186 Haemophilus influenzae 727 10011816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885351	15082	37238	249	82

Description

6500733681 dppb:hi1187 dipeptide transport system permease protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1187 HI1187 Haemophilus influenzae 727 -11537539 69230 dppb:hi1187 (de:dipeptide transport system permease protein dppb) (db:swissprot) DPPB_HAEIN P45096 HAEMOPHILUS INFLUENZAE 727 -11537539 166098 dppb transmembrane protein dppb (cl:transmembrane protein dppb) (db:pir2.dat) G64188 G64188 Haemophilus influenzae 727 -11537539 241582 dppb dppb (db:genpept-bct1) (de:haemophilus influenzae dppb, dppc, dppd, dppf, isn, artp, arti/j,artq, and artm genes, complete cds, and opa gene, partial cds.) (nt:similar to dipeptide transport system permease dppb) (le:91) (re:1092) (di:direct) HIU17295 U17295 g972895 Haemophilus influenzae 727 -11537539 7500880593 hi1187 dipeptide abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to sp:p37316 pid:349226 pid:466682) (le:3161) (re:4162) (di:complement) U32798 U32798 g1574114 Haemophilus influenzae Rd 71421 -11537539 5000694736 (de:(hi1187) (pn:dipeptide transport system permease protein :dipeptide transport system permease protein:dppb) (gn:dppb) (gtcfc:12.1) (ec:) (dppb_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1187 HI1187 Haemophilus influenzae 727 10011813

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885353	15083	37239	2334	777

Description

GTC ORF with score 135 to: (db:genpept-pln1) (de:aspergillus oryzae putative dna binding protein facb (facb) gene,complete cds.) (nt:description: homologue of the emericella nidulans) (le:1680:2223:2597:2927) (re:2148:2536:2877:3284) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885363	15084	37240	279	92

Description

6500733682 potd-b:hi1344 spermidine/putrescine-binding periplasmic protein precursor:potd:spbp (gtcfc:12.1:13.11) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1344 HI1344 Haemophilus influenzae 727 -11537540 167175 potd:potd-b spermidine/putrescine-binding protein 1 precursor hi1344 (db:pir2.dat) H64117 H64117 Haemophilus influenzae 727 -11537540 7500960739 hi1344 spermidine/putrescine abc transporter (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to pid:1142681 percent ident: 78.95;) (le:7549) (re:8688) (di:complement) U32813 U32813 g1574803 Haemophilus influenzae Rd 71421 -11537540 5000694737 (de:(hi1344) (pn:spermidine) (gn:potd-b) (gtcfc:12.1) (ec:) (potl_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1344 HI1344 Haemophilus influenzae 727 10088298

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885382	15085	37241	732	243

Description

6500733683 potc:hi1345 spermidine/putrescine transport system permease protein (gtcfc:12.1:13.11) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1345 HI1345 Haemophilus influenzae 727 -11537541 167173 potc spermidine/putrescine transport system permease potc (cl:spermidine/putrescine transport system permease protein potI) (db:pir2.dat) I64117 I64117 Haemophilus influenzae 727 -11537541 7500960737 hi1345 spermidine/putrescine abc transporter:permease (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to gb:m64519 sp:p23859 pid:147328 gb:u00096) (le:8761) (re:9504) (di:complement) U32813 U32813 g1574804 Haemophilus influenzae Rd 71421 -11537541 5000694738 (de:(hi1345) (pn:spermidine) (gn:potc) (gtcfc:12.1) (ec:) (potc_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1345 HI1345 Haemophilus influenzae 727 10088296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885390	15086	37242	405	134

Description

6500733684 potb:hi1346 spermidine/putrescine transport system permease protein (gtcfc:12.1:13.11) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1346 HI1346 Haemophilus influenzae 727 -11537542 90595 potb:hi1346 (de:spermidine/putrescine transport system permease protein potb) (db:swissprot) POTB_HAEIN P45170 HAEMOPHILUS INFLUENZAE 727 -11537542 167172 potb spermidine/putrescine transport system permease potb (cl:spermidine/putrescine transport system permease protein poth) (db:pir2.dat) A64118 A64118 Haemophilus influenzae 727 -11537542 7500888283 hi1346 spermidine/putrescine abc transporter:permease (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to gb:m64519 sp:p23860 pid:147327 gb:u00096) (le:9530) (re:10390) (di:complement) U32813 U32813 g1574805 Haemophilus influenzae Rd 71421 -11537542 5000694739 (de:(hi1346) (pn:spermidine) (gn:potb) (gtcfc:12.1) (ec:) (potb_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1346 HI1346 Haemophilus influenzae 727 10032717

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885392	15087	37243	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885393	15088	37244	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885412	15089	37245	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885423	15090	37246	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885431	15091	37247	219	72

Description

6500733685 pota:hi1347 spermidine/putrescine transport atp-binding protein (gtcfc:12.1:13.11) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1347 HI1347 Haemophilus influenzae 727 -11537543 90591 pota:hi1347 (de:spermidine/putrescine transport atp-binding protein pota) (db:swissprot) POTA_HAEIN P45171 HAEMOPHILUS INFLUENZAE 727 -11537543 167171 pota spermidine/putrescine transport protein pota (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64118 B64118 Haemophilus influenzae 727 -11537543 7500888280 hi1347 spermidine/putrescine abc transporter (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to gb:m64519 sp:p23858 pid:147326 gb:u00096) (le:10374) (re:11519) (di:complement) U32813 U32813 g1574806 Haemophilus influenzae Rd 71421 -11537543 5000694740 (de:(hi1347) (pn:spermidine) (gn:pota) (gtcfc:12.1) (ec:) (pota_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1347 HI1347 Haemophilus influenzae 727 10032713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885466	15092	37248	1188	396

Description

6500733686 glts:hi1530 sodium/glutamate symport carrier protein:glutamate permease (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1530 HI1530 Haemophilus influenzae 727 -11537544 74132 glts:hi1530 (de:sodium/glutamate symport carrier protein (glutamate permease)) (db:swissprot) GLTS_HAEIN P45240 HAEMOPHILUS INFLUENZAE 727 -11537544 153003 sodium--glutamate symport carrier protein:glutamate permease (cl:sodium--glutamate symport carrier protein) (db:pir2.dat) G64127 G64127 Haemophilus influenzae 727 -11537544 7500882565 hi1530 glutamate permease glts (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:similar to gb:l10328 sp:p19933 gb:d00626 gb:x17499) (le:12218) (re:13432) (di:direct) U32828 U32828 g1574371 Haemophilus influenzae Rd 71421 -11537544 5000694741 (de:(hi1530) (pn:sodium:glutamate permease:glts) (gn:glts) (gtcfc:12.1) (ec:) (glts_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1530 HI1530 Haemophilus influenzae 727 10016662

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885474	15093	37249	324	107

Description

6500733687 sapa:hi1638 peptide transport periplasmic protein precursor (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1638 HI1638 Haemophilus influenzae 727 -11537545 97913 sapa:hi1638 (de:peptide transport periplasmic protein sapa precursor) (db:swissprot) SAPA_HAEIN P45285 HAEMOPHILUS INFLUENZAE 727 -11537545 167076 periplasmic dipeptide transport protein dppa homolog (cl:dipeptide transport protein) (db:pir2.dat) A64134 A64134 Haemophilus influenzae 727 -11537545 7500891309 hi1638 peptide abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p36634 gb:x52093 gb:x74212 pid:414208) (le:65) (re:1762) (di:direct) U32837 U32837 g1574486 Haemophilus influenzae Rd 71421 -11537545 5000694742 (de:(hi1638) (pn:peptide transport periplasmic protein precursor:peptide transport periplasmic protein:sapa) (gn:sapa) (gtcfc:12.1) (ec:) (sapa_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1638 HI1638 Haemophilus influenzae 727 10039792

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885481	15094	37250	465	154

Description

6500733688 sapb:hi1639 peptide transport system permease protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1639 HI1639 Haemophilus influenzae 727 -11537546 97918 sapb:hi1639 (de:peptide transport system permease protein sapb) (db:swissprot) SAPB_HAEIN P45286 HAEMOPHILUS INFLUENZAE 727 -11537546 167079 sapb protein homolog (cl:transmembrane protein dppb) (db:pir2.dat) B64134 B64134 Haemophilus influenzae 727 -11537546 7500891311 hi1639 peptide abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p36668 gb:x52093 gb:x74212 pid:414209) (le:1762) (re:2727) (di:direct) U32837 U32837 g1574487 Haemophilus influenzae Rd 71421 -11537546 5000694743 (de:(hi1639) (pn:peptide transport system permease protein :peptide transport system permease protein:sapb) (gn:sapb) (gtcfc:12.1) (ec:) (sapb_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1639 HI1639 Haemophilus influenzae 727 10039797

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885490	15095	37251	987	329

Description

GTC ORF with score 106 to: (sr:streptococcus pyogenes type m15 opacity factor-positive serotype) (db:genpept-bct1) (de:vir regulon: mry15=mry homolog...scpa15=scpa15 (streptococcuspyogenes, type m15, opacity factor-positive serotype, genomic, 5genes, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885500	15096	37252	1335	444

Description

6500733689 sapc:dppc:hi1640 dipeptide transport system permease protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1640 HI1640 Haemophilus influenzae 727 -11537547 97922 sapc:hi1640 (de:peptide transport system permease protein sapc) (db:swissprot) SAPC_HAEIN P45287 HAEMOPHILUS INFLUENZAE 727 -11537547 166099 sapc protein homolog (db:pir2.dat) C64134 C64134 Haemophilus influenzae 727 -11537547 7500891312 hi1640 peptide abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p36669 gb:x74212 pid:414210 percent) (le:2717) (re:3604) (di:direct) U32837 U32837 g1574488 Haemophilus influenzae Rd 71421 -11537547 5000694744 (de:(hi1640) (pn:peptide transport system permease protein :dipeptide transport system permease protein:dppc) (gn:sapc) (gtcfc:12.1) (ec:) (sapc_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1640 HI1640 Haemophilus influenzae 727 10039801

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885512	15097	37253	201	66

Description

6500733690 sapd:hi1641 peptide transport system atp-binding protein (gtcfc:12.1) (keggfc:11.1) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1641 HI1641 Haemophilus influenzae 727 -11537548 97926 sapd:hi1641 (de:peptide transport system atp-binding protein sapd) (db:swissprot) SAPD_HAEIN P45288 HAEMOPHILUS INFLUENZAE 727 -11537548 167077 peptide transport system atp-binding protein hi1641 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) D64134 D64134 Haemophilus influenzae 727 -11537548 7500891313 hi1641 peptide abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p36636 gb:x74212 pid:414211 percent) (le:3608) (re:4657) (di:direct) U32837 U32837 g1574489 Haemophilus influenzae Rd 71421 -11537548 5000694745 (de:(hi1641) (pn:peptide transport system atp-binding protein :peptide transport system atp-binding protein:sapd) (gn:sapd) (gtcfc:12.1) (ec:) (sapd_haein) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1641 HI1641 Haemophilus influenzae 727 10039805

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885537	15098	37254	261	86

Description

6500733691 brab:hi1728 branched chain aa transport system ii carrier protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae) HI1728 HI1728 Haemophilus influenzae 727 -11537549 166033 hypothetical protein hi1728 (db:pir2.dat) G64138 G64138 Haemophilus influenzae 727 -11537549 7500960704 hi1728 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to sp:p42965 pid:707085 pid:1805475) (le:8107) (re:9300) (di:complement) U32845 U32845 g1574584 Haemophilus influenzae Rd 71421 -11537549 5000694746 (de:(hi1728) (pn:branched chain aa transport system ii carrier protein:brab) (gn:brab) (gtcfc:12.1) (ec:) (keggfc:11.2) (tigrfc:13.1) (db:gtc-haemophilus influenzae)) HI1728 HI1728 Haemophilus influenzae 727 10088060

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885539	15099	37255	786	261

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885544	15100	37256	366	121

Description

6500733692 tlyc:hi0301 hemolysin (gtcfc:12.10:12.11) (keggfc:14.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae) HI0301 HI0301 Haemophilus influenzae 727 -11537550 7500896705 hi0301 (de:hypothetical protein hi0301) (db:swissprot) YBEX_HAEIN Q57368 HAEMOPHILUS INFLUENZAE 727 -11537550 166188 conserved hypothetical protein hi0301 (cl:hypothetical protein b0658) (db:pir2.dat) G64060 G64060 Haemophilus influenzae 727 -11537550 7500896707 hi0301 hemolysin:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1778577 pid:1786879) (le:1275) (re:2174) (di:direct) U32716 U32716 g1573270 Haemophilus influenzae Rd 71421 -11537550 5000694761 (de:(hi0301) (pn:hemolysin:tlyc) (gn:tlyc) (gtcfc:12.10) (ec:) (keggfc:11.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae)) HI0301 HI0301 Haemophilus influenzae 727 10088100

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885551	15101	37257	864	287

Description

6500733693 lktb:hi1051 leukotoxin secretion atp-binding protein (gtcfc:12.14) (keggfc:14.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae) HI1051 HI1051 Haemophilus influenzae 727 -11537551 5500686460 hi1051 (de:hypothetical abc transporter atp-binding protein hi1051) (db:swissprot) YA51_HAEIN Q57180 HAEMOPHILUS INFLUENZAE 727 -11537551 166943 probable atp-binding transport protein hi1051 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) A64180 A64180 Haemophilus influenzae 727 -11537551 7500895871 hi1051 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the completegenome.) (nt:similar to gb:al009126 percent ident: 33.76;) (le:7304) (re:9148) (di:complement) U32785 U32785 g1574084 Haemophilus influenzae Rd 71421 -11537551 5000694762 (de:(hi1051) (pn:leukotoxin secretion atp-binding protein:lktb) (gn:lktb) (gtcfc:12.10) (ec:) (keggfc:11.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae)) HI1051 HI1051 Haemophilus influenzae 727 10088207

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885552	15102	37258	510	169

Description

5000694763 mukf:kicb:hi1372 killing protein suppressor:mukf protein homolog (gtcfc:10.2:14.3) (keggfc:14.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae) HI1372 HI1372 Haemophilus influenzae 727 -11537552 84675 mukf:kicb:hi1372 (de:mukf protein homolog) (db:swissprot) MUKF_HAEIN P45185 HAEMOPHILUS INFLUENZAE 727 -11537552 166933 kicb:mukf killing factor kicb:mukf protein (db:pir2.dat) B64120 B64120 Haemophilus influenzae 727 -11537552 7500886087 hi1372 killing protein kicb (db:genpept-bct1) (de:haemophilus influenzae rd section 132 of 163 of the completegenome.) (nt:similar to gb:d26440 sp:p36567 pid:450465 gb:u00096) (le:4291) (re:5718) (di:direct) U32817 U32817 g1574206 Haemophilus influenzae Rd 71421 -11537552 6500733694 mukf:kicb killing protein suppressor:mukf protein homolog (gtcfc:10.2:14.3) (keggfc:14.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae) HI1372 HI1372 Haemophilus influenzae 727 -11537552

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885558	15103	37259	687	228

Description

5000694764 muke:kica:hi1373 killing protein:kica:muke protein homolog (gtcfc:12.11) (keggfc:14.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae) HI1373 HI1373 Haemophilus influenzae 727 -11537553 84673 muke:kica:hi1373 (de:muke protein homolog) (db:swissprot) MUKE_HAEIN P45186 HAEMOPHILUS INFLUENZAE 727 -11537553 166932 kica:muke kica protein:muke protein (db:pir2.dat) C64120 C64120 Haemophilus influenzae 727 -11537553 7500886085 hi1373 killing protein suppressor kica (db:genpept-bct1) (de:haemophilus influenzae rd section 132 of 163 of the completegenome.) (nt:similar to gb:d26440 sp:p22524 gb:x57550 pid:450466) (le:5765) (re:6496) (di:direct) U32817 U32817 g1574207 Haemophilus influenzae Rd 71421 -11537553 6500733695 muke:kica killing protein:kica:muke protein homolog (gtcfc:12.11) (keggfc:14.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae) HI1373 HI1373 Haemophilus influenzae 727 -11537553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885566	15104	37260	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885567	15105	37261	756	251

Description

5000694765 hemolysin:21 kda:hly:hypothetical protein precursor (gtcfc:12.10:12.11) (keggfc:14.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae) HI1658 HI1658 Haemophilus influenzae 727 -11537554 116086 hi1658 (de:hypothetical protein hi1658 precursor) (db:swissprot) YRAP_HAEIN P45301 HAEMOPHILUS INFLUENZAE 727 -11537554 166189 hypothetical protein hi1658 (db:pir2.dat) A64135 A64135 Haemophilus influenzae 727 -11537554 7500952607 hi1658 hemolysin:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 153 of 163 of the completegenome.) (nt:similar to sp:p45467 pid:606090 gb:u00096) (le:9389) (re:9970) (di:direct) U32838 U32838 g1574507 Haemophilus influenzae Rd 71421 -11537554 6500733696 hemolysin:21 kda:hly:hypothetical protein precursor (gtcfc:12.10:12.11) (keggfc:14.2) (tigrfc:4.2) (db:gtc-haemophilus influenzae) HI1658 HI1658 Haemophilus influenzae 727 -11537554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885585	15106	37262	1686	561

Description

GTC ORF with score 1707 to: (db:genpept-pln1) (de:cochliobolus heterostrophus gtpase activating protein homolog(gap1), dna binding protein with alpha box domain (mat-1), and betaglucosidase homolog (bgl1) genes, complete cds.) (le:9022:9196:9629:9954) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885591	15107	37263	504	167

Description

GTC ORF with score 309 to: (fn:catalyzes the hydrolysis of glucosides) (db:genpept-pln1) (ec:3.2.1.21) (de:coccidioides immitis cytosolic beta-glucosidase (bgl1) gene,complete cds.) (nt:bgl1) (le:660:1500:1810) (re:1436:1751:3393) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885592	15108	37264	663	220

Description

6500733697 thdf:hi1002 thiophene and furan oxidation protein:possible thiophene and furan oxidation protein (gtcfc:12.12) (keggfc:14.2) (tigrfc:4.4) (db:gtc-haemophilus influenzae) HI1002 HI1002 Haemophilus influenzae 727 -11537555 101286 thdf:hi1002 (de:possible thiophene and furan oxidation protein thdf) (db:swissprot) THDF_HAEIN P43730 HAEMOPHILUS INFLUENZAE 727 -11537555 167189 conserved hypothetical protein hi1002 (cl:thiophen / furan oxidation protein:translation elongation factor tu homology) (db:pir2.dat) G64107 G64107 Haemophilus influenzae 727 -11537555 7500893024 hi1002 thiophene and furan oxidation protein thdf (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p25522 pid:290554 gb:u00096) (le:2614) (re:3999) (di:direct) U32781 U32781 g1574033 Haemophilus influenzae Rd 71421 -11537555 5000694766 (de:(hi1002) (pn:possible thiophene and furan oxidation protein :thiophene and furan oxidation protein:thdf) (gn:thdf) (gtcfc:12.12) (ec:) (thdf_haein) (keggfc:11.2) (tigrfc:4.4) (db:gtc-haemophilus influenzae)) HI1002 HI1002 Haemophilus influenzae 727 10043127

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885593	15109	37265	1083	360

Description

6500733698 soda:hi1088 superoxide dismutase:mn (gtcfc:12.12) (ec:1.15.1.1) (keggfc:14.1) (tigrfc:4.4) (db:gtc-haemophilus influenzae) HI1088 HI1088 Haemophilus influenzae 727 -11537556 137630 soda superoxide dismutase:mn (cl:superoxide dismutase (mn)) (ec:1.15.1.1) (db:pir2.dat) C64182 C64182 Haemophilus influenzae 727 -11537556 7500953943 hi1088 superoxide dismutase soda (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to gb:x73832 pid:1574643 percent ident:) (le:245) (re:892) (di:complement) U32789 U32789 g1574643 Haemophilus influenzae Rd 71421 -11537556 5000694767 (de:(hi1088) (pn:mn:superoxide dismutase:soda) (gn:soda) (gtcfc:12.12) (ec:1.15.1.1) (sodm_haein) (keggfc:11.1) (tigrfc:4.4) (db:gtc-haemophilus influenzae)) HI1088 HI1088 Haemophilus influenzae 727 10070169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885598	15110	37266	690	229

Description

6500733699 era:hi0013 gtp-binding protein (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0013 HI0013 Haemophilus influenzae 727 -11537557 70480 era:hi0013 (de:gtp-binding protein era) (db:swissprot) ERA_HAEIN P43728 HAEMOPHILUS INFLUENZAE 727 -11537557 143115 era gtp-binding protein era (cl:ras transforming protein:translation elongation factor tu homology) (db:pir2.dat) F64042 F64042 Haemophilus influenzae 727 -11537557 7500881108 hi0013 gtp-binding protein era (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to gb:m14658 sp:p06616 pid:416295 pid:42767) (le:1139) (re:2047) (di:complement) U32687 U32687 g1572957 Haemophilus influenzae Rd 71421 -11537557 5000694768 (de:(hi0013) (pn:gtp-binding protein :gtp-binding protein:era) (gn:era) (gtcfc:12.13) (ec:) (era_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0013 HI0013 Haemophilus influenzae 727 10013059

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885607	15111	37267	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885612	15112	37268	624	207

Description

6500733700 uxur:hi0054 uxu operon regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0054 HI0054 Haemophilus influenzae 727 -11537558 104083 uxur:hi0054 (de:uxu operon regulator) (db:swissprot) UXUR_HAEIN P44487 HAEMOPHILUS INFLUENZAE 727 -11537558 167261 regulatory protein uxur homolog (cl:regulatory protein uxur 2) (db:pir2.dat) D64045 D64045 Haemophilus influenzae 727 -11537558 7500893932 hi0054 uxu operon regulator uxur (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39161 pid:537165) (le:7748) (re:8548) (di:direct) U32690 U32690 g1573001 Haemophilus influenzae Rd 71421 -11537558 5000694769 (de:(hi0054) (pn:uxu operon regulator:uxur) (gn:uxur) (gtcfc:12.13) (ec:) (uxur_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0054 HI0054 Haemophilus influenzae 727 10045853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885615	15113	37269	540	179

Description

5000694770 30 kda protein:hypothetical protein (gtcfc:14.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0159 HI0159 Haemophilus influenzae 727 -11537559 110663 hi0159 (de:hypothetical protein hi0159) (db:swissprot) YCED_HAEIN P43790 HAEMOPHILUS INFLUENZAE 727 -11537559 165968 conserved hypothetical protein hi0159 (db:pir2.dat) H64051 H64051 Haemophilus influenzae 727 -11537559 241612 rpmf 30k protein (db:genpept-bct1) (de:haemophilus influenzae bola (bola), glutathione reductase (gor),phosphatidylserine decarboxylase (psd), 30k protein (rpmf), genes,complete cds.) (le:4247) (re:4771) (di:direct) HIU20229 U20229 g644856 Haemophilus influenzae 727 -11537559 7500921679 hi0159 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:similar to gb:m29698 sp:p14189 pid:146052) (le:9222) (re:9746) (di:complement) U32701 U32701 g1573116 Haemophilus influenzae Rd 71421 -11537559 6500733701 30 kda protein:hypothetical protein (gtcfc:14.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0159 HI0159 Haemophilus influenzae 727 -11537559

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885617	15114	37270	858	285

Description

6500733702 bola:hi0163 putative murein gene regulator:protein homolog (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0163 HI0163 Haemophilus influenzae 727 -11537560 61927 bola:hi0163 (de:bola protein homolog) (db:swissprot) BOLA_HAEIN P43780 HAEMOPHILUS INFLUENZAE 727 -11537560 167106 cell division protein bola homolog (cl:bola protein) (db:pir2.dat) B64052 B64052 Haemophilus influenzae 727 -11537560 241608 bola bola (fn:stationary phase regulatory protein) (db:genpept-bct1) (de:haemophilus influenzae bola (bola), glutathione reductase (gor),phosphatidylserine decarboxylase (psd), 30k protein (rpmf), genes,complete cds.) (le:519) (re:830) (di:complement) HIU20229 U20229 g644852 Haemophilus influenzae 727 -11537560 7500877883 hi0163 transcriptional regulator:putative bola (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to pid:663269 percent identity: 46.53;) (le:2364) (re:2675) (di:direct) U32702 U32702 g1573121 Haemophilus influenzae Rd 71421 -11537560 5000694771 (de:(hi0163) (pn:protein homolog:putative murein gene regulator:bola) (gn:bola) (gtcfc:12.13) (ec:) (bola_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0163 HI0163 Haemophilus influenzae 727 10004631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885640	15115	37271	1248	416

Description

6500733703 fur:hi0190 ferric uptake regulation protein (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0190 HI0190 Haemophilus influenzae 727 -11537561 72544 fur:hi0190 (de:ferric uptake regulation protein (ferric uptake regulator)) (db:swissprot) FUR_HAEIN P44561 HAEMOPHILUS INFLUENZAE 727 -11537561 166131 ferric uptake regulator (cl:ferric uptake regulator) (db:pir2.dat) B64053 B64053 Haemophilus influenzae 727 -11537561 7500881920 hi0190 ferric uptake regulation protein fur (db:genpept-bct1) (de:haemophilus influenzae rd section 19 of 163 of the complete genome.) (nt:similar to pid:1568605 percent identity: 69.39;) (le:4107) (re:4547) (di:complement) U32704 U32704 g1573148 Haemophilus influenzae Rd 71421 -11537561 5000694772 (de:(hi0190) (pn:ferric uptake regulation protein:fur) (gn:fur) (gtcfc:12.13) (ec:) (fur_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0190 HI0190 Haemophilus influenzae 727 10015095

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885641	15116	37272	1257	418

Description

GTC ORF with score 235 to: (or:Homo sapiens) (sr:homo sapiens male myeloblast cell_line:kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0209 gene, partial cds.) (nt:similar to a human major crk-binding protein) (le:<1) (re:5531) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885679	15117	37273	435	144

Description

6500733704 msbb:hi0199 multicopy suppressor of high-temperature requirement htrb protein:protein homolog (gtcfc:10.2:14.3) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0199 HI0199 Haemophilus influenzae 727 -11537562 84290 msbb:hi0199 (ec:2.3.1.-) (de:(ec 2.3.1.-)) (db:swissprot) MSBB_HAEIN P44567 HAEMOPHILUS INFLUENZAE 727 -11537562 167012 membrane-bound lytic transglycosylase homolog (db:pir2.dat) I64053 I64053 Haemophilus influenzae 727 -11537562 7500885917 hi0199 lipid a biosynthesis kdo 2-lauroyl -lipid iva (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:similar to gb:m77039 sp:p24205 gb:m87660 pid:146877) (le:1765) (re:2721) (di:direct) U32705 U32705 g1573159 Haemophilus influenzae Rd 71421 -11537562 5000694773 (de:(hi0199) (pn:protein homolog:multicopy suppressor of high-temperature requirement htrb protein:msbb) (gn:msbb) (gtcfc:12.13) (ec:) (msbb_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0199 HI0199 Haemophilus influenzae 727 10026491

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885708	15118	37274	366	121

Description

6500733705 arcb:hi0220 aerobic respiration control sensor protein arcb homolog (gtcfc:12.13) (ec:2.7.3.-) (keggfc:14.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0220 HI0220 Haemophilus influenzae 727 -11537563 59991 arcb:hi0220 (ec:2.7.3.-) (de:aerobic respiration control sensor protein arcb homolog,) (db:swissprot) ARCB_HAEIN P44578 HAEMOPHILUS INFLUENZAE 727 -11537563 165989 aerobic respiration control protein arcb homolog hi0220 (db:pir2.dat) G64055 G64055 Haemophilus influenzae 727 -11537563 5000694774 (de:(hi0220) (pn:aerobic respiration control sensor protein homolog:aerobic respiration control sensor protein:arcb) (gn:arcb) (gtcfc:12.13) (ec:2.7.3.-) (arcb_haein) (keggfc:11.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0220 HI0220 Haemophilus influenzae 727 10002724

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885711	15119	37275	1506	501

Description

6500733706 lrp:hi0224 leucine responsive regulatory protein (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0224 HI0224 Haemophilus influenzae 727 -11537564 108997 hi0224 (de:hypothetical transcriptional regulator hi0224) (db:swissprot) Y224_HAEIN P44580 HAEMOPHILUS INFLUENZAE 727 -11537564 166941 glutamate uptake regulatory protein homolog (db:pir2.dat) B64056 B64056 Haemophilus influenzae 727 -11537564 7500894908 hi0224 transcriptional regulator:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 23 of 163 of the complete genome.) (nt:similar to sp:p55658 pid:2182633 percent identity:) (le:8087) (re:8593) (di:direct) U32708 U32708 g1573188 Haemophilus influenzae Rd 71421 -11537564 5000694775 (de:(hi0224) (pn:leucine responsive regulatory protein:lrp) (gn:lrp) (gtcfc:12.13) (ec:) (y224_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0224 HI0224 Haemophilus influenzae 727 10050729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885713	15120	37276	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885745	15121	37277	630	209

Description

5000694776 arsc:arsg:hi0236 arsc protein:arsc:putative arsenate reductase:arsenical pump modifier (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0236 HI0236 Haemophilus influenzae 727 -11537565 60286 arsc:arsg:hi0236 (de:putative arsenate reductase (arsenical pump modifier)) (db:swissprot) ARSC_HAEIN P44589 HAEMOPHILUS INFLUENZAE 727 -11537565 166012 arsenate reductase homolog hi0236 (db:pir2.dat) G64056 G64056 Haemophilus influenzae 727 -11537565 7500877213 hi0236 arsenate reductase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:similar to pid:1805555 percent identity: 45.74;) (le:411) (re:761) (di:complement) U32710 U32710 g1573202 Haemophilus influenzae Rd 71421 -11537565 6500733707 arsc:arsg arsc protein:arsc:putative arsenate reductase:arsenical pump modifier (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0236 HI0236 Haemophilus influenzae 727 -11537565

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885746	15122	37278	564	187

Description

6500733708 narq:hi0267 nitrate sensor protein:sensor protein homolog (gtcfc:12.13:14.1) (ec:2.7.3.-) (keggfc:14.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0267 HI0267 Haemophilus influenzae 727 -11537566 85251 narq:hi0267 (ec:2.7.3.-) (de:sensor protein narq homolog,) (db:swissprot) NARQ_HAEIN P44604 HAEMOPHILUS INFLUENZAE 727 -11537566 167033 nitrate sensor protein homolog (cl:nitrate/nitrite sensor protein narq) (db:pir2.dat) F64058 F64058 Haemophilus influenzae 727 -11537566 7500886310 hi0267 nitrate/nitrite sensor protein narq (db:genpept-bct1) (de:haemophilus influenzae rd section 28 of 163 of the complete genome.) (nt:similar to gb:m94724 sp:p27896 gb:x65714 pid:146928) (le:713) (re:2416) (di:direct) U32713 U32713 g1573233 Haemophilus influenzae Rd 71421 -11537566 5000694777 (de:(hi0267) (pn:sensor protein homolog:nitrate sensor protein:narq) (gn:narq) (gtcfc:12.13) (ec:2.7.3.-) (narq_haein) (keggfc:11.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0267 HI0267 Haemophilus influenzae 727 10027432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885747	15123	37279	183	60

Description

6500733709 rpoh:hi0269 rna polymerase sigma-32 factor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0269 HI0269 Haemophilus influenzae 727 -11537567 95944 rpoh:hi0269 (de:rna polymerase sigma-32 factor) (db:swissprot) RP32_HAEIN P44404 HAEMOPHILUS INFLUENZAE 727 -11537567 139187 transcription initiation factor sigma 32 (cl:transcription initiation factor sigma katf:transcription initiation factor sigma katf homology) (db:pir2.dat) H64058 H64058 Haemophilus influenzae 727 -11537567 7500890504 hi0269 rna polymerase sigma-32 factor rpoh (db:genpept-bct1) (de:haemophilus influenzae rd section 28 of 163 of the complete genome.) (nt:similar to sp:p00580 gb:u00039 gb:k02177 gb:m20668) (le:3577) (re:4422) (di:direct) U32713 U32713 g1573235 Haemophilus influenzae Rd 71421 -11537567 5000694778 (de:(hi0269) (pn:rna polymerase sigma-32 factor:rpoh) (gn:rpoh) (gtcfc:12.13) (ec:) (rp32_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0269 HI0269 Haemophilus influenzae 727 10037890

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885748	15124	37280	600	199

Description

5000694779 mercury resistance homolog:yhdm:hypothetical transcriptional regulator hi0293 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0293 HI0293 Haemophilus influenzae 727 -11537568 109056 hi0293 (de:hypothetical transcriptional regulator hi0293) (db:swissprot) YBBI_HAEIN P44617 HAEMOPHILUS INFLUENZAE 727 -11537568 166986 mercuric resistance operon regulatory protein homolog hi0293 (cl:transcription repressor glnr) (db:pir2.dat) I64059 I64059 Haemophilus influenzae 727 -11537568 7500896571 hi0293 transcriptional regulator:merr family (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77565 pid:1773169) (le:7024) (re:7410) (di:direct) U32715 U32715 g1573261 Haemophilus influenzae Rd 71421 -11537568 6500733710 mercury resistance homolog:yhdm:hypothetical transcriptional regulator hi0293 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0293 HI0293 Haemophilus influenzae 727 -11537568

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885750	15125	37281	237	78

Description

6500733711 metj:hi0294 metf aporepressor:met repressor:met regulon regulatory protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0294 HI0294 Haemophilus influenzae 727 -11537569 154790 metj regulatory protein metj (cl:metj protein) (db:pir2.dat) A64060 A64060 Haemophilus influenzae 727 -11537569 7500955510 hi0294 met repressor metj (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p08338 gb:m12869 gb:m38202) (le:7424) (re:7741) (di:complement) U32715 U32715 g1573262 Haemophilus influenzae Rd 71421 -11537569 5000694780 (de:(hi0294) (pn:met repressor:met regulon regulatory protein :metf aporepressor:metj) (gn:metj) (gtcfc:12.13) (ec:) (metj_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0294 HI0294 Haemophilus influenzae 727 10081709

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885751	15126	37282	306	101

Description

6500733712 glnb:hi0337 nitrogen regulatory protein p-ii (gtcfc:10.2:2.7) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0337 HI0337 Haemophilus influenzae 727 -11537570 73971 glnb:hi0337 (de:nitrogen regulatory protein p-ii) (db:swissprot) GLNB_HAEIN P43795 HAEMOPHILUS INFLUENZAE 727 -11537570 154796 glnb nitrogen regulatory protein p-ii (cl:regulatory protein p-ii) (db:pir2.dat) F64062 F64062 Haemophilus influenzae 727 -11537570 7500882468 hi0337 nitrogen regulatory protein p-ii glnb (db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788904 pid:1799977) (le:7226) (re:7564) (di:direct) U32718 U32718 g1573306 Haemophilus influenzae Rd 71421 -11537570 5000694781 (de:(hi0337) (pn:nitrogen regulatory protein p-ii:glnb) (gn:glnb) (gtcfc:12.13) (ec:) (glnb_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0337 HI0337 Haemophilus influenzae 727 10016501

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885771	15127	37283	819	272

Description

5000694782 transcription activator:tena:hypothetical protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0358 HI0358 Haemophilus influenzae 727 -11537571 109113 hi0358 (de:hypothetical protein hi0358) (db:swissprot) Y358_HAEIN P44659 HAEMOPHILUS INFLUENZAE 727 -11537571 167199 transcription activator homolog hi0358 (db:pir2.dat) D64063 D64063 Haemophilus influenzae 727 -11537571 7500895187 hi0358 transcriptional activator:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to gb:ae000511 pid:2314455 percent) (le:3960) (re:4607) (di:direct) U32720 U32720 g1573326 Haemophilus influenzae Rd 71421 -11537571 6500733713 transcription activator:tena:hypothetical protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0358 HI0358 Haemophilus influenzae 727 -11537571

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885782	15128	37284	1308	435

Description

6500733714 icc:hi0399 lacz expression regulator:protein homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0399 HI0399 Haemophilus influenzae 727 -11537572 78691 icc:hi0399 (de:icc protein homolog) (db:swissprot) ICC_HAEIN P44685 HAEMOPHILUS INFLUENZAE 727 -11537572 166939 3:5-cyclic-nucleotide phosphodiesterase:cpda homolog:hypothetical protein hi0399:icc protein (cl:3',5'-cyclic-nucleotide phosphodiesterase cpda:3',5'-cyclic-nucleotide phosphodiesterase cpda homology:phosphoesterase core homology) (ec:3.1.4.17) (db:pir1.dat) E64065 E64065 Haemophilus influenzae 727 -11537572 7500883791 hi0399 lacz expression regulator icc (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to gb:d16557 sp:p36650 pid:453396) (le:6772) (re:7596) (di:direct) U32723 U32723 g1573370 Haemophilus influenzae Rd 71421 -11537572 5000694783 (de:(hi0399) (pn:protein homolog:lacz expression regulator:icc) (gn:icc) (gtcfc:12.13) (ec:) (icc_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0399 HI0399 Haemophilus influenzae 727 10021029

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885803	15129	37285	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885805	15130	37286	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885808	15131	37287	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885812	15132	37288	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885813	15133	37289	333	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885825	15134	37290	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885831	15135	37291	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885832	15136	37292	699	232

Description

6500733715 tyrr:hi0410 transcriptional regulatory protein:transcriptional regulatory protein homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0410 HI0410 Haemophilus influenzae 727 -11537573 102930 tyrr:hi0410 (de:transcriptional regulatory protein tyrr homolog) (db:swissprot) TYRR_HAEIN P44694 HAEMOPHILUS INFLUENZAE 727 -11537573 167205 transcription regulator tyrr homolog (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) C64066 C64066 Haemophilus influenzae 727 -11537573 7500893616 hi0410 transcriptional regulatory protein tyrr (db:genpept-bct1) (de:haemophilus influenzae rd section 39 of 163 of the complete genome.) (nt:similar to gb:m12114 sp:p07604 pid:148092 gb:u00096) (le:4409) (re:5365) (di:direct) U32724 U32724 g1573383 Haemophilus influenzae Rd 71421 -11537573 5000694784 (de:(hi0410) (pn:transcriptional regulatory protein homolog:transcriptional regulatory protein:tyrr) (gn:tyrr) (gtcfc:12.13) (ec:) (tyrr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0410 HI0410 Haemophilus influenzae 727 10044742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885844	15137	37293	201	67

Description

5000694785 lon:lon-a:hi0462 atp-dependent proteinase:lon:atp-dependent protease la (gtcfc:12.13:14.1) (ec:3.4.21.53) (keggfc:14.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0462 HI0462 Haemophilus influenzae 727 -11537574 82323 lon:lon-a:hi0462 (ec:3.4.21.53) (de:atp-dependent protease la,) (db:swissprot) LON_HAEIN P43864 HAEMOPHILUS INFLUENZAE 727 -11537574 140621 lon:lon-a endopeptidase la (cl:atp-dependent serine proteinase la) (ec:3.4.21.53) (db:pir2.dat) A64070 A64070 Haemophilus influenzae 727 -11537574 7500885102 hi0462 atp-dependent proteinase lon (db:genpept-bct1) (de:haemophilus influenzae rd section 44 of 163 of the complete genome.) (nt:similar to gb:m38347 sp:p08177 gb:j03896 gb:l12349) (le:127) (re:2538) (di:direct) U32729 U32729 g1573440 Haemophilus influenzae Rd 71421 -11537574 6500733716 lon:lon-a atp-dependent proteinase:lon:atp-dependent protease la (gtcfc:12.13:14.1) (ec:3.4.21.53) (keggfc:14.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0462 HI0462 Haemophilus influenzae 727 -11537574

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885851	15138	37294	1029	342

Description

6500733717 rbsr:hi0506 rbs repressor:ribose operon repressor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0506 HI0506 Haemophilus influenzae 727 -11537575 167132 rbs repressor homolog (cl:lac repressor) (db:pir2.dat) C64073 C64073 Haemophilus influenzae 727 -11537575 7500960729 hi0506 rbs repressor rbsr (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p25551 gb:d10466 gb:m13169) (le:6364) (re:7362) (di:direct) U32732 U32732 g1573487 Haemophilus influenzae Rd 71421 -11537575 5000694786 (de:(hi0506) (pn:ribose operon repressor:rbs repressor:rbsr) (gn:rbsr) (gtcfc:12.13) (ec:) (rbsr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0506 HI0506 Haemophilus influenzae 727 10088291

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885855	15139	37295	297	98

Description

6500733718 rpod:hi0533 rna polymerase sigma-70 factor:rna polymerase sigma factor:sigma-70 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0533 HI0533 Haemophilus influenzae 727 -11537576 96328 rpod:hi0533 (de:rna polymerase sigma factor rpod (sigma-70)) (db:swissprot) RPSD_HAEIN P43766 HAEMOPHILUS INFLUENZAE 727 -11537576 139159 transcription initiation factor sigma 70 (cl:transcription initiation factor sigma 70:transcription initiation factor sigma katf homology:transcription initiation factor sigma region 1 homology) (db:pir2.dat) B64075 B64075 Haemophilus influenzae 727 -11537576 7500890684 hi0533 rna polymerase sigma-70 factor rpod (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:similar to gb:j01687 sp:p00579 pid:147756) (le:6686) (re:8575) (di:direct) U32735 U32735 g1573517 Haemophilus influenzae Rd 71421 -11537576 5000694787 (de:(hi0533) (pn:rna polymerase sigma factor :sigma-70:rna polymerase sigma-70 factor:rpod) (gn:rpod) (gtcfc:12.13) (ec:) (rpsd_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0533 HI0533 Haemophilus influenzae 727 10038271

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885860	15140	37296	1167	388

Description

6500733719 asnc:hi0563 regulatory protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0563 HI0563 Haemophilus influenzae 727 -11537577 60373 asnc:hi0563 (de:regulatory protein asnc) (db:swissprot) ASNC_HAEIN P44337 HAEMOPHILUS INFLUENZAE 727 -11537577 154784 asnc regulatory protein asnc (cl:regulatory protein asnc) (db:pir2.dat) G64077 G64077 Haemophilus influenzae 727 -11537577 7500877252 hi0563 transcriptional regulatory protein asnc (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p03809 gb:k00826 pid:290592) (le:608) (re:1060) (di:complement) U32738 U32738 g1573550 Haemophilus influenzae Rd 71421 -11537577 5000694788 (de:(hi0563) (pn:regulatory protein :regulatory protein:asnc) (gn:asnc) (gtcfc:12.13) (ec:) (asnc_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0563 HI0563 Haemophilus influenzae 727 10003099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885870	15141	37297	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885889	15142	37298	1602	533

Description

6500733720 oxyr:hi0571 hydrogen peroxide-inducible activator:hydrogen peroxide-inducible genes activator (gtcfc:12.13:12.12) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0571 HI0571 Haemophilus influenzae 727 -11537578 88031 oxyr:hi0571 (de:hydrogen peroxide-inducible genes activator) (db:swissprot) OXYR_HAEIN P44418 HAEMOPHILUS INFLUENZAE 727 -11537578 154801 oxyr regulatory protein oxyr (cl:regulatory protein ilvy) (db:pir2.dat) C64078 C64078 Haemophilus influenzae 727 -11537578 243352 oxyr oxyr (fn:transcriptional activator) (sr:haemophilus influenzae strain=tn106) (db:genpept-bct1) (de:haemophilus influenzae oxyr (oxyr) gene, complete cds.) (le:1) (re:906) (di:direct) HIU49355 U49355 g1491811 Haemophilus influenzae 727 -11537578 297234 hi0571 hydrogen peroxide-inducible genes activator (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to sp:p11721 gb:j04553 gb:m34102 gb:x16531) (le:9931) (re:10836) (di:complement) U32738 U32738 g1573558 Haemophilus influenzae Rd 71421 -11537578 5000694789 (de:(hi0571) (pn:hydrogen peroxide-inducible genes activator:hydrogen peroxide-inducible activator:oxyr) (gn:oxyr) (gtcfc:12.13) (ec:) (oxyr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0571 HI0571 Haemophilus influenzae 727 10030172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885907	15143	37299	297	98

Description

6500733721 fucr:hi0615 l-fucose operon activator (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0615 HI0615 Haemophilus influenzae 727 -11537579 72512 fucr:hi0615 (de:l-fucose operon activator) (db:swissprot) FUCR_HAEIN P44780 HAEMOPHILUS INFLUENZAE 727 -11537579 166934 fuc operon regulatory protein homolog (db:pir2.dat) G64081 G64081 Haemophilus influenzae 727 -11537579 7500881909 hi0615 l-fucose operon activator fucr (db:genpept-bct1) (de:haemophilus influenzae rd section 59 of 163 of the complete genome.) (nt:similar to sp:p11554 gb:x15025 pid:41508 pid:882700) (le:121) (re:870) (di:complement) U32744 U32744 g1573609 Haemophilus influenzae Rd 71421 -11537579 5000694790 (de:(hi0615) (pn:l-fucose operon activator:fucr) (gn:fucr) (gtcfc:12.13) (ec:) (fucr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0615 HI0615 Haemophilus influenzae 727 10015063

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885908	15144	37300	591	196

Description

6500733722 glpr:hi0619 glycerol-3-phosphate regulon repressor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0619 HI0619 Haemophilus influenzae 727 -11537580 74049 glpr:hi0619 (de:glycerol-3-phosphate regulon repressor) (db:swissprot) GLPR_HAEIN P44784 HAEMOPHILUS INFLUENZAE 727 -11537580 166164 glycerol-3-phosphate regulon repressor homolog hi0619 (db:pir2.dat) A64082 A64082 Haemophilus influenzae 727 -11537580 7500882517 hi0619 glycerol-3-phosphate regulon repressor glpr (db:genpept-bct1) (de:haemophilus influenzae rd section 59 of 163 of the complete genome.) (nt:similar to sp:p09392 gb:m96795 pid:146186) (le:5136) (re:5903) (di:direct) U32744 U32744 g1573613 Haemophilus influenzae Rd 71421 -11537580 5000694791 (de:(hi0619) (pn:glycerol-3-phosphate regulon repressor:glpr) (gn:glpr) (gtcfc:12.13) (ec:) (glpr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0619 HI0619 Haemophilus influenzae 727 10016579

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885912	15145	37301	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885927	15146	37302	729	242

Description

6500733723 rpoe:hi0628 rna polymerase sigma-e factor:sigma-24 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0628 HI0628 Haemophilus influenzae 727 -11537581 96273 rpoe:hi0628 (de:rna polymerase sigma-e factor (sigma-24)) (db:swissprot) RPOE_HAEIN P44790 HAEMOPHILUS INFLUENZAE 727 -11537581 167148 transcription initiation factor sigma e (cl:transcription initiation factor sigma e) (db:pir2.dat) F64082 F64082 Haemophilus influenzae 727 -11537581 7500890649 hi0628 rna polymerase sigma-e factor rpoe (db:genpept-bct1) (de:haemophilus influenzae rd section 60 of 163 of the complete genome.) (nt:similar to sp:p34086 pid:1045628 pid:987648) (le:9143) (re:9712) (di:direct) U32745 U32745 g1573624 Haemophilus influenzae Rd 71421 -11537581 5000694792 (de:(hi0628) (pn:sigma-24:rna polymerase sigma-e factor:rpoe) (gn:rpoe) (gtcfc:12.13) (ec:) (rpoe_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0628 HI0628 Haemophilus influenzae 727 10038216

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885939	15147	37303	567	188

Description

5000694793 rsea:mcla:hi0629 negative rpo regulator:mcla:sigma-e factor negative regulatory protein homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0629 HI0629 Haemophilus influenzae 727 -11537582 97458 rsea:mcla:hi0629 (de:sigma-e factor negative regulatory protein homolog) (db:swissprot) RSEA_HAEIN P44791 HAEMOPHILUS INFLUENZAE 727 -11537582 167032 mcla protein homolog (db:pir2.dat) G64082 G64082 Haemophilus influenzae 727 -11537582 7500891145 hi0629 sigma-e factor negative regulatory protein (db:genpept-bct1) (de:haemophilus influenzae rd section 60 of 163 of the complete genome.) (nt:similar to sp:p38106 gb:u10148 gb:u00096) (le:9737) (re:10324) (di:direct) U32745 U32745 g1573625 Haemophilus influenzae Rd 71421 -11537582 6500733724 rsea:mcla negative rpo regulator:mcla:sigma-e factor negative regulatory protein homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0629 HI0629 Haemophilus influenzae 727 -11537582

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885941	15148	37304	510	169

Description

6500733725 ilvy:hi0681 transcriptional activator protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0681 HI0681 Haemophilus influenzae 727 -11537583 79279 ilvy:hi0681 (de:transcriptional activator protein ilvy) (db:swissprot) ILVY_HAEIN P44821 HAEMOPHILUS INFLUENZAE 727 -11537583 167203 regulatory protein ilvy homolog (cl:regulatory protein ilvy) (db:pir2.dat) A64086 A64086 Haemophilus influenzae 727 -11537583 7500884066 hi0681 transcriptional activator ilvy (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p05827 gb:m32253 pid:146476) (le:8823) (re:9701) (di:complement) U32750 U32750 g1573681 Haemophilus influenzae Rd 71421 -11537583 5000694794 (de:(hi0681) (pn:transcriptional activator protein :transcriptional activator protein:ilvy) (gn:ilvy) (gtcfc:12.13) (ec:) (ilvy_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0681 HI0681 Haemophilus influenzae 727 10021607

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885971	15149	37305	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885978	15150	37306	486	161

Description

6500733726 relb:hi0710 negative regulator of translation (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0710 HI0710 Haemophilus influenzae 727 -11537584 167031 hypothetical protein hi0710 (db:pir2.dat) A64088 A64088 Haemophilus influenzae 727 -11537584 7500960671 hi0710 h. influenzae predicted coding region hi0710 (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:144) (re:440) (di:direct) U32754 U32754 g1573712 Haemophilus influenzae Rd 71421 -11537584 5000694795 (de:(hi0710) (pn:negative regulator of translation:relb) (gn:relb) (gtcfc:12.13) (ec:) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0710 HI0710 Haemophilus influenzae 727 10088262

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885979	15151	37307	264	87

Description

6500733727 narp:hi0726 nitrate/nitrite response regulator protein:nitrate/nitrite response regulator protein homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0726 HI0726 Haemophilus influenzae 727 -11537585 85248 narp:hi0726 (de:nitrate/nitrite response regulator protein homolog) (db:swissprot) NARP_HAEIN P44845 HAEMOPHILUS INFLUENZAE 727 -11537585 167035 narp nitrate/nitrite response regulator protein narp (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) A64089 A64089 Haemophilus influenzae 727 -11537585 7500886308 hi0726 nitrate/nitrite response regulator protein (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:similar to gb:u00008 sp:p31802 gb:l11273 pid:304917) (le:61) (re:687) (di:complement) U32756 U32756 g1573730 Haemophilus influenzae Rd 71421 -11537585 5000694796 (de:(hi0726) (pn:nitrate) (gn:narp) (gtcfc:12.13) (ec:) (narp_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0726 HI0726 Haemophilus influenzae 727 10027429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885985	15152	37308	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885986	15153	37309	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885988	15154	37310	450	149

Description

6500733728 lexa:hi0749 lexa repressor:repressor (gtcfc:12.13:14.1) (ec:3.4.21.88) (keggfc:14.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0749 HI0749 Haemophilus influenzae 727 -11537586 154698 lexa lexa protein:repressor lexa (cl:lexa repressor) (db:pir2.dat) E64090 E64090 Haemophilus influenzae 727 -11537586 7500955488 hi0749 lexa repressor lexa (db:genpept-bct1) (de:haemophilus influenzae rd section 74 of 163 of the complete genome.) (nt:similar to sp:p03033 gb:j01643 pid:146608) (le:155) (re:784) (di:direct) U32759 U32759 g1573757 Haemophilus influenzae Rd 71421 -11537586 5000694797 (de:(hi0749) (pn:repressor:lexa repressor:lexa) (gn:lexa) (gtcfc:12.13) (ec:3.4.21.88) (lexa_haein) (keggfc:11.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0749 HI0749 Haemophilus influenzae 727 10081684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885991	15155	37311	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885993	15156	37312	600	199

Description

5000694798 glucokinase regulator:hypothetical protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0754 HI0754 Haemophilus influenzae 727 -11537587 109276 hi0754 (de:hypothetical protein hi0754) (db:swissprot) YFEU_HAEIN P44862 HAEMOPHILUS INFLUENZAE 727 -11537587 166155 glucokinase regulator homolog (cl:conserved hypothetical protein b2428) (db:pir2.dat) I64090 I64090 Haemophilus influenzae 727 -11537587 7500923424 hi0754 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 74 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p76535 pid:1788768 percent) (le:8339) (re:9250) (di:direct) U32759 U32759 g1573762 Haemophilus influenzae Rd 71421 -11537587 6500733729 glucokinase regulator:hypothetical protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0754 HI0754 Haemophilus influenzae 727 -11537587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501885996	15157	37313	1146	381

Description

6500733730 nadr:hi0763 nadab transcriptional regulator:transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0763 HI0763 Haemophilus influenzae 727 -11537588 85151 nadr:hi0763 (de:transcriptional regulator nadr) (db:swissprot) NADR_HAEIN P44308 HAEMOPHILUS INFLUENZAE 727 -11537588 167029 nadr transcription regulator nadr (db:pir2.dat) D64091 D64091 Haemophilus influenzae 727 -11537588 7500886250 hi0763 transcriptional regulator nadr (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p27278 pid:537230 gb:u00096) (le:6424) (re:7689) (di:complement) U32760 U32760 g1573771 Haemophilus influenzae Rd 71421 -11537588 5000694799 (de:(hi0763) (pn:transcriptional regulator :nadab transcriptional regulator:nadr) (gn:nadr) (gtcfc:12.13) (ec:) (nadr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0763 HI0763 Haemophilus influenzae 727 10027332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886000	15158	37314	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886008	15159	37315	573	191

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886009	15160	37316	285	94

Description

6500733731 csra:hi0813 carbon storage regulator:carbon storage regulator homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0813 HI0813 Haemophilus influenzae 727 -11537589 66695 csra:hi0813 (de:carbon storage regulator homolog) (db:swissprot) CSRA_HAEIN P44879 HAEMOPHILUS INFLUENZAE 727 -11537589 166039 carbon storage regulator csra homolog (cl:glycogen biosynthesis inhibitor) (db:pir2.dat) H64095 H64095 Haemophilus influenzae 727 -11537589 7500879504 hi0813 carbon storage regulator csra (db:genpept-bct1) (de:haemophilus influenzae rd section 78 of 163 of the complete genome.) (nt:similar to gb:l07596 sp:p31803 pid:304882 gb:u00096) (le:9006) (re:9197) (di:complement) U32763 U32763 g1573825 Haemophilus influenzae Rd 71421 -11537589 5000694800 (de:(hi0813) (pn:carbon storage regulator homolog:carbon storage regulator:csra) (gn:csra) (gtcfc:12.13) (ec:) (csra_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0813 HI0813 Haemophilus influenzae 727 10009313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886011	15161	37317	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886014	15162	37318	1479	492

Description

5000694801 galr:gals:hi0821 gals:galactose operon repressor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0821 HI0821 Haemophilus influenzae 727 -11537590 73089 galr:gals:hi0821 (de:galactose operon repressor) (db:swissprot) GALR_HAEIN P31766 HAEMOPHILUS INFLUENZAE 727 -11537590 153217 galr gal repressor (cl:lac repressor) (db:pir2.dat) F64096 F64096 Haemophilus influenzae 727 -11537590 7500882094 hi0821 galactose operon repressor galr (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to sp:p31766 gb:x65934 pid:1573834 percent) (le:6194) (re:7192) (di:direct) U32764 U32764 g1573834 Haemophilus influenzae Rd 71421 -11537590 6500733732 galr:gals gals:galactose operon repressor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0821 HI0821 Haemophilus influenzae 727 -11537590

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886046	15163	37319	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886054	15164	37320	1149	382

Description

5000694802 p14 protein:p14:hypothetical protein precursor (gtcfc:14.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0827 HI0827 Haemophilus influenzae 727 -11537591 110801 hi0827 (de:hypothetical protein hi0827 precursor) (db:swissprot) YCIA_HAEIN P44886 HAEMOPHILUS INFLUENZAE 727 -11537591 167066 conserved hypothetical protein hi0827 precursor (db:pir2.dat) A64097 A64097 Haemophilus influenzae 727 -11537591 7500921822 hi0827 conserved hypothetical (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to gb:k00431 sp:p04379 pid:455187) (le:1400) (re:1864) (di:direct) U32765 U32765 g1573841 Haemophilus influenzae Rd 71421 -11537591 6500733733 p14 protein:p14:hypothetical protein precursor (gtcfc:14.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0827 HI0827 Haemophilus influenzae 727 -11537591

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886058	15165	37321	183	61

Description

6500733734 trpr:hi0830 tryptophan repressor:trp operon repressor homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0830 HI0830 Haemophilus influenzae 727 -11537592 102465 trpr:hi0830 (de:trp operon repressor homolog) (db:swissprot) TRPR_HAEIN P44889 HAEMOPHILUS INFLUENZAE 727 -11537592 167230 trp operon repressor (cl:trp repressor) (db:pir1.dat) D64097 D64097 Haemophilus influenzae 727 -11537592 7500893506 hi0830 trp operon repressor trpr (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to gb:l26582 sp:p39439 pid:433054 percent) (le:4012) (re:4317) (di:direct) U32765 U32765 g1573844 Haemophilus influenzae Rd 71421 -11537592 5000694803 (de:(hi0830) (pn:trp operon repressor homolog:tryptophan repressor:trpr) (gn:trpr) (gtcfc:12.13) (ec:) (trpr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0830 HI0830 Haemophilus influenzae 727 10044284

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886066	15166	37322	579	192

Description

6500733735 vacb:hi0861 virulence associated protein homolog:protein homolog (gtcfc:14.3) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0861 HI0861 Haemophilus influenzae 727 -11537593 104382 vacb:hi0861 (de:vacb protein homolog) (db:swissprot) VACB_HAEIN P44907 HAEMOPHILUS INFLUENZAE 727 -11537593 167267 virulence-associated protein vacb homolog hi0861 (cl:virulence-associated protein vacb homolog) (db:pir2.dat) G64098 G64098 Haemophilus influenzae 727 -11537593 7500893949 hi0861 virulence-associated protein vacb (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p21499 pid:537020 gb:u00096) (le:10841) (re:13189) (di:complement) U32767 U32767 g1573876 Haemophilus influenzae Rd 71421 -11537593 5000694804 (de:(hi0861) (pn:protein homolog:virulence associated protein homolog:vacb) (gn:vacb) (gtcfc:12.13) (ec:) (vacb_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0861 HI0861 Haemophilus influenzae 727 10046149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886079	15167	37323	1335	445

Description

5000694805 gtp-binding protein:obg:hypothetical 43 (gtcfc:14.3) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0877 HI0877 Haemophilus influenzae 727 -11537594 112656 hi0877 (de:hypothetical 43.4 kd gtp-binding protein hi0877) (db:swissprot) YHBZ_HAEIN P44915 HAEMOPHILUS INFLUENZAE 727 -11537594 166176 gtp-binding protein obg:gtp-binding protein homolog hi0877 (cl:gtp-binding protein obg:translation elongation factor tu homology) (db:pir1.dat) E64099 E64099 Haemophilus influenzae 727 -11537594 7500936791 hi0877 gtp-binding protein yhbz (db:genpept-bct1) (de:haemophilus influenzae rd section 84 of 163 of the complete genome.) (nt:similar to sp:p42641 pid:606121 gb:u00096) (le:7268) (re:8440) (di:complement) U32769 U32769 g1573894 Haemophilus influenzae Rd 71421 -11537594 6500733736 gtp-binding protein:obg:hypothetical 43 (gtcfc:14.3) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0877 HI0877 Haemophilus influenzae 727 -11537594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886081	15168	37324	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886085	15169	37325	1590	529

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886093	15170	37326	669	222

Description

6500733737 arca:hi0884 aerobic respiration control protein arca:aerobic respiration control protein homolog (gtcfc:12.13:2.1) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0884 HI0884 Haemophilus influenzae 727 -11537595 59985 arca:hi0884 (de:aerobic respiration control protein arca homolog) (db:swissprot) ARCA_HAEIN P44918 HAEMOPHILUS INFLUENZAE 727 -11537595 154749 aerobic respiration control protein arca homolog (cl:ompr protein:response regulator homology) (db:pir2.dat) I64099 I64099 Haemophilus influenzae 727 -11537595 7500877073 hi0884 aerobic respiration control protein arca arca (db:genpept-bct1) (de:haemophilus influenzae rd section 85 of 163 of the complete genome.) (nt:similar to sp:p03026 gb:l34010 gb:m10044) (le:3741) (re:4451) (di:complement) U32770 U32770 g1573901 Haemophilus influenzae Rd 71421 -11537595 5000694806 (de:(hi0884) (pn:aerobic respiration control protein homolog:aerobic respiration control protein arca:arca) (gn:arca) (gtcfc:12.13) (ec:) (arca_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI0884 HI0884 Haemophilus influenzae 727 10002718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886099	15171	37327	393	130

Description

5000694807 repressor for cytochrome p450:bm3r1:hypothetical transcriptional regulator hi0893 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0893 HI0893 Haemophilus influenzae 727 -11537596 109308 hi0893 (de:hypothetical transcriptional regulator hi0893) (db:swissprot) Y893_HAEIN P44923 HAEMOPHILUS INFLUENZAE 727 -11537596 167135 hypothetical protein hi0893 (db:pir2.dat) F64100 F64100 Haemophilus influenzae 727 -11537596 7500895627 hi0893 transcriptional repressor bm3r1 (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to gb:s87512 sp:p43506 pid:623036) (le:3854) (re:4417) (di:direct) U32771 U32771 g1573912 Haemophilus influenzae Rd 71421 -11537596 6500733738 repressor for cytochrome p450:bm3r1:hypothetical transcriptional regulator hi0893 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0893 HI0893 Haemophilus influenzae 727 -11537596

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886102	15172	37328	408	135

Description

GTC ORF with score 92 to: (db:genpept-vrl) (de:molluscum contagiosum virus subtype 1 clone h-i hypotheticalprotein (b-h-1) gene, partial cds, homolog of vaccinia a33r (b-h-2)and homolog of vaccinia a34r (b-h-3) genes, complete cds,hypothetical protein ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886103	15173	37329	534	177

Description

GTC ORF with score 115 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid zk512, complete sequence.) (nt:contains proline-rich region; cdna est embl:t00517) (le:13445:13833:13927:14086) (re:13459:13872:14026:14253) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886109	15174	37330	309	102

Description

5000694808 crp:cap:hi0957 cyclic amp receptor protein:crp:catabolite gene activator:camp receptor protein:camp-regulatory protein (gtcfc:12.13:11.3) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0957 HI0957 Haemophilus influenzae 727 -11537597 66480 crp:cap:hi0957 (de:protein)) (db:swissprot) CRP_HAEIN P29281 HAEMOPHILUS INFLUENZAE 727 -11537597 131440 crp camp receptor protein:cap:catabolite gene activator protein (cl:regulatory protein fnr:camp receptor protein cyclic nucleotide-binding domain homology) (db:pir1.dat) B38225 B38225 Haemophilus influenzae 727 -11537597 241255 crp cyclic amp receptor protein (sr:haemophilus influenzae dna) (db:genpept-bct1) (de:haemophilus influenzae cyclic amp receptor protein, complete cds.) (nt:putative) (le:501) (re:1175) (di:direct) HEACRPO M77207 g148880 Haemophilus influenzae 727 -11537597 7500879412 hi0957 catabolite gene activator crp (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to pid:1146416 percent ident: 78.85;) (le:9245) (re:9919) (di:direct) U32776 U32776 g1573982 Haemophilus influenzae Rd 71421 -11537597 6500733739 crp:cap cyclic amp receptor protein:crp:catabolite gene activator:camp receptor protein:camp-regulatory protein (gtcfc:12.13:11.3) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0957 HI0957 Haemophilus influenzae 727 -11537597

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886111	15175	37331	765	255

Description

GTC ORF with score 98 to: (fn:transmission-blocking target antigen) (sr:plasmodium falciparum (individual_isolate nf54) gametocyte cdna t) (db:genpept-inv) (de:plasmodium falciparum transmission blocking target antigen (ps230)mrna, complete cds.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886123	15176	37332	1128	375

Description

6500733740 lytb:hi1007 penicillin tolerance protein:protein homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1007 HI1007 Haemophilus influenzae 727 -11537598 82776 lytb:hi1007 (de:lytb protein homolog) (db:swissprot) LYTB_HAEIN P44976 HAEMOPHILUS INFLUENZAE 727 -11537598 7500885222 hi1007 penicillin tolerance protein lytb (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p22565 gb:x54945 pid:216456) (le:8285) (re:9229) (di:direct) U32781 U32781 g1574037 Haemophilus influenzae Rd 71421 -11537598 5000694809 (de:(hi1007) (pn:protein homolog:penicillin tolerance protein:lytb) (gn:lytb) (gtcfc:12.13) (ec:) (lytb_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1007 HI1007 Haemophilus influenzae 727 10024996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886126	15177	37333	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886149	15178	37334	1461	486

Description

6500733741 glpr:hi1009 glycerol-3-phosphate regulon repressor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1009 HI1009 Haemophilus influenzae 727 -11537599 112272 hi1009 (de:hypothetical transcriptional regulator hi1009) (db:swissprot) YGBI_HAEIN P44978 HAEMOPHILUS INFLUENZAE 727 -11537599 7500924023 hi1009 glycerol-3-phosphate regulon repressor glpr (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to sp:p09392 gb:m96795 pid:146186) (le:9793) (re:10563) (di:complement) U32781 U32781 g1574039 Haemophilus influenzae Rd 71421 -11537599 5000694810 (de:(hi1009) (pn:glycerol-3-phosphate regulon repressor:glpr) (gn:glpr) (gtcfc:12.13) (ec:) (ygbi_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1009 HI1009 Haemophilus influenzae 727 10126704

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886160	15179	37335	978	325

Description

5000694811 arac-like transcription regulator:hypothetical transcriptional regulator hi1052 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1052 HI1052 Haemophilus influenzae 727 -11537600 109419 hi1052 (de:hypothetical transcriptional regulator hi1052) (db:swissprot) YA52_HAEIN P45008 HAEMOPHILUS INFLUENZAE 727 -11537600 166006 arac-like transcription regulator homolog (db:pir2.dat) B64180 B64180 Haemophilus influenzae 727 -11537600 7500895875 hi1052 transcriptional regulator:arac family (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to sp:p35319 pid:581707 percent ident:) (le:69) (re:965) (di:complement) U32786 U32786 g1574606 Haemophilus influenzae Rd 71421 -11537600 6500733742 arac-like transcription regulator:hypothetical transcriptional regulator hi1052 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1052 HI1052 Haemophilus influenzae 727 -11537600

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886167	15180	37336	609	203

Description

6500733743 xylr:hi1106 xylose operon regluatory protein:xylose operon regulatory protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1106 HI1106 Haemophilus influenzae 727 -11537601 108240 xylr:hi1106 (de:xylose operon regulatory protein) (db:swissprot) XYLR_HAEIN P45043 HAEMOPHILUS INFLUENZAE 727 -11537601 167271 xylr xylose operon regluatory protein xylr (db:pir2.dat) H64182 H64182 Haemophilus influenzae 727 -11537601 7500894496 hi1106 xylose operon regluatory protein xylr (db:genpept-bct1) (de:haemophilus influenzae rd section 105 of 163 of the completegenome.) (nt:similar to sp:p37390 pid:466707 gb:u00096) (le:6251) (re:7414) (di:complement) U32790 U32790 g1574660 Haemophilus influenzae Rd 71421 -11537601 5000694812 (de:(hi1106) (pn:xylose operon regulatory protein:xylose operon regluatory protein:xylr) (gn:xylr) (gtcfc:12.13) (ec:) (xylr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1106 HI1106 Haemophilus influenzae 727 10049972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886168	15181	37337	324	107

Description

GTC ORF with score 92 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886186	15182	37338	297	98

Description

GTC ORF with score 93 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana fatty acid desaturase/cytochrome b5 fusionprotein mrna, complete cds.) (nt:member of the mono-oxygenase-related fatty acid) (le:159) (re:1499) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886195	15183	37339	849	283

Description

6500733744 gcva:hi1194 glycine cleavage system transcriptional activator:glycine cleavage system transcriptional activator homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1194 HI1194 Haemophilus influenzae 727 -11537602 73474 gcva:hi1194 (de:glycine cleavage system transcriptional activator homolog) (db:swissprot) GCVA_HAEIN P45099 HAEMOPHILUS INFLUENZAE 727 -11537602 166170 glycine cleavage system transcription activator (db:pir2.dat) B64189 B64189 Haemophilus influenzae 727 -11537602 7500882302 hi1194 glycine cleavage system transcriptional (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to sp:p32064 gb:u01030 gb:x73413 pid:312766) (le:261) (re:1166) (di:direct) U32799 U32799 g1574123 Haemophilus influenzae Rd 71421 -11537602 5000694813 (de:(hi1194) (pn:glycine cleavage system transcriptional activator homolog:glycine cleavage system transcriptional activator:gcva) (gn:gcva) (gtcfc:12.13) (ec:) (gcva_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influen) HI1194 HI1194 Haemophilus influenzae 727 10016008

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886205	15184	37340	345	114

Description

6500733745 cysb:hi1200 cys regulon transcriptional activator (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1200 HI1200 Haemophilus influenzae 727 -11537603 67639 cysb:hi1200 (de:cys regulon transcriptional activator) (db:swissprot) CYSB_HAEIN P45105 HAEMOPHILUS INFLUENZAE 727 -11537603 154783 cysb regulatory protein cysb (cl:regulatory protein lysr) (db:pir2.dat) E64189 E64189 Haemophilus influenzae 727 -11537603 7500879900 hi1200 cys regulon transcriptional activator cysb (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to gb:m15041 sp:p06613 gb:m34332 pid:145665) (le:6212) (re:7183) (di:direct) U32799 U32799 g1574129 Haemophilus influenzae Rd 71421 -11537603 5000694814 (de:(hi1200) (pn:cys regulon transcriptional activator:cys regulon transcriptional activator:cysb) (gn:cysb) (gtcfc:12.13) (ec:) (cysb_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1200 HI1200 Haemophilus influenzae 727 10010237

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886206	15185	37341	294	97

Description

6500733746 argr:hi1209 arginine repressor protein:arginine repressor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1209 HI1209 Haemophilus influenzae 727 -11537604 60100 argr:hi1209 (de:arginine repressor) (db:swissprot) ARGR_HAEIN P45110 HAEMOPHILUS INFLUENZAE 727 -11537604 166007 arginine repressor protein (db:pir2.dat) B64110 B64110 Haemophilus influenzae 727 -11537604 7500877144 hi1209 arginine repressor argr (db:genpept-bct1) (de:haemophilus influenzae rd section 115 of 163 of the completegenome.) (nt:similar to gb:m17532 sp:p15282 gb:x13968 pid:145356) (le:4978) (re:5433) (di:complement) U32800 U32800 g1574139 Haemophilus influenzae Rd 71421 -11537604 5000694815 (de:(hi1209) (pn:arginine repressor:arginine repressor protein:argr) (gn:argr) (gtcfc:12.13) (ec:) (argr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1209 HI1209 Haemophilus influenzae 727 10002826

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886207	15186	37342	789	262

Description

6500733747 phob:hi1379 phosphate regulon transcriptional regulatory protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1379 HI1379 Haemophilus influenzae 727 -11537605 89624 phob:hi1379 (de:phosphate regulon transcriptional regulatory protein phob) (db:swissprot) PHOB_HAEIN P45189 HAEMOPHILUS INFLUENZAE 727 -11537605 154753 phob phosphate regulon regulatory protein phob (cl:ompr protein:response regulator homology) (db:pir2.dat) F64120 F64120 Haemophilus influenzae 727 -11537605 7500888041 hi1379 phosphate regulon transcriptional regulatory (db:genpept-bct1) (de:haemophilus influenzae rd section 133 of 163 of the completegenome.) (nt:similar to sp:p08402 gb:x04026 pid:42388 gb:u00096) (le:5251) (re:5946) (di:complement) U32818 U32818 g1574213 Haemophilus influenzae Rd 71421 -11537605 5000694816 (de:(hi1379) (pn:phosphate regulon transcriptional regulatory protein :phosphate regulon transcriptional regulatory protein:phob) (gn:phob) (gtcfc:12.13) (ec:) (phob_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenz) HI1379 HI1379 Haemophilus influenzae 727 10031746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886212	15187	37343	594	197

Description

6500733748 fnr:hi1425 fumarate:and nitrate reduction regulatory protein:fumarate and nitrate reduction regulatory protein homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1425 HI1425 Haemophilus influenzae 727 -11537606 72214 fnr:hi1425 (de:fumarate and nitrate reduction regulatory protein homolog) (db:swissprot) FNR_HAEIN P45199 HAEMOPHILUS INFLUENZAE 727 -11537606 154726 regulatory protein fnr homolog (cl:regulatory protein fnr:camp receptor protein cyclic nucleotide-binding domain homology) (db:pir2.dat) E64122 E64122 Haemophilus influenzae 727 -11537606 7500881691 hi1425 fumarate and nitrate reduction regulatory (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:similar to gb:j01608 sp:p03019 pid:146961 gb:u00096) (le:7653) (re:8426) (di:direct) U32821 U32821 g1574259 Haemophilus influenzae Rd 71421 -11537606 5000694817 (de:(hi1425) (pn:fumarate and nitrate reduction regulatory protein homolog:fumarate:and nitrate reduction regulatory protein:fnr) (gn:fnr) (gtcfc:12.13) (ec:) (fnr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1425 HI1425 Haemophilus influenzae 727 10014765

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886215	15188	37344	453	150

Description

6500733749 sspb:hi1440 stringent starvation protein:stringent starvation protein b homolog (gtcfc:13.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1440 HI1440 Haemophilus influenzae 727 -11537607 99579 sspb:hi1440 (de:stringent starvation protein b homolog) (db:swissprot) SSPB_HAEIN P45206 HAEMOPHILUS INFLUENZAE 727 -11537607 167178 sspb stringent starvation protein sspb (cl:stringent starvation protein sspb) (db:pir2.dat) D64123 D64123 Haemophilus influenzae 727 -11537607 7500892144 hi1440 stringent starvation protein b sspb (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to gb:m69028 sp:p25663 gb:x05088 pid:147872) (le:12819) (re:13271) (di:complement) U32822 U32822 g1574279 Haemophilus influenzae Rd 71421 -11537607 5000694818 (de:(hi1440) (pn:stringent starvation protein b homolog:stringent starvation protein:sspb) (gn:sspb) (gtcfc:12.13) (ec:) (sspb_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1440 HI1440 Haemophilus influenzae 727 10041436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886219	15189	37345	351	116

Description

GTC ORF with score 131 to: (db:genpept-pln1) (de:gdh=nad(+)-specific glutamate dehydrogenase (neurospora crassa,genomic, 4919 nt).) (nt:this sequence comes from fig. 2; nad-gdh) (le:1105:1358:2354:4322) (re:1303:2354:4264:4358) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886231	15190	37346	1548	515

Description

GTC ORF with score 1370 to: (db:genpept-pln1) (de:gdh=nad(+)-specific glutamate dehydrogenase (neurospora crassa,genomic, 4919 nt).) (nt:this sequence comes from fig. 2; nad-gdh) (le:1105:1358:2354:4322) (re:1303:2354:4264:4358) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886245	15191	37347	591	196

Description

6500733750 sspa:hi1441 stringent starvation protein a:stringent starvation protein a homolog (gtcfc:13.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1441 HI1441 Haemophilus influenzae 727 -11537608 99576 sspa:hi1441 (de:stringent starvation protein a homolog) (db:swissprot) SSPA_HAEIN P45207 HAEMOPHILUS INFLUENZAE 727 -11537608 154880 stringent starvation protein homolog (cl:stringent starvation protein) (db:pir2.dat) E64123 E64123 Haemophilus influenzae 727 -11537608 7500892142 hi1441 stringent starvation protein a sspa (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to sp:p31784 pid:241868 percent ident:) (le:13271) (re:13909) (di:complement) U32822 U32822 g1574280 Haemophilus influenzae Rd 71421 -11537608 5000694819 (de:(hi1441) (pn:stringent starvation protein a homolog:stringent starvation protein a:sspa) (gn:sspa) (gtcfc:12.13) (ec:) (sspa_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1441 HI1441 Haemophilus influenzae 727 10041433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886249	15192	37348	696	231

Description

6500733751 pilb:hi1453 fimbrial transcription regulation repressor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1453 HI1453 Haemophilus influenzae 727 -11537609 7500922703 hi1453 (de:hypothetical protein hi1453 precursor) (db:swissprot) YE53_HAEIN Q57127 HAEMOPHILUS INFLUENZAE 727 -11537609 166137 regulatory protein pilb homolog (db:pir2.dat) D64124 D64124 Haemophilus influenzae 727 -11537609 7500922705 hi1453 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:al009126 percent ident: 30.84;) (le:7573) (re:8043) (di:complement) U32823 U32823 g1574291 Haemophilus influenzae Rd 71421 -11537609 5000694820 (de:(hi1453) (pn:fimbrial transcription regulation repressor:pilb) (gn:pilb) (gtcfc:12.13) (ec:) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1453 HI1453 Haemophilus influenzae 727 10088085

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886271	15193	37349	693	230

Description

5000694821 fimbrial transcription regulation repressor:pilb:hypothetical protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1455 HI1455 Haemophilus influenzae 727 -11537610 111431 hi1455 (de:hypothetical protein hi1455) (db:swissprot) YE55_HAEIN P45213 HAEMOPHILUS INFLUENZAE 727 -11537610 166138 peptide methionine sulfoxide reductase (db:pir2.dat) E64124 E64124 Haemophilus influenzae 727 -11537610 7500922709 hi1455 peptide methionine sulfoxide reductase msra (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:ae000511 pid:2313314 percent) (le:8738) (re:9799) (di:complement) U32823 U32823 g1574293 Haemophilus influenzae Rd 71421 -11537610 6500733752 fimbrial transcription regulation repressor:pilb:hypothetical protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1455 HI1455 Haemophilus influenzae 727 -11537610

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886301	15194	37350	390	129

Description

6500733753 modd:hi1473 molybdenum transport system alternative nitrogenase regulator (gtcfc:12.6:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1473 HI1473 Haemophilus influenzae 727 -11537611 5500685568 modd:hi1473 (de:molybdenum transport system protein modd homolog) (db:swissprot) MODD_HAEIN Q57278 HAEMOPHILUS INFLUENZAE 727 -11537611 167001 modd protein homolog (db:pir2.dat) H64125 H64125 Haemophilus influenzae 727 -11537611 7500885752 hi1473 molybdenum transport system protein modd (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to sp:p94777 pid:1816657 percent ident:) (le:6720) (re:7565) (di:complement) U32825 U32825 g1574314 Haemophilus influenzae Rd 71421 -11537611 5000694822 (de:(hi1473) (pn:molybdenum transport system alternative nitrogenase regulator:modd) (gn:modd) (gtcfc:12.13) (ec:) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1473 HI1473 Haemophilus influenzae 727 10088252

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886302	15195	37351	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886306	15196	37352	1035	344

Description

6500733754 lrp:hi1596 leucine responsive regulatory protein:leucine-responsive regulatory protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1596 HI1596 Haemophilus influenzae 727 -11537612 82481 lrp:hi1596 (de:leucine-responsive regulatory protein) (db:swissprot) LRP_HAEIN P45265 HAEMOPHILUS INFLUENZAE 727 -11537612 154785 transcription regulator hi1596:leucine-responsive:leucine-responsive regulatory protein (cl:regulatory protein asnc) (db:pir2.dat) H64131 H64131 Haemophilus influenzae 727 -11537612 7500885159 hi1596 leucine responsive regulatory protein lrp (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:similar to sp:p37403 gb:u02273 gb:x52093 pid:407916) (le:7088) (re:7588) (di:complement) U32833 U32833 g1574439 Haemophilus influenzae Rd 71421 -11537612 5000694823 (de:(hi1596) (pn:leucine-responsive regulatory protein:leucine responsive regulatory protein:lrp) (gn:lrp) (gtcfc:12.13) (ec:) (lrp_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1596 HI1596 Haemophilus influenzae 727 10024702

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886309	15197	37353	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886331	15198	37354	1908	635

Description

6500733755 purr:hi1635 purine nucleotide synthesis repressor protein:purine nucleotide synthesis repressor (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1635 HI1635 Haemophilus influenzae 727 -11537613 92478 purr:hi1635 (de:purine nucleotide synthesis repressor) (db:swissprot) PURR_HAEIN P46456 HAEMOPHILUS INFLUENZAE 727 -11537613 7500889092 hi1635 purine nucleotide synthesis repressor purr (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:similar to gb:j04212 sp:p15039 gb:x51368 pid:147428) (le:6589) (re:7599) (di:direct) U32836 U32836 g1574481 Haemophilus influenzae Rd 71421 -11537613 5000694824 (de:(hi1635) (pn:purine nucleotide synthesis repressor:purine nucleotide synthesis repressor protein:purr) (gn:purr) (gtcfc:12.13) (ec:) (purr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1635 HI1635 Haemophilus influenzae 727 10126723

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886339	15199	37355	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886345	15200	37356	432	143

Description

6500733756 sensor protein for basr:bass:probable sensor protein hi1707 (gtcfc:12.13:14.1) (ec:2.7.3.-) (keggfc:14.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1707 HI1707 Haemophilus influenzae 727 -11537614 112408 hi1707 (ec:2.7.3.-) (de:probable sensor protein hi1707,) (db:swissprot) YGIY_HAEIN P45336 HAEMOPHILUS INFLUENZAE 727 -11537614 167155 hypothetical protein hi1707 (cl:hypothetical protein hi1707:sensor histidine kinase homology) (db:pir2.dat) E64137 E64137 Haemophilus influenzae 727 -11537614 7500924278 hi1707 sensor protein ygiy (db:genpept-bct1) (de:haemophilus influenzae rd section 158 of 163 of the completegenome.) (nt:similar to sp:p40719 pid:882556 gb:u00096) (le:9622) (re:10977) (di:complement) U32843 U32843 g1574561 Haemophilus influenzae Rd 71421 -11537614 5000694825 (de:(hi1707) (pn:probable sensor protein hi1707:sensor protein for basr:bass) (gtcfc:12.13) (ec:2.7.3.-) (ygiy_haein) (keggfc:11.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1707 HI1707 Haemophilus influenzae 727 10054136

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886349	15201	37357	828	275

Description

5000694826 transcriptional regulatory protein:basr:probable transcriptional regulatory protein hi1708 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1708 HI1708 Haemophilus influenzae 727 -11537615 112406 hi1708 (de:probable transcriptional regulatory protein hi1708) (db:swissprot) YGIX_HAEIN P45337 HAEMOPHILUS INFLUENZAE 727 -11537615 167204 regulatory protein basr homolog (cl:ompr protein:response regulator homology) (db:pir2.dat) F64137 F64137 Haemophilus influenzae 727 -11537615 7500924276 hi1708 transcriptional regulatory protein ygix (db:genpept-bct1) (de:haemophilus influenzae rd section 158 of 163 of the completegenome.) (nt:similar to pid:882555 sp:p52076 gb:u00096) (le:10974) (re:11639) (di:complement) U32843 U32843 g1574562 Haemophilus influenzae Rd 71421 -11537615 6500733757 transcriptional regulatory protein:basr:probable transcriptional regulatory protein hi1708 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1708 HI1708 Haemophilus influenzae 727 -11537615

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886364	15202	37358	390	130

Description

6500733758 metr:hi1739 trans-activator of mete and meth:transcriptional activator protein (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1739 HI1739 Haemophilus influenzae 727 -11537616 83593 metr:hi1739 (de:transcriptional activator protein metr) (db:swissprot) METR_HAEIN P45349 HAEMOPHILUS INFLUENZAE 727 -11537616 167198 metr protein homolog (db:pir2.dat) D64139 D64139 Haemophilus influenzae 727 -11537616 7500885564 hi1739 transcriptional activator metr (db:genpept-bct1) (de:haemophilus influenzae rd section 161 of 163 of the completegenome.) (nt:similar to gb:j04155 sp:p19797 gb:m37630) (le:10570) (re:11499) (di:complement) U32846 U32846 g1574593 Haemophilus influenzae Rd 71421 -11537616 5000694827 (de:(hi1739) (pn:transcriptional activator protein :trans-activator of mete and meth:metr) (gn:metr) (gtcfc:12.13) (ec:) (metr_haein) (keggfc:11.2) (tigrfc:9.1) (db:gtc-haemophilus influenzae)) HI1739 HI1739 Haemophilus influenzae 727 10025807

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886379	15203	37359	852	284

Description

6500733759 sodit1:hi0020 2-oxoglutarate/malate translocator (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0020 HI0020 Haemophilus influenzae 727 -11537617 4000709415 hi0020 (de:hypothetical protein hi0020) (db:swissprot) YBHI_HAEIN Q57048 HAEMOPHILUS INFLUENZAE 727 -11537617 165963 conserved hypothetical protein hi0020 (cl:2-oxoglutarate/malate translocator) (db:pir2.dat) B64043 B64043 Haemophilus influenzae 727 -11537617 7500896773 hi0020 transport protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p75763 pid:1786986 percent) (le:8964) (re:10403) (di:complement) U32687 U32687 g1572964 Haemophilus influenzae Rd 71421 -11537617 5000694834 (de:(hi0020) (pn:2-oxoglutarate) (gn:sodit1) (gtcfc:12.2) (ec:) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0020 HI0020 Haemophilus influenzae 727 10088045

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886380	15204	37360	1032	343

Description

6500733760 dcub:hi0153 anaerobic c4-dicarboxylate membrane transporter protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0153 HI0153 Haemophilus influenzae 727 -11537618 166013 dicarboxylate transport protein homolog hi0153 (db:pir2.dat) B64051 B64051 Haemophilus influenzae 727 -11537618 5000694835 (de:(hi0153) (pn:anaerobic c4-dicarboxylate membrane transporter protein:dcub) (gn:dcub) (gtcfc:12.2) (ec:) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0153 HI0153 Haemophilus influenzae 727 10088057

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886388	15205	37361	702	233

Description

6500733761 foca:hi0181 formate transporter:formate channel (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0181 HI0181 Haemophilus influenzae 727 -11537619 72217 foca:hi0181 (de:probable formate transporter (formate channel)) (db:swissprot) FOCA_HAEIN P43756 HAEMOPHILUS INFLUENZAE 727 -11537619 166142 foca probable formate transport protein:probable formate channel protein (cl:formate dehydrogenase focb) (db:pir2.dat) G64052 G64052 Haemophilus influenzae 727 -11537619 7500881695 hi0181 formate transporter (db:genpept-bct1) (de:haemophilus influenzae rd section 18 of 163 of the complete genome.) (nt:similar to sp:p21501 pid:147154 gb:u00096) (le:4683) (re:5537) (di:complement) U32703 U32703 g1573137 Haemophilus influenzae Rd 71421 -11537619 5000694836 (de:(hi0181) (pn:probable formate transporter:formate transporter:formate channel) (gn:foca) (gtcfc:12.2) (ec:) (foca_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0181 HI0181 Haemophilus influenzae 727 10014768

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886395	15206	37362	843	280

Description

6500733762 rbsd:hi0501 high affinity ribose transport protein (gtcfc:12.2) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0501 HI0501 Haemophilus influenzae 727 -11537620 93577 rbsd:hi0501 (de:high affinity ribose transport protein rbsd) (db:swissprot) RBSD_HAEIN P44734 HAEMOPHILUS INFLUENZAE 727 -11537620 166194 rbsd ribose transport protein rbsd (cl:fucose operon u protein) (db:pir2.dat) G64072 G64072 Haemophilus influenzae 727 -11537620 7500889476 hi0501 high affinity ribose transport protein rbsd (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p04982 gb:m13169 gb:x68551) (le:1522) (re:1941) (di:direct) U32732 U32732 g1573482 Haemophilus influenzae Rd 71421 -11537620 5000694837 (de:(hi0501) (pn:high affinity ribose transport protein :high affinity ribose transport protein:rbsd) (gn:rbsd) (gtcfc:12.2) (ec:) (rbsd_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0501 HI0501 Haemophilus influenzae 727 10035570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886419	15207	37363	2226	741

Description

6500733763 rbsa:hi0502 high affinity ribose transport protein:ribose transport atp-binding protein (gtcfc:12.2) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0502 HI0502 Haemophilus influenzae 727 -11537621 93563 rbsa:hi0502 (de:ribose transport atp-binding protein rbsa) (db:swissprot) RBSA_HAEIN P44735 HAEMOPHILUS INFLUENZAE 727 -11537621 166192 ribose transport protein (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) H64072 H64072 Haemophilus influenzae 727 -11537621 7500889468 hi0502 d-ribose abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p04983 gb:m13169 pid:147513) (le:1955) (re:3436) (di:direct) U32732 U32732 g1573483 Haemophilus influenzae Rd 71421 -11537621 5000694838 (de:(hi0502) (pn:ribose transport atp-binding protein :high affinity ribose transport protein:rbsa) (gn:rbsa) (gtcfc:12.2) (ec:) (rbsa_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0502 HI0502 Haemophilus influenzae 727 10035556

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886443	15208	37364	1248	415

Description

6500733764 rbsc:hi0503 high affinity ribose transport protein:ribose transport system permease protein (gtcfc:12.2) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0503 HI0503 Haemophilus influenzae 727 -11537622 93573 rbsc:hi0503 (de:ribose transport system permease protein rbsc) (db:swissprot) RBSC_HAEIN P44736 HAEMOPHILUS INFLUENZAE 727 -11537622 166193 rbsc ribose transport protein rbsc (cl:l-arabinose transport system permease arah) (db:pir2.dat) I64072 I64072 Haemophilus influenzae 727 -11537622 7500889473 hi0503 d-ribose abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p04984 gb:m13169 pid:147514) (le:3449) (re:4420) (di:direct) U32732 U32732 g1573484 Haemophilus influenzae Rd 71421 -11537622 5000694839 (de:(hi0503) (pn:ribose transport system permease protein :high affinity ribose transport protein:rbsc) (gn:rbsc) (gtcfc:12.2) (ec:) (rbsc_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0503 HI0503 Haemophilus influenzae 727 10035566

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886466	15209	37365	2157	718

Description

6500733765 rbsb:hi0504 periplasmic ribose-binding protein:d-ribose-binding periplasmic protein precursor (gtcfc:12.2:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0504 HI0504 Haemophilus influenzae 727 -11537623 93567 rbsb:hi0504 (de:d-ribose-binding periplasmic protein precursor) (db:swissprot) RBSB_HAEIN P44737 HAEMOPHILUS INFLUENZAE 727 -11537623 153218 d-ribose-binding protein (cl:lac repressor) (db:pir2.dat) A64073 A64073 Haemophilus influenzae 727 -11537623 7500889471 hi0504 d-ribose abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p02925 gb:k00511 gb:m13169) (le:4440) (re:5318) (di:direct) U32732 U32732 g1573485 Haemophilus influenzae Rd 71421 -11537623 5000694840 (de:(hi0504) (pn:d-ribose-binding periplasmic protein precursor:periplasmic ribose-binding protein:rbsb) (gn:rbsb) (gtcfc:12.2) (ec:) (rbsb_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0504 HI0504 Haemophilus influenzae 727 10035560

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886478	15210	37366	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886482	15211	37367	207	68

Description

6500733766 fucp:hi0610 l-fucose permease (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0610 HI0610 Haemophilus influenzae 727 -11537624 72510 fucp:hi0610 (de:l-fucose permease) (db:swissprot) FUCP_HAEIN P44776 HAEMOPHILUS INFLUENZAE 727 -11537624 166935 fucose permease homolog (db:pir2.dat) B64081 B64081 Haemophilus influenzae 727 -11537624 7500881907 hi0610 l-fucose permease fucp (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to sp:p11551 gb:x15025 pid:146041 pid:41504) (le:5752) (re:7038) (di:complement) U32743 U32743 g1573603 Haemophilus influenzae Rd 71421 -11537624 5000694841 (de:(hi0610) (pn:l-fucose permease:fucp) (gn:fucp) (gtcfc:12.2) (ec:) (fucp_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0610 HI0610 Haemophilus influenzae 727 10015061

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886494	15212	37368	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886507	15213	37369	483	160

Description

6500733767 fucu:hi0612 fucose operon protein:fucose operon protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0612 HI0612 Haemophilus influenzae 727 -11537625 72515 fucu:hi0612 (de:fucose operon fucu protein) (db:swissprot) FUCU_HAEIN P44778 HAEMOPHILUS INFLUENZAE 727 -11537625 157268 hypothetical protein hi0612 (cl:fucose operon u protein) (db:pir2.dat) D64081 D64081 Haemophilus influenzae 727 -11537625 7500881911 hi0612 fucose operon protein fucu (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to pid:882699 gb:u00096 pid:1789169 percent) (le:7747) (re:8181) (di:complement) U32743 U32743 g1573605 Haemophilus influenzae Rd 71421 -11537625 5000694842 (de:(hi0612) (pn:fucose operon protein:fucose operon protein:fucu) (gn:fucu) (gtcfc:12.2) (ec:) (fucu_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0612 HI0612 Haemophilus influenzae 727 10015066

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886511	15214	37370	228	75

Description

6500733768 glpt:hi0686 glycerol-3-phosphatase transporter (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0686 HI0686 Haemophilus influenzae 727 -11537626 153208 glycerol-3-phosphate transport protein homolog hi0686:truncated (cl:hexose phosphate transport protein uhpt) (db:pir2.dat) F64086 F64086 Haemophilus influenzae 727 -11537626 5000694843 (de:(hi0686) (pn:glycerol-3-phosphatase transporter:glpt) (gn:glpt) (gtcfc:12.2) (ec:) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0686 HI0686 Haemophilus influenzae 727 10080841

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886514	15215	37371	549	182

Description

6500733769 glpf:hi0690 glycerol uptake facilitator protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0690 HI0690 Haemophilus influenzae 727 -11537627 74029 glpf:hi0690 (de:glycerol uptake facilitator protein) (db:swissprot) GLPF_HAEIN P44826 HAEMOPHILUS INFLUENZAE 727 -11537627 154809 glycerol facilitator protein (cl:glycerol facilitator protein) (db:pir2.dat) H64086 H64086 Haemophilus influenzae 727 -11537627 7500882498 hi0690 glycerol uptake facilitator protein glpf (db:genpept-bct1) (de:haemophilus influenzae rd section 67 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p11244 gb:m55990 gb:u13915) (le:145) (re:939) (di:direct) U32752 U32752 g1573694 Haemophilus influenzae Rd 71421 -11537627 5000694844 (de:(hi0690) (pn:glycerol uptake facilitator protein:glpf) (gn:glpf) (gtcfc:12.2) (ec:) (glpf_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0690 HI0690 Haemophilus influenzae 727 10016559

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886526	15216	37372	495	164

Description

5000694845 sodium-dependent noradrenaline transporter:hypothetical sodium-dependent transporter hi0736 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0736 HI0736 Haemophilus influenzae 727 -11537628 109273 hi0736 (de:hypothetical sodium-dependent transporter hi0736) (db:swissprot) Y736_HAEIN P44849 HAEMOPHILUS INFLUENZAE 727 -11537628 167169 probable transport protein hi0736 (cl:gamma-aminobutyric acid transporter) (db:pir2.dat) E64089 E64089 Haemophilus influenzae 727 -11537628 7500895485 hi0736 sodium-dependent transporter:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 72 of 163 of the complete genome.) (nt:similar to gb:ae000782 percent ident: 42.45;) (le:1016) (re:2542) (di:complement) U32757 U32757 g1573742 Haemophilus influenzae Rd 71421 -11537628 6500733770 sodium-dependent noradrenaline transporter:hypothetical sodium-dependent transporter hi0736 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0736 HI0736 Haemophilus influenzae 727 -11537628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886531	15217	37373	726	241

Description

6500733771 dcub:hi0746 anaerobic c4-dicarboxylate membrane transporter protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0746 HI0746 Haemophilus influenzae 727 -11537629 68140 dcub:hi0746 (de:anaerobic c4-dicarboxylate transporter dcub) (db:swissprot) DCUB_HAEIN P44855 HAEMOPHILUS INFLUENZAE 727 -11537629 166014 dicarboxylate transport protein homolog hi0746 (db:pir2.dat) B64090 B64090 Haemophilus influenzae 727 -11537629 7500880095 hi0746 anaerobic c4-dicarboxylate membrane transporter (db:genpept-bct1) (de:haemophilus influenzae rd section 73 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p14409 gb:m27058 gb:x79886) (le:4649) (re:5971) (di:direct) U32758 U32758 g1573753 Haemophilus influenzae Rd 71421 -11537629 5000694846 (de:(hi0746) (pn:anaerobic c4-dicarboxylate transporter :anaerobic c4-dicarboxylate membrane transporter protein:dcub) (gn:dcub) (gtcfc:12.2) (ec:) (dcub_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0746 HI0746 Haemophilus influenzae 727 10010733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886534	15218	37374	297	98

Description

6500733772 mglb:hi0822 d-galactose-binding periplasmic protein:d-galactose-binding periplasmic protein precursor:gbp:d-galactose/ d-glucose binding protein:ggbp (gtcfc:12.2:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0822 HI0822 Haemophilus influenzae 727 -11537630 153223 d-galactose-binding protein (cl:d-galactose-binding protein) (db:pir2.dat) G64096 G64096 Haemophilus influenzae 727 -11537630 7500955304 hi0822 galactose abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to sp:p02927 gb:k00419 gb:x05646 pid:146853) (le:7283) (re:8332) (di:direct) U32764 U32764 g1573835 Haemophilus influenzae Rd 71421 -11537630 5000694847 (de:(hi0822) (pn:d-galactose-binding periplasmic protein precursor:gbp:d-galactose:d-galactose-binding periplasmic protein:mglb) (gn:mglb) (gtcfc:12.2) (ec:) (dgal_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenz) HI0822 HI0822 Haemophilus influenzae 727 10080846

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886535	15219	37375	378	125

Description

6500733773 mgla:hi0823 methylgalactoside permease atp-binding protein:galactoside transport atp-binding protein (gtcfc:12.2) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0823 HI0823 Haemophilus influenzae 727 -11537631 83638 mgla:hi0823 (de:galactoside transport atp-binding protein mgla) (db:swissprot) MGLA_HAEIN P44884 HAEMOPHILUS INFLUENZAE 727 -11537631 166992 mgla probable atp-binding transport protein mgla (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) H64096 H64096 Haemophilus influenzae 727 -11537631 7500885589 hi0823 galactoside abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to gb:m59444 sp:p23199 pid:146854 gb:u00096) (le:8398) (re:9918) (di:direct) U32764 U32764 g1573836 Haemophilus influenzae Rd 71421 -11537631 5000694848 (de:(hi0823) (pn:galactoside transport atp-binding protein :methylgalactoside permease atp-binding protein:mgla) (gn:mgla) (gtcfc:12.2) (ec:) (mgla_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0823 HI0823 Haemophilus influenzae 727 10025852

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886546	15220	37376	615	204

Description

GTC ORF with score 606 to: (sr:aspergillus niger strain a733) (db:genpept-pln1) (de:leu2b=beta-isopropylmalate dehydrogenase (aspergillus niger, straina733, mrna, 1364 nt).) (nt:isozyme; this sequence comes from fig. 1b) (le:40) (re:1155) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886547	15221	37377	240	79

Description

GTC ORF with score 262 to: (sr:aspergillus niger strain a733) (db:genpept-pln1) (de:leu2b=beta-isopropylmalate dehydrogenase (aspergillus niger, straina733, mrna, 1364 nt).) (nt:isozyme; this sequence comes from fig. 1b) (le:40) (re:1155) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886552	15222	37378	939	312

Description

GTC ORF with score 627 to: (sr:aspergillus niger strain a733) (db:genpept-pln1) (de:leu2b=beta-isopropylmalate dehydrogenase (aspergillus niger, straina733, mrna, 1364 nt).) (nt:isozyme; this sequence comes from fig. 1b) (le:40) (re:1155) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886573	15223	37379	843	281

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886576	15224	37380	1044	347

Description

6500733774 mglc:hi0824 mglc protein:galactoside transport system permease protein (gtcfc:12.2) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0824 HI0824 Haemophilus influenzae 727 -11537632 83642 mglc:hi0824 (de:galactoside transport system permease protein mglc) (db:swissprot) MGLC_HAEIN P44885 HAEMOPHILUS INFLUENZAE 727 -11537632 166993 mglc transmembrane pore-generating protein mglc (db:pir2.dat) I64096 I64096 Haemophilus influenzae 727 -11537632 7500885594 hi0824 galactoside abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to gb:m59444 sp:p23200 pid:146855 gb:u00096) (le:9935) (re:10945) (di:direct) U32764 U32764 g1573837 Haemophilus influenzae Rd 71421 -11537632 5000694849 (de:(hi0824) (pn:galactoside transport system permease protein :mglc protein:mglc) (gn:mglc) (gtcfc:12.2) (ec:) (mglc_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI0824 HI0824 Haemophilus influenzae 727 10025856

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886584	15225	37381	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886585	15226	37382	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886600	15227	37383	1623	540

Description

5000694850 potassium channel homolog:kch:hypothetical protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0828 HI0828 Haemophilus influenzae 727 -11537633 110816 hi0828 (de:hypothetical protein hi0828) (db:swissprot) YCII_HAEIN P44887 HAEMOPHILUS INFLUENZAE 727 -11537633 167099 hypothetical protein hi0828 (db:pir2.dat) B64097 B64097 Haemophilus influenzae 727 -11537633 7500921828 hi0828 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to sp:p31070 percent ident: 67.35;) (le:1881) (re:2177) (di:direct) U32765 U32765 g1573842 Haemophilus influenzae Rd 71421 -11537633 6500733775 potassium channel homolog:kch:hypothetical protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI0828 HI0828 Haemophilus influenzae 727 -11537633

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886605	15228	37384	456	151

Description

GTC ORF with score 237 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t6a23 genomic sequence,complete sequence.) (nt:unknown protein) (le:6887:7383:7674:7982) (re:7303:7472:7736:8068) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886611	15229	37385	837	278

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886612	15230	37386	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886615	15231	37387	750	249

Description

6500733776 gntp:hi1015 gluconate permease (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1015 HI1015 Haemophilus influenzae 727 -11537634 166156 gluconate transport protein homolog:gluconate permease homolog (cl:d-serine permease) (db:pir2.dat) D64108 D64108 Haemophilus influenzae 727 -11537634 7500960655 hi1015 gluconate permease gntp (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to sp:p39835 pid:606350 gb:u00096) (le:4679) (re:6145) (di:direct) U32782 U32782 g1574047 Haemophilus influenzae Rd 71421 -11537634 5000694851 (de:(hi1015) (pn:gluconate permease:gntp) (gn:gntp) (gtcfc:12.2) (ec:) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI1015 HI1015 Haemophilus influenzae 727 10088089

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886626	15232	37388	801	266

Description

6500733777 xylh:hi1109 ribose transport permease protein:xylose transport permease protein (gtcfc:12.2) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1109 HI1109 Haemophilus influenzae 727 -11537635 108231 xylh:hi1109 (de:xylose transport permease protein xylh) (db:swissprot) XYLH_HAEIN P45045 HAEMOPHILUS INFLUENZAE 727 -11537635 167143 xylh xylose transport protein xylh (cl:l-arabinose transport system permease arah) (db:pir2.dat) A64183 A64183 Haemophilus influenzae 727 -11537635 7500894494 hi1109 d-xylose abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 106 of 163 of the completegenome.) (nt:similar to sp:p37389 pid:466706 gb:u00096) (le:168) (re:1295) (di:complement) U32791 U32791 g1574663 Haemophilus influenzae Rd 71421 -11537635 5000694852 (de:(hi1109) (pn:xylose transport permease protein :ribose transport permease protein:xylh) (gn:xylh) (gtcfc:12.2) (ec:) (xylh_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI1109 HI1109 Haemophilus influenzae 727 10049963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886628	15233	37389	504	167

Description

6500733778 xylg:hi1110 d-xylose transport atp-binding protein (gtcfc:12.2) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1110 HI1110 Haemophilus influenzae 727 -11537636 108228 xylg:hi1110 (de:d-xylose transport atp-binding protein xylg) (db:swissprot) XYLG_HAEIN P45046 HAEMOPHILUS INFLUENZAE 727 -11537636 166082 xylg d-xylose transport atp-binding protein xylg (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64183 B64183 Haemophilus influenzae 727 -11537636 7500894492 hi1110 d-xylose abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 106 of 163 of the completegenome.) (nt:similar to sp:p37388 pid:466705 gb:u00096) (le:1299) (re:2810) (di:complement) U32791 U32791 g1574664 Haemophilus influenzae Rd 71421 -11537636 5000694853 (de:(hi1110) (pn:d-xylose transport atp-binding protein :d-xylose transport atp-binding protein:xylg) (gn:xylg) (gtcfc:12.2) (ec:) (xylg_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI1110 HI1110 Haemophilus influenzae 727 10049960

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886636	15234	37390	516	171

Description

6500733779 xylf:hi1111 d-xylose-binding periplasmic protein:rbsb:d-xylose-binding periplasmic protein precursor (gtcfc:12.2:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1111 HI1111 Haemophilus influenzae 727 -11537637 108225 xylf:hi1111 (de:d-xylose-binding periplasmic protein precursor) (db:swissprot) XYLF_HAEIN P45047 HAEMOPHILUS INFLUENZAE 727 -11537637 166083 xylf xylf protein (db:pir2.dat) C64183 C64183 Haemophilus influenzae 727 -11537637 7500894490 hi1111 d-xylose abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 106 of 163 of the completegenome.) (nt:similar to sp:p37387 pid:466704 gb:u00096) (le:2861) (re:3859) (di:complement) U32791 U32791 g1574665 Haemophilus influenzae Rd 71421 -11537637 5000694854 (de:(hi1111) (pn:d-xylose-binding periplasmic protein precursor:d-xylose-binding periplasmic protein:rbsb) (gn:xylf) (gtcfc:12.2) (ec:) (xylf_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI1111 HI1111 Haemophilus influenzae 727 10049957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886700	15235	37391	2343	781

Description

GTC ORF with score 1734 to: (fn:required for conidial pigmentation) (db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene, completecds.) (nt:alb1) (le:598:932:1268:4755:5584) (re:884:1220:4699:5510:7260) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886716	15236	37392	900	299

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886739	15237	37393	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886740	15238	37394	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886741	15239	37395	405	134

Description

6500733780 lctp:hi1218 l-lactate permease (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1218 HI1218 Haemophilus influenzae 727 -11537638 1500686285 hi1218 (de:putative l-lactate permease) (db:swissprot) YC18_HAEIN Q57251 HAEMOPHILUS INFLUENZAE 727 -11537638 166936 l-lactate permease homolog (cl:l-lactate permease) (db:pir2.dat) H64110 H64110 Haemophilus influenzae 727 -11537638 7500921440 hi1218 l-lactate permease lctp (db:genpept-bct1) (de:haemophilus influenzae rd section 116 of 163 of the completegenome.) (nt:similar to gb:ae000782 percent ident: 34.25;) (le:6361) (re:7959) (di:complement) U32801 U32801 g1574148 Haemophilus influenzae Rd 71421 -11537638 5000694855 (de:(hi1218) (pn:l-lactate permease:lctp) (gn:lctp) (gtcfc:12.2) (ec:) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI1218 HI1218 Haemophilus influenzae 727 10061045

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886742	15240	37396	375	124

Description

5000694856 na+ and cl-dependent gamma-aminobutryic acid transporter:hypothetical sodium-dependent transporter hi1690 (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1690 HI1690 Haemophilus influenzae 727 -11537639 112240 hi1690 (de:hypothetical sodium-dependent transporter hi1690) (db:swissprot) YG90_HAEIN P45320 HAEMOPHILUS INFLUENZAE 727 -11537639 167024 neurotransmitter transport protein homolog (cl:gamma-aminobutyric acid transporter) (db:pir2.dat) H64136 H64136 Haemophilus influenzae 727 -11537639 7500923988 hi1690 sodium-dependent transporter:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to gb:al009126 percent ident: 38.41;) (le:816) (re:2189) (di:direct) U32842 U32842 g1574543 Haemophilus influenzae Rd 71421 -11537639 6500733781 na+ and cl-dependent gamma-aminobutryic acid transporter:hypothetical sodium-dependent transporter hi1690 (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1690 HI1690 Haemophilus influenzae 727 -11537639

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886744	15241	37397	330	109

Description

6500733782 ptsi:hi1712 enzyme i:phosphoenolpyruvate-protein phosphotransferase:phosphotransferase system:enzyme i (gtcfc:12.2) (ec:2.7.3.9) (keggfc:14.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1712 HI1712 Haemophilus influenzae 727 -11537640 92089 ptsi:hi1712 (ec:2.7.3.9) (de:(phosphotransferase system, enzyme i)) (db:swissprot) PT1_HAEIN P43922 HAEMOPHILUS INFLUENZAE 727 -11537640 139003 phosphotransferase system enzyme i (cl:phosphotransferase system enzyme i:phosphotransferase system enzyme i homology) (ec:2.7.3.9) (db:pir2.dat) H64137 H64137 Haemophilus influenzae 727 -11537640 7500888904 hi1712 phosphoenolpyruvate-protein phosphotransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:similar to gb:m76176 sp:p12654 gb:x52093 pid:153937) (le:1497) (re:3224) (di:complement) U32844 U32844 g1574567 Haemophilus influenzae Rd 71421 -11537640 5000694857 (de:(hi1712) (pn:phosphoenolpyruvate-protein phosphotransferase:phosphotransferase system, enzyme i:enzyme i:ptsi) (gn:ptsi) (gtcfc:12.2) (ec:2.7.3.9) (pt1_haein) (keggfc:11.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae)) HI1712 HI1712 Haemophilus influenzae 727 10034123

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886757	15242	37398	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886766	15243	37399	585	194

Description

6500733783 ptsh:hi1713 phosphohistidinoprotein-hexose phosphotransferase:phosphocarrier protein hpr:histidine-containing protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1713 HI1713 Haemophilus influenzae 727 -11537641 92322 ptsh:hi1713 (de:phosphocarrier protein hpr (histidine-containing protein)) (db:swissprot) PTHP_HAEIN P43921 HAEMOPHILUS INFLUENZAE 727 -11537641 152983 phosphotransferase system phosphohistidine-containing protein (cl:phosphotransferase system phosphohistidine-containing protein:phosphotransferase system phosphohistidine-containing protein homology) (db:pir2.dat) I64137 I64137 Haemophilus influenzae 727 -11537641 7500888956 hi1713 phosphocarrier protein hpr ptsh (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:similar to sp:p07006 pid:153936 pid:47845 percent) (le:3304) (re:3561) (di:complement) U32844 U32844 g1574568 Haemophilus influenzae Rd 71421 -11537641 5000694858 (de:(hi1713) (pn:phosphocarrier protein hhistidine-containing protein:phosphohistidinoprotein-hexose phosphotransferase:ptsh) (gn:ptsh) (gtcfc:12.2) (ec:) (ptsh_haein) (keggfc:11.2) (tigrfc:13.3) (db:gtc-haemophilus influenza) HI1713 HI1713 Haemophilus influenzae 727 10034354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886770	15244	37400	678	225

Description

5000694859 lactam utilization protein:lamb:hypothetical protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1729 HI1729 Haemophilus influenzae 727 -11537642 112589 hi1729 (de:hypothetical protein hi1729) (db:swissprot) YBGL_HAEIN P45347 HAEMOPHILUS INFLUENZAE 727 -11537642 166937 lactam utilization protein homolog (cl:bacillus subtilis lactam utilization protein ycsf) (db:pir2.dat) H64138 H64138 Haemophilus influenzae 727 -11537642 7500896752 hi1729 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75746 pid:1786931 percent) (le:9344) (re:10117) (di:complement) U32845 U32845 g1574585 Haemophilus influenzae Rd 71421 -11537642 6500733784 lactam utilization protein:lamb:hypothetical protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1729 HI1729 Haemophilus influenzae 727 -11537642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886775	15245	37401	807	268

Description

5000694860 ribonucleotide transport atp-binding protein:mkl:hypothetical abc transporter atp-binding protein hi1087 (gtcfc:12.3) (keggfc:14.2) (tigrfc:13.5) (db:gtc-haemophilus influenzae) HI1087 HI1087 Haemophilus influenzae 727 -11537643 116107 hi1087 (de:hypothetical abc transporter atp-binding protein hi1087) (db:swissprot) YRBF_HAEIN P45031 HAEMOPHILUS INFLUENZAE 727 -11537643 167142 hypothetical protein hi1087 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64182 B64182 Haemophilus influenzae 727 -11537643 7500952619 hi1087 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to sp:p45393 pid:606133 gb:u00096) (le:9408) (re:10202) (di:complement) U32788 U32788 g1574641 Haemophilus influenzae Rd 71421 -11537643 6500733785 ribonucleotide transport atp-binding protein:mkl:hypothetical abc transporter atp-binding protein hi1087 (gtcfc:12.3) (keggfc:14.2) (tigrfc:13.5) (db:gtc-haemophilus influenzae) HI1087 HI1087 Haemophilus influenzae 727 -11537643

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886781	15246	37402	870	289

Description

6500733786 uraa:hi1227 uracil permease:probable uracil permease:uracil transporter (gtcfc:12.3) (keggfc:14.2) (tigrfc:13.5) (db:gtc-haemophilus influenzae) HI1227 HI1227 Haemophilus influenzae 727 -11537644 103805 uraa:hi1227 (de:probable uracil permease (uracil transporter)) (db:swissprot) URAA_HAEIN P45117 HAEMOPHILUS INFLUENZAE 727 -11537644 167250 uracil transport protein homolog (cl:uracil transport protein uraa) (db:pir2.dat) D64111 D64111 Haemophilus influenzae 727 -11537644 7500893838 hi1227 uracil permease uraa (db:genpept-bct1) (de:haemophilus influenzae rd section 117 of 163 of the completegenome.) (nt:similar to gb:x76083 sp:p41006 pid:431231 percent) (le:3767) (re:5011) (di:complement) U32802 U32802 g1574157 Haemophilus influenzae Rd 71421 -11537644 5000694861 (de:(hi1227) (pn:probable uracil permease:uracil transporter:uracil permease:uraa) (gn:uraa) (gtcfc:12.3) (ec:) (uraa_haein) (keggfc:11.2) (tigrfc:13.5) (db:gtc-haemophilus influenzae)) HI1227 HI1227 Haemophilus influenzae 727 10045575

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886782	15247	37403	405	135

Description

5000694862 nitrate transporter atpase component:nasd:hypothetical abc transporter atp-binding protein hi0354 (gtcfc:12.4) (keggfc:14.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_)) HI0354 HI0354 Haemophilus influenzae 727 -11537645 109110 hi0354 (de:hypothetical abc transporter atp-binding protein hi0354) (db:swissprot) Y354_HAEIN P44656 HAEMOPHILUS INFLUENZAE 727 -11537645 167034 nasd protein homolog (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64063 B64063 Haemophilus influenzae 727 -11537645 7500895178 hi0354 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to pid:1184189 gb:u00096 sp:q47538) (le:1528) (re:2250) (di:direct) U32720 U32720 g1573323 Haemophilus influenzae Rd 71421 -11537645 6500733787 nitrate transporter atpase component:nasd:hypothetical abc transporter atp-binding protein hi0354 (gtcfc:12.4) (keggfc:14.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae) HI0354 HI0354 Haemophilus influenzae 727 -11537645

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886792	15248	37404	354	117

Description

6500733788 psta:hi1381 integral membrane protein:phosphate transport system permease protein (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) HI1381 HI1381 Haemophilus influenzae 727 -11537646 92038 psta:hi1381 (de:phosphate transport system permease protein psta) (db:swissprot) PSTA_HAEIN P45190 HAEMOPHILUS INFLUENZAE 727 -11537646 154444 phot phot protein (cl:phot protein) (db:pir2.dat) G64120 G64120 Haemophilus influenzae 727 -11537646 7500888875 hi1381 phosphate abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 133 of 163 of the completegenome.) (nt:similar to gb:l10328 sp:p07654 gb:k01992 gb:x02723) (le:6819) (re:7667) (di:complement) U32818 U32818 g1574214 Haemophilus influenzae Rd 71421 -11537646 5000694311 (de:(hi13891) (pn:indole-3-glycerol phosphate synthase:igps) (gn:trpc) (gtcfc:5.15) (ec:4.1.1.48) (trpc_haein) (keggfc:5.15) (db:gtc-haemophilus influenzae)) HI13891 HI13891 Haemophilus influenzae 727 10034072

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886795	15249	37405	285	94

Description

6500733789 pstc:hi1382 peripheral membrane protein c:phosphate transport system permease protein (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) HI1382 HI1382 Haemophilus influenzae 727 -11537647 92043 pstc:hi1382 (de:phosphate transport system permease protein pstc) (db:swissprot) PSTC_HAEIN P45191 HAEMOPHILUS INFLUENZAE 727 -11537647 154443 phow phow protein:peripheral membrane protein c (cl:phow protein) (db:pir2.dat) H64120 H64120 Haemophilus influenzae 727 -11537647 7500888888 hi1382 phosphate abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 133 of 163 of the completegenome.) (nt:similar to gb:l10328 sp:p07653 gb:k01992 gb:x02723) (le:7669) (re:8616) (di:complement) U32818 U32818 g1574215 Haemophilus influenzae Rd 71421 -11537647 5000694863 (de:(hi1382) (pn:phosphate transport system permease protein :peripheral membrane protein c:pstc) (gn:pstc) (gtcfc:12.4) (ec:) (pstc_haein) (keggfc:11.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae)) HI1382 HI1382 Haemophilus influenzae 727 10034077

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886796	15250	37406	258	85

Description

6500733790 psts:hi1383 periplasmic phosphate-binding protein:phosphate-binding periplasmic protein precursor:pbp (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) HI1383 HI1383 Haemophilus influenzae 727 -11537648 153017 phosphate-binding protein:phosphate-repressible (cl:phosphate-repressible phosphate-binding protein) (db:pir2.dat) I64120 I64120 Haemophilus influenzae 727 -11537648 7500955186 hi1383 phosphate abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 133 of 163 of the completegenome.) (nt:similar to pid:1052826 percent ident: 55.35;) (le:8707) (re:9483) (di:complement) U32818 U32818 g1574216 Haemophilus influenzae Rd 71421 -11537648 5000694864 (de:(hi1383) (pn:phosphate-binding periplasmic protein precursor:pbp:periplasmic phosphate-binding protein:psts) (gn:psts) (gtcfc:12.4) (ec:) (psts_haein) (keggfc:11.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae)) HI1383 HI1383 Haemophilus influenzae 727 10080737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886800	15251	37407	1305	434

Description

5000694865 phosphate permease:ybr296c:putative phosphate permease hi1604 (gtcfc:12.4) (keggfc:14.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_)) HI1604 HI1604 Haemophilus influenzae 727 -11537649 112038 hi1604 (de:putative phosphate permease hi1604) (db:swissprot) YG04_HAEIN P45268 HAEMOPHILUS INFLUENZAE 727 -11537649 167087 amphotropic murine retrovirus receptor homolog (db:pir2.dat) A64132 A64132 Haemophilus influenzae 727 -11537649 7500923605 hi1604 phosphate permease:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:similar to pid:1814405 percent ident: 41.05;) (le:3569) (re:4831) (di:direct) U32834 U32834 g1574446 Haemophilus influenzae Rd 71421 -11537649 6500733791 phosphate permease:ybr296c:putative phosphate permease hi1604 (gtcfc:12.4) (keggfc:14.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae) HI1604 HI1604 Haemophilus influenzae 727 -11537649

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886805	15252	37408	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886808	15253	37409	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886814	15254	37410	606	201

Description

6500733792 modc:hi1691 molybdate uptake system hydrophilic membrane-bound protein:molybdenum transport atp-binding protein (gtcfc:12.4) (keggfc:14.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_)) HI1691 HI1691 Haemophilus influenzae 727 -11537650 83988 modc:hi1691 (de:molybdenum transport atp-binding protein modc) (db:swissprot) MODC_HAEIN P45321 HAEMOPHILUS INFLUENZAE 727 -11537650 153030 chld molybdenum transport protein chld (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) I64136 I64136 Haemophilus influenzae 727 -11537650 7500885751 hi1691 molybdenum abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to pid:973216 gb:u00096 pid:1651350) (le:2213) (re:3268) (di:complement) U32842 U32842 g1574544 Haemophilus influenzae Rd 71421 -11537650 5000694866 (de:(hi1691) (pn:molybdenum transport atp-binding protein :molybdate uptake system hydrophilic membrane-bound protein:modc) (gn:modc) (gtcfc:12.4) (ec:) (modc_haein) (keggfc:11.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae)) HI1691 HI1691 Haemophilus influenzae 727 10026194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886820	15255	37411	492	163

Description

6500733793 modb:hi1692 molybdate uptake system hydrophobic membrane-bound protein:molybdenum transport system permease protein (gtcfc:12.4) (keggfc:14.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_)) HI1692 HI1692 Haemophilus influenzae 727 -11537651 83984 modb:hi1692 (de:molybdenum transport system permease protein modb) (db:swissprot) MODB_HAEIN P45322 HAEMOPHILUS INFLUENZAE 727 -11537651 153205 molybdenum transport protein (cl:maltose transport protein malg) (db:pir2.dat) A64137 A64137 Haemophilus influenzae 727 -11537651 7500885750 hi1692 molybdenum abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to gb:l34009 sp:p09834 pid:504499) (le:3255) (re:3944) (di:complement) U32842 U32842 g1574545 Haemophilus influenzae Rd 71421 -11537651 5000694867 (de:(hi1692) (pn:molybdenum transport system permease protein :molybdate uptake system hydrophobic membrane-bound protein:modb) (gn:modb) (gtcfc:12.4) (ec:) (modb_haein) (keggfc:11.2) (tigrfc:13.2) (db:gtc-haemophilus influenzae) HI1692 HI1692 Haemophilus influenzae 727 10026190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886821	15256	37412	2772	924

Description

5000694868 fbp:hi0097 major ferric iron binding protein precursor:fbp:iron-regulated 40 kd protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0097 HI0097 Haemophilus influenzae 727 -11537652 153242 major ferric iron-binding protein:major iron-regulated protein (cl:sfua protein) (db:pir2.dat) C64048 C64048 Haemophilus influenzae 727 -11537652 7500955308 hi0097 iron iii abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:similar to pid:2340838 percent identity: 80.72;) (le:4006) (re:4890) (di:direct) U32695 U32695 g1573048 Haemophilus influenzae Rd 71421 -11537652 6500733794 fbp major ferric iron binding protein precursor:fbp:iron-regulated 40 kd protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) HI0097 HI0097 Haemophilus influenzae 727 -11537652

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886850	15257	37413	3246	1082

Description

6500733795 sfub:hi0098 periplasmic-binding-protein-dependent iron transport protein:periplasmic-binding-protein-dependent irontransport protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0098 HI0098 Haemophilus influenzae 727 -11537653 167084 hitb iron utilization protein hitb (cl:sfub protein) (db:pir2.dat) D64048 D64048 Haemophilus influenzae 727 -11537653 7500955478 hi0098 iron iii abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:similar to gb:m33815 sp:p21409 pid:152861 percent) (le:5107) (re:6528) (di:direct) U32695 U32695 g1573049 Haemophilus influenzae Rd 71421 -11537653 5000694869 (de:(hi0098) (pn:periplasmic-binding-protein-dependent irontransport protein:periplasmic-binding-protein-dependent iron transport protein:sfub) (gn:sfub) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) HI0098 HI0098 Haemophilus influenzae 727 10088279

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886851	15258	37414	405	134

Description

GTC ORF with score 116 to: (sr:fruit fly) (db:genpept-inv) (de:drosophila melanogaster tart-b1 transposon putative single-strandednucleic acid binding protein and putative reverse transcriptasegenes, complete cds.) (nt:putative single-stranded nucleic ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886876	15259	37415	450	149

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886877	15260	37416	2205	734

Description

6500733796 nhaa:hi0225 na:/h:antiporter 1 (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0225 HI0225 Haemophilus influenzae 727 -11537654 85769 nhaa:hi0225 (de:na(+)/h(+) antiporter 1) (db:swissprot) NHAA_HAEIN P44581 HAEMOPHILUS INFLUENZAE 727 -11537654 167023 na+/h+-exchanging protein:na+/h+ antiporter (cl:na+/h+-exchanging protein nhaa) (db:pir2.dat) C64056 C64056 Haemophilus influenzae 727 -11537654 7500886414 hi0225 na+/h+ antiporter nhaa (db:genpept-bct1) (de:haemophilus influenzae rd section 23 of 163 of the complete genome.) (nt:similar to gb:d28504 pid:551299 percent identity:) (le:8632) (re:9834) (di:complement) U32708 U32708 g1573189 Haemophilus influenzae Rd 71421 -11537654 5000694870 (de:(hi0225) (pn:na:na) (gn:nhaa) (gtcfc:12.5) (ec:) (nhaa_haein) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI0225 HI0225 Haemophilus influenzae 727 10027936

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886878	15261	37417	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886890	15262	37418	549	182

Description

6500733797 tonb:hi0251 energy transducer:protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0251 HI0251 Haemophilus influenzae 727 -11537655 101772 tonb:hi0251 (de:tonb protein) (db:swissprot) TONB_HAEIN P42872 HAEMOPHILUS INFLUENZAE 727 -11537655 166118 tonb energy transducer tonb (db:pir2.dat) F64057 F64057 Haemophilus influenzae 727 -11537655 7500893255 hi0251 tonb protein (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to gb:u04996 percent identity: 96.18;) (le:3858) (re:4670) (di:complement) U32711 U32711 g1573217 Haemophilus influenzae Rd 71421 -11537655 5000694871 (de:(hi0251) (pn:protein:energy transducer:tonb) (gn:tonb) (gtcfc:12.5) (ec:) (tonb_haein) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI0251 HI0251 Haemophilus influenzae 727 10043601

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886895	15263	37419	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886903	15264	37420	855	284

Description

6500733798 bcp:hi0254 bacterioferritin comigratory protein:bacterioferritin comigratory protein homolog (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0254 HI0254 Haemophilus influenzae 727 -11537656 61510 bcp:hi0254 (de:bacterioferritin comigratory protein homolog) (db:swissprot) BCP_HAEIN P44411 HAEMOPHILUS INFLUENZAE 727 -11537656 166026 bacterioferritin comigratory protein (cl:bacterioferritin comigratory protein:alkyl hydroperoxidase c22 protein homology) (db:pir2.dat) I64057 I64057 Haemophilus influenzae 727 -11537656 7500877728 hi0254 bacterioferritin comigratory protein bcp (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to gb:m63654 sp:p23480 pid:147017 gb:u00096) (le:5748) (re:6215) (di:complement) U32711 U32711 g1573220 Haemophilus influenzae Rd 71421 -11537656 5000694872 (de:(hi0254) (pn:bacterioferritin comigratory protein homolog:bacterioferritin comigratory protein:bcp) (gn:bcp) (gtcfc:12.5) (ec:) (bcp_haein) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI0254 HI0254 Haemophilus influenzae 727 10004219

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886936	15265	37421	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886942	15266	37422	564	187

Description

GTC ORF with score 106 to: (db:genpept-bct1) (de:methanobacterium thermoautotrophicum from bases 36267 to 48321(section 4 of 148) of the complete genome.) (nt:function code:10.02 - metabolism of macromolecules,) (le:6961) (re:8172) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886946	15267	37423	696	231

Description

6500733799 merp:hi0292 mercury scavenger protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0292 HI0292 Haemophilus influenzae 727 -11537657 166988 probable mercuric ion-binding protein hi0292:periplasmic mercuric ion-binding protein merp homolog (cl:mercuric resistance operon regulatory protein:heavy-metal-associated homology) (db:pir1.dat) H64059 H64059 Haemophilus influenzae 727 -11537657 7500960723 hi0292 mercuric ion scavenger protein merp (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:x73112 pid:483769 sp:q51770 percent) (le:6741) (re:6947) (di:complement) U32715 U32715 g1573260 Haemophilus influenzae Rd 71421 -11537657 5000694873 (de:(hi0292) (pn:mercury scavenger protein:merp) (gn:merp) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI0292 HI0292 Haemophilus influenzae 727 10088248

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886968	15268	37424	651	216

Description

6500733800 fece:hi0361 iii dicitrate transport atp-binding protein fece:iron:iii dicitrate transport atp-binding protein homolog (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) HI0361 HI0361 Haemophilus influenzae 727 -11537658 71280 fece:hi0361 (de:iron(iii) dicitrate transport atp-binding protein fece homolog) (db:swissprot) FECE_HAEIN P44662 HAEMOPHILUS INFLUENZAE 727 -11537658 166925 atp-binding protein yfeb homolog (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F64063 F64063 Haemophilus influenzae 727 -11537658 7500881391 hi0361 iron chelated transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to pid:1245464 pid:1245465 percent) (le:6367) (re:7287) (di:complement) U32720 U32720 g1573329 Haemophilus influenzae Rd 71421 -11537658 5000694874 (de:(hi0361) (pn:iii dicitrate transport atp-binding protein homolog:iron:iii dicitrate transport atp-binding protein fece) (gn:fece) (gtcfc:12.5) (ec:) (fece_haein) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI0361 HI0361 Haemophilus influenzae 727 10013853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501886971	15269	37425	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887011	15270	37426	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887027	15271	37427	1281	426

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887066	15272	37428	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887084	15273	37429	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887085	15274	37430	294	97

Description

6500733801 nhab:hi0427 na+/h+ antiporter (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0427 HI0427 Haemophilus influenzae 727 -11537659 85773 nhab:hi0427 (de:na(+)/h(+) antiporter 2) (db:swissprot) NHAB_HAEIN P44706 HAEMOPHILUS INFLUENZAE 727 -11537659 167025 nhab na+/h+-exchanging protein nhab:na+/h+ antiporter (db:pir2.dat) B64067 B64067 Haemophilus influenzae 727 -11537659 7500886416 hi0427 na+/h+ antiporter nhab (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:m83655 sp:p27377 pid:146957 gb:u00096) (le:2342) (re:3910) (di:direct) U32726 U32726 g1573402 Haemophilus influenzae Rd 71421 -11537659 5000694875 (de:(hi0427) (pn:na) (gn:nhab) (gtcfc:12.5) (ec:) (nhab_haein) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI0427 HI0427 Haemophilus influenzae 727 10027940

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887091	15275	37431	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887093	15276	37432	420	139

Description

5000694876 trkh:hi0723 sp_p21166:trk system potassium uptake protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0723 HI0723 Haemophilus influenzae 727 -11537660 166500 hypothetical protein hi0723 (cl:potassium uptake protein trkg) (db:pir2.dat) E64157 E64157 Haemophilus influenzae 727 -11537660 102256 trkh:hi0723 (de:trk system potassium uptake protein trkh) (db:swissprot) TRKH_HAEIN P44843 HAEMOPHILUS INFLUENZAE 727 -11537660 6500733802 trkh sp_p21166:trk system potassium uptake protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) HI0723 HI0723 Haemophilus influenzae 727 -11537660

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887094	15277	37433	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887116	15278	37434	582	193

Description

6500733803 kefbc:hi0911 potassium efflux system:kefc:glutathione-regulated potassium-efflux system protein:k:/h:antiporter (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI0911 HI0911 Haemophilus influenzae 727 -11537661 80617 kefbc:hi0911 (de:antiporter)) (db:swissprot) KEFX_HAEIN P44933 HAEMOPHILUS INFLUENZAE 727 -11537661 167100 glutathione-regulated potassium efflux system protein kefc homolog (cl:glutathione-regulated potassium efflux system protein kefc) (db:pir2.dat) A64102 A64102 Haemophilus influenzae 727 -11537661 7500884588 hi0911 glutathione-regulated potassium efflux system (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p03819 gb:x56742 pid:216472) (le:9611) (re:11467) (di:direct) U32772 U32772 g1573928 Haemophilus influenzae Rd 71421 -11537661 5000694877 (de:(hi0911) (pn:glutathione-regulated potassium-efflux system protein:k:potassium efflux system:kefc) (gn:kefbc) (gtcfc:12.5) (ec:) (kefx_haein) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI0911 HI0911 Haemophilus influenzae 727 10022859

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887126	15279	37435	1179	392

Description

GTC ORF with score 161 to: (db:genpept-bct1) (de:pseudomonas aeruginosa pyoverdine chromophore biosynthesis genecluster including pvca (pvca), pvcb (pvcb), pvcc (pvcc), and pvcd(pvcd) genes, complete cds, and transcriptional activator ptxr(ptxr) gene, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887138	15280	37436	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887151	15281	37437	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887153	15282	37438	1242	413

Description

6500733804 cora:hi1035 magnesium and cobalt transport protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1035 HI1035 Haemophilus influenzae 727 -11537662 65478 cora:hi1035 (de:magnesium and cobalt transport protein cora) (db:swissprot) CORA_HAEIN P44998 HAEMOPHILUS INFLUENZAE 727 -11537662 166976 cora magnesium transport protein cora (db:pir2.dat) A64109 A64109 Haemophilus influenzae 727 -11537662 7500879122 hi1035 magnesium and cobalt transport protein cora (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to sp:p27841 gb:m87049 gb:l11042 gb:u00096) (le:2822) (re:3769) (di:direct) U32784 U32784 g1574068 Haemophilus influenzae Rd 71421 -11537662 5000694878 (de:(hi1035) (pn:magnesium and cobalt transport protein :magnesium and cobalt transport protein:cora) (gn:cora) (gtcfc:12.5) (ec:) (cora_haein) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1035 HI1035 Haemophilus influenzae 727 10008126

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887160	15283	37439	357	119

Description

GTC ORF with score 92 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t23e7.) (nt:coded for by c. elegans cdna yk35g10.5; coded for) (le:9863:11265:11487) (re:9974:11329:11588) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887161	15284	37440	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887162	15285	37441	1104	367

Description

6500733805 mert:hi1049 mercuric transport protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1049 HI1049 Haemophilus influenzae 727 -11537663 5500686459 hi1049 (de:hypothetical protein hi1049) (db:swissprot) YA49_HAEIN Q57347 HAEMOPHILUS INFLUENZAE 727 -11537663 166985 hypothetical protein hi1049 (db:pir2.dat) H64109 H64109 Haemophilus influenzae 727 -11537663 7500895864 hi1049 mercuric ion transport protein mert (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the completegenome.) (nt:similar to sp:p04140 gb:z00027 pid:154899 pid:43716) (le:6599) (re:6892) (di:direct) U32785 U32785 g1574082 Haemophilus influenzae Rd 71421 -11537663 5000694879 (de:(hi1049) (pn:mercuric transport protein:mert) (gn:mert) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1049 HI1049 Haemophilus influenzae 727 10088246

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887168	15286	37442	366	121

Description

6500733806 merp:hi1050 mercury scavenger protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1050 HI1050 Haemophilus influenzae 727 -11537664 166989 mercury reductase homolog (db:pir2.dat) I64109 I64109 Haemophilus influenzae 727 -11537664 7500960713 hi1050 mercuric ion scavenger protein merp (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the completegenome.) (nt:similar to pid:1143574 sp:q54463 percent ident:) (le:6901) (re:7179) (di:direct) U32785 U32785 g1574083 Haemophilus influenzae Rd 71421 -11537664 5000694880 (de:(hi1050) (pn:mercury scavenger protein:merp) (gn:merp) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1050 HI1050 Haemophilus influenzae 727 10088249

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887175	15287	37443	357	118

Description

6500733807 nhac:hi1107 na+/h+ antiporter (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1107 HI1107 Haemophilus influenzae 727 -11537665 4000708966 hi1107 (de:hypothetical na+/h+ antiporter hi1107) (db:swissprot) YB07_HAEIN Q57007 HAEMOPHILUS INFLUENZAE 727 -11537665 167026 na+/h+-exchanging protein homolog:na+/h+ antiporter (cl:na+/h+-exchanging protein) (db:pir2.dat) I64182 I64182 Haemophilus influenzae 727 -11537665 7500896299 hi1107 na+/h+ antiporter nhac (db:genpept-bct1) (de:haemophilus influenzae rd section 105 of 163 of the completegenome.) (nt:similar to gb:m73530 sp:p27611 pid:143245) (le:7526) (re:8932) (di:complement) U32790 U32790 g1574661 Haemophilus influenzae Rd 71421 -11537665 5000694881 (de:(hi1107) (pn:na) (gn:nhac) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1107 HI1107 Haemophilus influenzae 727 10088260

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887188	15288	37444	324	107

Description

6500733808 fepc:hi1272 ferric enterobactin transport atp-binding protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1272 HI1272 Haemophilus influenzae 727 -11537666 5500686488 hi1272 (de:hypothetical abc transporter atp-binding protein hi1272) (db:swissprot) YC72_HAEIN Q57243 HAEMOPHILUS INFLUENZAE 727 -11537666 166129 ferric enterobactin transport atp-binding protein homolog hi1272 (cl:atp-binding cassette homology) (db:pir2.dat) F64113 F64113 Haemophilus influenzae 727 -11537666 7500921508 hi1272 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:similar to gb:ae000511 sp:o05732 pid:2072456) (le:1202) (re:1993) (di:direct) U32807 U32807 g1574727 Haemophilus influenzae Rd 71421 -11537666 5000694882 (de:(hi1272) (pn:ferric enterobactin transport atp-binding protein:fepc) (gn:fepc) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1272 HI1272 Haemophilus influenzae 727 10088080

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887209	15289	37445	1266	422

Description

6500733809 putp:hi1352 sodium/proline symporter:proline permease (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1352 HI1352 Haemophilus influenzae 727 -11537667 92496 putp:hi1352 (de:sodium/proline symporter (proline permease)) (db:swissprot) PUTP_HAEIN P45174 HAEMOPHILUS INFLUENZAE 727 -11537667 153168 putp sodium/proline symporter:proline carrier protein:proline permease:proline transport protein (cl:proline carrier protein) (db:pir2.dat) E64118 E64118 Haemophilus influenzae 727 -11537667 7500889108 hi1352 sodium/proline symporter proline permease (db:genpept-bct1) (de:haemophilus influenzae rd section 129 of 163 of the completegenome.) (nt:similar to gb:d32069 pid:509694 pid:913690 percent) (le:4606) (re:6120) (di:complement) U32814 U32814 g1574814 Haemophilus influenzae Rd 71421 -11537667 5000694883 (de:(hi1352) (pn:sodium) (gn:putp) (gtcfc:12.5) (ec:) (putp_haein) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1352 HI1352 Haemophilus influenzae 727 10034528

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887211	15290	37446	612	203

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887216	15291	37447	249	82

Description

5000694884 ftna:rsga-a:hi1384 ferritin like protein:rsga:ferritin like protein 1 (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1384 HI1384 Haemophilus influenzae 727 -11537668 72426 ftna:rsga-a:hi1384 (de:ferritin like protein 1) (db:swissprot) FTN1_HAEIN P43707 HAEMOPHILUS INFLUENZAE 727 -11537668 166133 bacterioferritin homolog hi1384 (cl:ferritin) (db:pir2.dat) A64121 A64121 Haemophilus influenzae 727 -11537668 7500881780 hi1384 ferritin rsga (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to sp:p23887 gb:x53513 pid:42898 gb:u00096) (le:372) (re:920) (di:direct) U32819 U32819 g1574219 Haemophilus influenzae Rd 71421 -11537668 6500733810 ftna:rsga-a ferritin like protein:rsga:ferritin like protein 1 (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) HI1384 HI1384 Haemophilus influenzae 727 -11537668

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887234	15292	37448	417	138

Description

5000694885 ftnb:rsga-b:hi1385 ferritin like protein:rsga:ferritin like protein 2 (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1385 HI1385 Haemophilus influenzae 727 -11537669 72427 ftnb:rsga-b:hi1385 (de:ferritin like protein 2) (db:swissprot) FTN2_HAEIN P43708 HAEMOPHILUS INFLUENZAE 727 -11537669 166134 bacterioferritin homolog hi1385 (cl:ferritin) (db:pir2.dat) B64121 B64121 Haemophilus influenzae 727 -11537669 7500881781 hi1385 ferritin rsga (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to sp:p23887 gb:x53513 pid:42898 gb:u00096) (le:936) (re:1433) (di:direct) U32819 U32819 g1574220 Haemophilus influenzae Rd 71421 -11537669 6500733811 ftnb:rsga-b ferritin like protein:rsga:ferritin like protein 2 (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) HI1385 HI1385 Haemophilus influenzae 727 -11537669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887241	15293	37449	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887244	15294	37450	201	67

Description

5000694886 ferrichrome-iron receptor:fhua:hypothetical protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1466 HI1466 Haemophilus influenzae 727 -11537670 111436 hi1466 (de:hypothetical protein hi1466) (db:swissprot) YE66_HAEIN P45220 HAEMOPHILUS INFLUENZAE 727 -11537670 166132 ferrichrome-iron receptor homolog (db:pir2.dat) C64125 C64125 Haemophilus influenzae 727 -11537670 7500922728 hi1466 h. influenzae predicted coding region hi1466 (db:genpept-bct1) (de:haemophilus influenzae rd section 139 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8731) (re:9276) (di:direct) U32824 U32824 g1574305 Haemophilus influenzae Rd 71421 -11537670 6500733812 ferrichrome-iron receptor:fhua:hypothetical protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) HI1466 HI1466 Haemophilus influenzae 727 -11537670

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887245	15295	37451	615	204

Description

6500733813 fepc:hi1470 ferric enterobactin transport atp-binding protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1470 HI1470 Haemophilus influenzae 727 -11537671 5500686561 hi1470 (de:hypothetical abc transporter atp-binding protein hi1470) (db:swissprot) YE70_HAEIN Q57399 HAEMOPHILUS INFLUENZAE 727 -11537671 166130 ferric enterobactin transport atp-binding protein homolog hi1470 (cl:atp-binding cassette homology) (db:pir2.dat) F64125 F64125 Haemophilus influenzae 727 -11537671 7500922735 hi1470 iron chelatin abc transporter:atp-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to gb:ae000511 sp:o05732 pid:2072456) (le:3843) (re:4604) (di:complement) U32825 U32825 g1574311 Haemophilus influenzae Rd 71421 -11537671 5000694887 (de:(hi1470) (pn:ferric enterobactin transport atp-binding protein:fepc) (gn:fepc) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1470 HI1470 Haemophilus influenzae 727 10088081

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887248	15296	37452	1389	462

Description

6500733814 sfuc:hi1474 periplasmic-binding-protein-dependent iron transport protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1474 HI1474 Haemophilus influenzae 727 -11537672 5500686563 hi1474 (de:hypothetical abc transporter atp-binding protein hi1474) (db:swissprot) YE74_HAEIN Q57213 HAEMOPHILUS INFLUENZAE 727 -11537672 167085 nucleotide-binding protein sfuc homolog (cl:atp-binding cassette homology) (db:pir2.dat) I64125 I64125 Haemophilus influenzae 727 -11537672 7500922753 hi1474 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to gb:ae000511 pid:2313950 percent) (le:7575) (re:8174) (di:complement) U32825 U32825 g1574315 Haemophilus influenzae Rd 71421 -11537672 5000694888 (de:(hi1474) (pn:periplasmic-binding-protein-dependent iron transport protein:sfuc) (gn:sfuc) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1474 HI1474 Haemophilus influenzae 727 10088280

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887258	15297	37453	330	109

Description

6500733815 modb:hi1525 molybdate-binding periplasmic protein precursor (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HI1525 HI1525 Haemophilus influenzae 727 -11537673 166998 molybdenum transport protein molb homolog hi1525 (cl:molybdate-binding periplasmic protein) (db:pir2.dat) B64127 B64127 Haemophilus influenzae 727 -11537673 7500960714 hi1525 molybdate-binding periplasmic protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:similar to gb:ae000666 percent ident: 32.51;) (le:4508) (re:5245) (di:complement) U32828 U32828 g1574366 Haemophilus influenzae Rd 71421 -11537673 5000694889 (de:(hi1525) (pn:molybdate-binding periplasmic protein precursor:modb) (gn:modb) (gtcfc:12.5) (ec:) (keggfc:11.2) (tigrfc:13.4) (db:gtc-haemophilus influenzae)) HI1525 HI1525 Haemophilus influenzae 727 10088251

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887275	15298	37454	441	146

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887279	15299	37455	741	246

Description

6500733816 tbpa:hi1019 thiamin-binding periplasmic protein precursor (gtcfc:12.6) (keggfc:11.1) (db:gtc-haemophilus influenzae) HI1019 HI1019 Haemophilus influenzae 727 -11537674 100800 tbpa:hi1019 (de:thiamin-binding periplasmic protein precursor) (db:swissprot) TBPA_HAEIN P44984 HAEMOPHILUS INFLUENZAE 727 -11537674 166606 thiamine-binding periplasmic protein precursor homolog hi1019 (db:pir2.dat) C64164 C64164 Haemophilus influenzae 727 -11537674 7500892806 hi1019 thiamin abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p31550 gb:u09984 pid:216488) (le:8450) (re:9448) (di:direct) U32782 U32782 g1574048 Haemophilus influenzae Rd 71421 -11537674 5000695534 (de:(hi1019) (pn:thiamin-binding periplasmic protein precursor) (gn:tbpa) (gtcfc:13.7) (ec:) (tbpa_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI1019 HI1019 Haemophilus influenzae 727 10042647

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887282	15300	37456	834	277

Description

5000695176 gb:d10483_53:hypothetical protein (gtcfc:12.6:14.1) (keggfc:11.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1020 HI1020 Haemophilus influenzae 727 -11537675 109553 hi1020 (de:hypothetical protein hi1020) (db:swissprot) YABK_HAEIN P44985 HAEMOPHILUS INFLUENZAE 727 -11537675 166607 hypothetical protein hi1020 (cl:sfub protein) (db:pir2.dat) D64164 D64164 Haemophilus influenzae 727 -11537675 7500896007 hi1020 thiamin abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p31549 pid:216487 gb:u00096) (le:9453) (re:11069) (di:direct) U32782 U32782 g1574049 Haemophilus influenzae Rd 71421 -11537675 6500733817 gb:d10483_53:hypothetical protein (gtcfc:12.6:14.1) (keggfc:11.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1020 HI1020 Haemophilus influenzae 727 -11537675

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887292	15301	37457	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887308	15302	37458	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887312	15303	37459	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887317	15304	37460	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887322	15305	37461	666	221

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887332	15306	37462	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887337	15307	37463	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887338	15308	37464	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887365	15309	37465	1293	430

Description

5000695177 hypothetical protein:gb:d10483_52:hypothetical abc transporter atp-binding protein hi1021 (gtcfc:12.6:14.1) (keggfc:11.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1021 HI1021 Haemophilus influenzae 727 -11537676 7500976270 hi1021 thiamin abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p31548 pid:216486 gb:u00096) (le:11053) (re:11700) (di:direct) U32782 U32782 g1574050 Haemophilus influenzae Rd 71421 -11537676 6500733818 hypothetical protein:gb:d10483_52:hypothetical abc transporter atp-binding protein hi1021 (gtcfc:12.6:14.1) (keggfc:11.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1021 HI1021 Haemophilus influenzae 727 -11537676

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887401	15310	37466	189	62

Description

6500733819 hi1079:hin_1068 glutamine transport system permease protein:glnp (gtcfc:12.6) (keggfc:11.1) (db:gtc-haemophilus influenzae) HIN_1068 HIN_1068 Haemophilus influenzae 727 -11537677 109445 hi1079 (de:hypothetical amino-acid abc transporter permease protein hi0179) (db:swissprot) YA79_HAEIN P45023 HAEMOPHILUS INFLUENZAE 727 -11537677 7500895918 hi1079 amino acid abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to gb:ae000511 pid:2314077 percent) (le:3773) (re:4405) (di:complement) U32788 U32788 g1574633 Haemophilus influenzae Rd 71421 -11537677 5000695546 (de:(hin106811) (pn:glutamine transport system permease protein:glnp) (gn:hi1079) (gtcfc:13.7) (ec:) (ya79_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN106811 HIN106811 Haemophilus influenzae 727 10126710

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887414	15311	37467	1566	521

Description

6500733820 hi1124:hin_1110 oligopeptide binding protein:oppa (gtcfc:12.6) (keggfc:11.1) (db:gtc-haemophilus influenzae) HIN_1110 HIN_1110 Haemophilus influenzae 727 -11537678 7500976272 hi1124 oligopeptide abc transporter (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:similar to sp:p06202 gb:x05491 gb:x52093 pid:47802) (le:5638) (re:7263) (di:complement) U32792 U32792 g1574679 Haemophilus influenzae Rd 71421 -11537678 5000695551 (de:(hin111011) (pn:oligopeptide binding protein:oppa) (gn:hi1124) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN111011 HIN111011 Haemophilus influenzae 727 10126711

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887417	15312	37468	1110	369

Description

5000694890 msba:msh-1:hi0060 atp dependent translocator homolog:msba:probable transport atp-binding protein msba (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0060 HI0060 Haemophilus influenzae 727 -11537679 84288 msba:msh-1:hi0060 (de:probable transport atp-binding protein msba) (db:swissprot) MSBA_HAEIN P44407 HAEMOPHILUS INFLUENZAE 727 -11537679 166015 msba:msh-1 probable abc-type transport protein msba (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) H64045 H64045 Haemophilus influenzae 727 -11537679 7500885916 hi0060 abc transporter:atp-binding protein msba (db:genpept-bct1) (de:haemophilus influenzae rd section 6 of 163 of the complete genome.) (nt:similar to sp:p27299 gb:z11796 pid:42023 gb:u00096) (le:3816) (re:5579) (di:complement) U32691 U32691 g1573008 Haemophilus influenzae Rd 71421 -11537679 6500733821 msba:msh-1 atp dependent translocator homolog:msba:probable transport atp-binding protein msba (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0060 HI0060 Haemophilus influenzae 727 -11537679

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887418	15313	37469	759	252

Description

5000694891 hemin receptor precursor:hemr:probable tonb-dependent receptor hi0262 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0262 HI0262 Haemophilus influenzae 727 -11537680 109034 hi0262 (de:probable tonb-dependent receptor hi0262 precursor) (db:swissprot) Y262_HAEIN P44600 HAEMOPHILUS INFLUENZAE 727 -11537680 166187 hxuc outer membrane protein hxuc (cl:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pir2.dat) C64058 C64058 Haemophilus influenzae 727 -11537680 7500894992 hi0262 heme-hemopexin utilization protein c (db:genpept-bct1) (de:haemophilus influenzae rd section 27 of 163 of the complete genome.) (nt:similar to sp:p45357 pid:595326 percent identity:) (le:2837) (re:5008) (di:direct) U32712 U32712 g1573228 Haemophilus influenzae Rd 71421 -11537680 6500733822 hemin receptor precursor:hemr:probable tonb-dependent receptor hi0262 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0262 HI0262 Haemophilus influenzae 727 -11537680

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887423	15314	37470	492	163

Description

6500733823 hxua:hi0264 heme-hemopexin-binding protein:hemopexin-binding protein precursor:heme:hemopexin utilization protein a (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0264 HI0264 Haemophilus influenzae 727 -11537681 78234 hxua:hi0264 (de:protein a)) (db:swissprot) HXA1_HAEIN P44602 HAEMOPHILUS INFLUENZAE 727 -11537681 166185 hxua hemopexin-heme complex-binding protein precursor (db:pir2.dat) E64058 E64058 Haemophilus influenzae 727 -11537681 7500883638 hi0264 heme-hemopexin utilization protein a hxua (db:genpept-bct1) (de:haemophilus influenzae rd section 27 of 163 of the complete genome.) (nt:similar to gb:u08348 pid:540014 percent identity:) (le:6792) (re:9509) (di:direct) U32712 U32712 g1573230 Haemophilus influenzae Rd 71421 -11537681 5000694892 (de:(hi0264) (pn:hemopexin-binding protein precursor:heme:hemopexin utilization protein a:heme-hemopexin-binding protein:hxua) (gn:hxua) (gtcfc:12.6) (ec:) (hxa1_haein) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI0264 HI0264 Haemophilus influenzae 727 10020573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887424	15315	37471	192	63

Description

6500733824 abc:hi0621 atp-binding protein:atp-binding protein abc (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0621 HI0621 Haemophilus influenzae 727 -11537682 57914 abc:hi0621 (de:atp-binding protein abc) (db:swissprot) ABC_HAEIN P44785 HAEMOPHILUS INFLUENZAE 727 -11537682 166017 atp-binding protein homolog hi0621 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) C64082 C64082 Haemophilus influenzae 727 -11537682 7500876262 hi0621 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 59 of 163 of the complete genome.) (nt:similar to sp:p30750 gb:l08626 pid:1208966) (le:7745) (re:8782) (di:complement) U32744 U32744 g1573615 Haemophilus influenzae Rd 71421 -11537682 5000694893 (de:(hi0621) (pn:atp-binding protein abc:atp-binding protein:abc) (gn:abc) (gtcfc:12.6) (ec:) (abc_haein) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI0621 HI0621 Haemophilus influenzae 727 10000694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887439	15316	37472	2352	783

Description

5000694894 transferrin-binding protein 1:tbp2:probable tonb-dependent receptor hi0635 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0635 HI0635 Haemophilus influenzae 727 -11537683 109238 hi0635 (de:probable tonb-dependent receptor hi0635 precursor) (db:swissprot) Y635_HAEIN P44795 HAEMOPHILUS INFLUENZAE 727 -11537683 167210 hemoglobin-binding protein homolog hi0635 (cl:tonb-dependent receptor amino-terminal homology) (db:pir2.dat) B64083 B64083 Haemophilus influenzae 727 -11537683 7500895432 hi0635 hemoglobin-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 61 of 163 of the complete genome.) (nt:similar to pid:1000292 pid:984513 percent ident:) (le:5676) (re:8537) (di:complement) U32746 U32746 g1573631 Haemophilus influenzae Rd 71421 -11537683 6500733825 transferrin-binding protein 1:tbp2:probable tonb-dependent receptor hi0635 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0635 HI0635 Haemophilus influenzae 727 -11537683

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887440	15317	37473	690	229

Description

5000694895 lactoferrin binding protein:lbpa:probable tonb-dependent receptor hi0661 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0661 HI0661 Haemophilus influenzae 727 -11537684 166938 hemoglobin receptor homolog (cl:tonb-dependent receptor carboxyl-terminal homology) (db:pir2.dat) I64084 I64084 Haemophilus influenzae 727 -11537684 109249 hi0661 (de:probable tonb-dependent receptor hi0661 precursor) (db:swissprot) Y661_HAEIN P44809 HAEMOPHILUS INFLUENZAE 727 -11537684 6500733826 lactoferrin binding protein:lbpa:probable tonb-dependent receptor hi0661 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0661 HI0661 Haemophilus influenzae 727 -11537684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887443	15318	37474	441	147

Description

6500733827 tbp1:hi0712 transferrin-binding protein 1 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0712 HI0712 Haemophilus influenzae 727 -11537685 109269 hi0712 (de:probable tonb-dependent receptor hi0712 precursor) (db:swissprot) Y712_HAEIN P44836 HAEMOPHILUS INFLUENZAE 727 -11537685 167209 hemoglobin-binding protein homolog hi0712 (cl:tonb-dependent receptor amino-terminal homology) (db:pir2.dat) B64088 B64088 Haemophilus influenzae 727 -11537685 7500895469 hi0712 hemoglobin-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to pid:1000292 pid:984513 percent ident:) (le:805) (re:4059) (di:complement) U32754 U32754 g1573714 Haemophilus influenzae Rd 71421 -11537685 5000694896 (de:(hi0712) (pn:transferrin-binding protein 1:tbp1) (gn:tbp1) (gtcfc:12.6) (ec:) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI0712 HI0712 Haemophilus influenzae 727 10051001

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887466	15319	37475	534	177

Description

GTC ORF with score 132 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887473	15320	37476	516	171

Description

GTC ORF with score 103 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t27a16 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:46311:46543:46813:46958) (re:46498:46734:46922:47149) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887491	15321	37477	195	64

Description

5000694897 hbpa:dppa:hi0853 heme-binding lipoprotein:dppa:heme-binding protein a precursor:hemin-binding lipoprotein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0853 HI0853 Haemophilus influenzae 727 -11537686 166182 hbpa heme-binding protein a precursor (cl:dipeptide transport protein) (db:pir2.dat) D64098 D64098 Haemophilus influenzae 727 -11537686 7500955175 hi0853 heme-binding lipoprotein dppa (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to gb:m84028 sp:p33950 pid:1573869 percent) (le:101) (re:1750) (di:direct) U32767 U32767 g1573869 Haemophilus influenzae Rd 71421 -11537686 6500733828 hbpa:dppa heme-binding lipoprotein:dppa:heme-binding protein a precursor:hemin-binding lipoprotein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0853 HI0853 Haemophilus influenzae 727 -11537686

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887494	15322	37478	1461	486

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887497	15323	37479	273	90

Description

6500733829 tfba:hi0973 transferrin-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0973 HI0973 Haemophilus influenzae 727 -11537687 5500686453 hi0973 (de:hypothetical protein hi0973) (db:swissprot) Y973_HAEIN Q57133 HAEMOPHILUS INFLUENZAE 727 -11537687 167208 transferrin-binding protein tfba homolog (db:pir2.dat) G64105 G64105 Haemophilus influenzae 727 -11537687 7500895772 hi0973 h. influenzae predicted coding region hi0973 (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2245) (re:3114) (di:direct) U32778 U32778 g1574000 Haemophilus influenzae Rd 71421 -11537687 5000694898 (de:(hi0973) (pn:transferrin-binding protein:tfba) (gn:tfba) (gtcfc:12.6) (ec:) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI0973 HI0973 Haemophilus influenzae 727 10088307

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887526	15324	37480	354	117

Description

6500733830 panf:hi0975 sodium/pantothenate symporter:pantothenate permease (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0975 HI0975 Haemophilus influenzae 727 -11537688 88581 panf:hi0975 (de:sodium/pantothenate symporter (pantothenate permease)) (db:swissprot) PANF_HAEIN P44963 HAEMOPHILUS INFLUENZAE 727 -11537688 167069 pantothenate transport protein:pantothenate permease (cl:proline carrier protein) (db:pir2.dat) H64105 H64105 Haemophilus influenzae 727 -11537688 7500887652 hi0975 sodium/pantothenate symporter panf (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:similar to pid:606198 gb:u00096 pid:1789656 percent) (le:4989) (re:6443) (di:direct) U32778 U32778 g1574003 Haemophilus influenzae Rd 71421 -11537688 5000694899 (de:(hi0975) (pn:sodium:pantothenate permease:panf) (gn:panf) (gtcfc:12.6) (ec:) (panf_haein) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI0975 HI0975 Haemophilus influenzae 727 10030708

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887535	15325	37481	1608	535

Description

6500733831 tbp1:hi0994 transferrin binding protein 1 precursor:probable transferrin binding protein 1 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0994 HI0994 Haemophilus influenzae 727 -11537689 100789 tbp1:hi0994 (de:probable transferrin binding protein 1 precursor) (db:swissprot) TBP1_HAEIN P44970 HAEMOPHILUS INFLUENZAE 727 -11537689 151710 tbp1 transferrin-binding protein 1 precursor (cl:bacterial pathogen transferrin-binding protein:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pir2.dat) C64107 C64107 Haemophilus influenzae 727 -11537689 7500892802 hi0994 transferrin-binding protein 1 precursor tbp1 (db:genpept-bct1) (de:haemophilus influenzae rd section 95 of 163 of the complete genome.) (nt:similar to gb:z15129 sp:q06987 gb:s64486 gb:x75168) (le:3901) (re:6639) (di:complement) U32780 U32780 g1574024 Haemophilus influenzae Rd 71421 -11537689 5000694900 (de:(hi0994) (pn:probable transferrin binding protein 1 precursor:transferrin binding protein 1 precursor:tbp1) (gn:tbp1) (gtcfc:12.6) (ec:) (tbp1_haein) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI0994 HI0994 Haemophilus influenzae 727 10042636

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887545	15326	37482	447	148

Description

6500733832 tbp2:hi0995 transferrin binding protein 2 precursor:probable transferrin binding protein 2 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI0995 HI0995 Haemophilus influenzae 727 -11537690 100795 tbp2:hi0995 (de:probable transferrin binding protein 2 precursor) (db:swissprot) TBP2_HAEIN P44971 HAEMOPHILUS INFLUENZAE 727 -11537690 167207 tbp2 transferrin-binding protein 2 precursor (db:pir2.dat) D64107 D64107 Haemophilus influenzae 727 -11537690 7500892803 hi0995 transferrin-binding protein 2 precursor tbp2 (db:genpept-bct1) (de:haemophilus influenzae rd section 95 of 163 of the complete genome.) (nt:similar to pid:1177569 percent ident: 39.97;) (le:6667) (re:8544) (di:complement) U32780 U32780 g1574025 Haemophilus influenzae Rd 71421 -11537690 5000694901 (de:(hi0995) (pn:probable transferrin binding protein 2 precursor:transferrin binding protein 2 precursor:tbp2) (gn:tbp2) (gtcfc:12.6) (ec:) (tbp2_haein) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI0995 HI0995 Haemophilus influenzae 727 10042642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887554	15327	37483	258	85

Description

6500733833 cydd:hi1157 transport atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI1157 HI1157 Haemophilus influenzae 727 -11537691 67475 cydd:hi1157 (de:transport atp-binding protein cydd) (db:swissprot) CYDD_HAEIN P45082 HAEMOPHILUS INFLUENZAE 727 -11537691 167223 cydd abc-type transport protein cydd (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F64186 F64186 Haemophilus influenzae 727 -11537691 7500879840 hi1157 atp-binding protein protein cydd (db:genpept-bct1) (de:haemophilus influenzae rd section 110 of 163 of the completegenome.) (nt:similar to gb:l21749 sp:p29018 gb:l25859 pid:146416) (le:6353) (re:8113) (di:complement) U32795 U32795 g1574714 Haemophilus influenzae Rd 71421 -11537691 5000694902 (de:(hi1157) (pn:transport atp-binding protein :transport atp-binding protein:cydd) (gn:cydd) (gtcfc:12.6) (ec:) (cydd_haein) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI1157 HI1157 Haemophilus influenzae 727 10010074

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887562	15328	37484	282	93

Description

6500733834 tbp1:hi1217 transferrin binding protein 1 precursor (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI1217 HI1217 Haemophilus influenzae 727 -11537692 110451 hi1217 (de:probable tonb-dependent receptor hi1217 precursor) (db:swissprot) YC17_HAEIN P45114 HAEMOPHILUS INFLUENZAE 727 -11537692 167206 hypothetical protein hi1217 (db:pir2.dat) G64110 G64110 Haemophilus influenzae 727 -11537692 7500921439 hi1217 transferrin-binding protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 116 of 163 of the completegenome.) (nt:similar to gp:2764817 percent ident: 25.44;) (le:3365) (re:6106) (di:complement) U32801 U32801 g1574147 Haemophilus influenzae Rd 71421 -11537692 5000694903 (de:(hi1217) (pn:transferrin binding protein 1 precursor:tbp1) (gn:tbp1) (gtcfc:12.6) (ec:) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI1217 HI1217 Haemophilus influenzae 727 10052182

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887581	15329	37485	390	129

Description

GTC ORF with score 175 to: (sr:baker"s yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 9672.) (nt:similar to mouse mpv17 protein (swissprot accession) (le:24166) (re:24759) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887595	15330	37486	879	292

Description

6500733835 hemu:hi1471 hemin permease (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI1471 HI1471 Haemophilus influenzae 727 -11537693 5500686562 hi1471 (de:hypothetical abc transporter permease protein hi1471) (db:swissprot) YE71_HAEIN Q57130 HAEMOPHILUS INFLUENZAE 727 -11537693 166186 hemin transport protein homolog hi1471:hemin permease homolog hi1471 (cl:ferrichrome abc transporter) (db:pir2.dat) G64125 G64125 Haemophilus influenzae 727 -11537693 7500922739 hi1471 iron chelatin abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to gb:ae000511 sp:o05731 pid:2072455) (le:4597) (re:5610) (di:complement) U32825 U32825 g1574312 Haemophilus influenzae Rd 71421 -11537693 5000694904 (de:(hi1471) (pn:hemin permease:hemu) (gn:hemu) (gtcfc:12.6) (ec:) (keggfc:11.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae)) HI1471 HI1471 Haemophilus influenzae 727 10088099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887598	15331	37487	342	113

Description

5000694905 cystic fibrosis transmembrane conductance regulator:hypothetical protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI1619 HI1619 Haemophilus influenzae 727 -11537694 112048 hi1619 (de:hypothetical protein hi1619) (db:swissprot) YG19_HAEIN P45276 HAEMOPHILUS INFLUENZAE 727 -11537694 166070 hypothetical protein hi1619 (db:pir2.dat) B64133 B64133 Haemophilus influenzae 727 -11537694 6500733836 cystic fibrosis transmembrane conductance regulator:hypothetical protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI1619 HI1619 Haemophilus influenzae 727 -11537694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887600	15332	37488	492	163

Description

5000694906 high-affinity choline transport protein:bett:probable transport protein hi1706 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI1706 HI1706 Haemophilus influenzae 727 -11537695 112569 hi1706 (de:probable transport protein hi1706) (db:swissprot) YH06_HAEIN P45335 HAEMOPHILUS INFLUENZAE 727 -11537695 166195 bett protein homolog (cl:choline transport protein bett) (db:pir2.dat) D64137 D64137 Haemophilus influenzae 727 -11537695 7500936673 hi1706 high-affinity choline transport protein bett (db:genpept-bct1) (de:haemophilus influenzae rd section 158 of 163 of the completegenome.) (nt:similar to sp:p17447 gb:x52905 pid:48716 gb:u00096) (le:7318) (re:9327) (di:complement) U32843 U32843 g1574560 Haemophilus influenzae Rd 71421 -11537695 6500733837 high-affinity choline transport protein:bett:probable transport protein hi1706 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-haemophilus influenzae) HI1706 HI1706 Haemophilus influenzae 727 -11537695

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887609	15333	37489	480	159

Description

6500733838 htpg:hi0104 heat shock protein c62.5:high temperature protein g (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae) HI0104 HI0104 Haemophilus influenzae 727 -11537696 78022 htpg:hi0104 (de:heat shock protein htpg (high temperature protein g)) (db:swissprot) HTPG_HAEIN P44516 HAEMOPHILUS INFLUENZAE 727 -11537696 152095 htpg heat shock protein htpg:heat shock protein htpg c62.5 (cl:heat shock protein 90) (db:pir2.dat) G64048 G64048 Haemophilus influenzae 727 -11537696 7500883600 hi0104 heat shock protein htpg (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:similar to pid:862902 sp:p54649 percent identity:) (le:9885) (re:11780) (di:complement) U32695 U32695 g1573053 Haemophilus influenzae Rd 71421 -11537696 5000694907 (de:(hi0104) (pn:heat shock protein :high temperature protein g:heat shock protein c62) (gn:htpg) (gtcfc:12.7) (ec:) (htpg_haein) (keggfc:11.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae)) HI0104 HI0104 Haemophilus influenzae 727 10020361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887625	15334	37490	591	196

Description

6500733839 hsca:hi0373 heat shock cognate 66:heat shock protein:hsc66 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae) HI0373 HI0373 Haemophilus influenzae 727 -11537697 77869 hsca:hi0373 (de:chaperone protein hsca (hsc66)) (db:swissprot) HSCA_HAEIN P44669 HAEMOPHILUS INFLUENZAE 727 -11537697 166177 heat shock cognate protein 66 (cl:heat shock protein 70) (db:pir2.dat) B64064 B64064 Haemophilus influenzae 727 -11537697 7500883559 hi0373 heat shock protein hsca (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to gb:u05338 sp:p36541 gb:u01827 pid:402675) (le:5257) (re:7116) (di:complement) U32721 U32721 g1573342 Haemophilus influenzae Rd 71421 -11537697 5000694908 (de:(hi0373) (pn:heat shock protein :heat shock cognate 66:hsc66) (gn:hsca) (gtcfc:12.7) (ec:) (hsca_haein) (keggfc:11.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae)) HI0373 HI0373 Haemophilus influenzae 727 10020228

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887626	15335	37491	339	112

Description

5000694909 mopb:groes:hi0542 heat shock protein groes:10 kd chaperonin:protein cpn10:protein groes (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae) HI0542 HI0542 Haemophilus influenzae 727 -11537698 64046 mopb:groes:hi0542 (de:10 kd chaperonin (protein cpn10) (protein groes)) (db:swissprot) CH10_HAEIN P43734 HAEMOPHILUS INFLUENZAE 727 -11537698 154469 groes chaperonin groes (cl:chaperonin groes) (db:pir2.dat) B64076 B64076 Haemophilus influenzae 727 -11537698 7500878585 hi0542 chaperonin groes (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to pid:1144301 sp:q59686 percent ident:) (le:5712) (re:6002) (di:direct) U32736 U32736 g1573527 Haemophilus influenzae Rd 71421 -11537698 6500733840 mopb:groes heat shock protein groes:10 kd chaperonin:protein cpn10:protein groes (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae) HI0542 HI0542 Haemophilus influenzae 727 -11537698

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887634	15336	37492	756	251

Description

5000694910 mopa:groel:hi0543 heat shock protein:groel:mopa:60 kd chaperonin:protein cpn60:groel protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae) HI0543 HI0543 Haemophilus influenzae 727 -11537699 64136 mopa:groel:hi0543 (de:60 kd chaperonin (protein cpn60) (groel protein)) (db:swissprot) CH60_HAEIN P43733 HAEMOPHILUS INFLUENZAE 727 -11537699 154545 groel chaperonin groel (cl:chaperonin groel) (db:pir2.dat) C64076 C64076 Haemophilus influenzae 727 -11537699 7500878595 hi0543 heat shock protein groel (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to pid:1144302 sp:q59687 percent ident:) (le:6025) (re:7671) (di:direct) U32736 U32736 g1573528 Haemophilus influenzae Rd 71421 -11537699 6500733841 mopa:groel heat shock protein:groel:mopa:60 kd chaperonin:protein cpn60:groel protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae) HI0543 HI0543 Haemophilus influenzae 727 -11537699

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887638	15337	37493	486	161

Description

GTC ORF with score 530 to: (sr:a.nidulans, cdna to mrna, (bases 471 to 4014), dna (bases 1 t) (db:genpept-pln1) (de:a.nidulans kinesin-like protein (bimc) mrna, complete cds.) (nt:kinesin-like protein (bimc)) (le:142) (re:3696) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887640	15338	37494	645	214

Description

GTC ORF with score 768 to: (sr:a.nidulans, cdna to mrna, (bases 471 to 4014), dna (bases 1 t) (db:genpept-pln1) (de:a.nidulans kinesin-like protein (bimc) mrna, complete cds.) (nt:kinesin-like protein (bimc)) (le:142) (re:3696) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887641	15339	37495	495	164

Description

GTC ORF with score 416 to: (sr:a.nidulans, cdna to mrna, (bases 471 to 4014), dna (bases 1 t) (db:genpept-pln1) (de:a.nidulans kinesin-like protein (bimc) mrna, complete cds.) (nt:kinesin-like protein (bimc)) (le:142) (re:3696) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887642	15340	37496	1476	491

Description

GTC ORF with score 1292 to: (sr:a.nidulans, cdna to mrna, (bases 471 to 4014), dna (bases 1 t) (db:genpept-pln1) (de:a.nidulans kinesin-like protein (bimc) mrna, complete cds.) (nt:kinesin-like protein (bimc)) (le:142) (re:3696) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887644	15341	37497	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887648	15342	37498	657	218

Description

GTC ORF with score 969 to: (sr:a.nidulans, cdna to mrna, (bases 471 to 4014), dna (bases 1 t) (db:genpept-pln1) (de:a.nidulans kinesin-like protein (bimc) mrna, complete cds.) (nt:kinesin-like protein (bimc)) (le:142) (re:3696) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887668	15343	37499	597	199

Description

6500733842 dnak:hi1237 protein:heat shock protein 70:hsp70 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae) HI1237 HI1237 Haemophilus influenzae 727 -11537700 152044 dnak-type molecular chaperone:heat shock protein 70 (cl:heat shock protein 70) (db:pir2.dat) B64112 B64112 Haemophilus influenzae 727 -11537700 7500955121 hi1237 heat shock protein 70 dnak (db:genpept-bct1) (de:haemophilus influenzae rd section 118 of 163 of the completegenome.) (nt:similar to sp:p48209 pid:825786 percent ident:) (le:7134) (re:9041) (di:direct) U32803 U32803 g1574167 Haemophilus influenzae Rd 71421 -11537700 5000694911 (de:(hi1237) (pn:protein:hsp70:heat shock protein 70:dnak) (gn:dnak) (gtcfc:12.7) (ec:) (dnak_haein) (keggfc:11.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae)) HI1237 HI1237 Haemophilus influenzae 727 10080100

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887673	15344	37500	885	294

Description

6500733843 dnaj:hi1238 heat shock protein:protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae) HI1238 HI1238 Haemophilus influenzae 727 -11537701 152143 dnaj heat shock protein dnaj (cl:heat shock protein dnaj:dnaj amino-terminal homology) (db:pir2.dat) C64112 C64112 Haemophilus influenzae 727 -11537701 7500955125 hi1238 heat shock protein dnaj (db:genpept-bct1) (de:haemophilus influenzae rd section 118 of 163 of the completegenome.) (nt:similar to sp:p48208 pid:825787 percent ident:) (le:9092) (re:10276) (di:direct) U32803 U32803 g1574168 Haemophilus influenzae Rd 71421 -11537701 5000694912 (de:(hi1238) (pn:protein:heat shock protein:dnaj) (gn:dnaj) (gtcfc:12.7) (ec:) (dnaj_haein) (keggfc:11.2) (tigrfc:4.3) (db:gtc-haemophilus influenzae)) HI1238 HI1238 Haemophilus influenzae 727 10080170

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887676	15345	37501	1878	625

Description

6500733844 ftsy:hi0768 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI0768 HI0768 Haemophilus influenzae 727 -11537702 72473 ftsy:hi0768 (de:cell division protein ftsy) (db:swissprot) FTSY_HAEIN P44870 HAEMOPHILUS INFLUENZAE 727 -11537702 154437 ftsy cell division protein ftsy (cl:cell division protein ftsy) (db:pir2.dat) G64091 G64091 Haemophilus influenzae 727 -11537702 7500881853 hi0768 cell division protein ftsy (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to sp:p10121 gb:u00039 gb:x04398 pid:41498) (le:10596) (re:11840) (di:direct) U32760 U32760 g1573776 Haemophilus influenzae Rd 71421 -11537702 5000694913 (de:(hi0768) (pn:cell division protein :cell division protein:ftsy) (gn:ftsy) (gtcfc:12.8) (ec:) (ftsy_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI0768 HI0768 Haemophilus influenzae 727 10015024

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887706	15346	37502	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887709	15347	37503	855	284

Description

6500733845 ftse:hi0769 cell division atp-binding protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI0769 HI0769 Haemophilus influenzae 727 -11537703 72445 ftse:hi0769 (de:cell division atp-binding protein ftse) (db:swissprot) FTSE_HAEIN P44871 HAEMOPHILUS INFLUENZAE 727 -11537703 153032 cell division protein ftse (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) H64091 H64091 Haemophilus influenzae 727 -11537703 7500881815 hi0769 cell division atp-binding protein ftse (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to sp:p10115 gb:u00039 gb:x04398 pid:41499) (le:11859) (re:12515) (di:direct) U32760 U32760 g1573777 Haemophilus influenzae Rd 71421 -11537703 5000694914 (de:(hi0769) (pn:cell division atp-binding protein :cell division atp-binding protein:ftse) (gn:ftse) (gtcfc:12.8) (ec:) (ftse_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI0769 HI0769 Haemophilus influenzae 727 10014996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887730	15348	37504	1107	368

Description

6500733846 ftsx:hi0770 cell division membrane protein:cell division protein homolog (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI0770 HI0770 Haemophilus influenzae 727 -11537704 72470 ftsx:hi0770 (de:cell division protein ftsx homolog) (db:swissprot) FTSX_HAEIN P44872 HAEMOPHILUS INFLUENZAE 727 -11537704 166044 cell division protein homolog (db:pir2.dat) I64091 I64091 Haemophilus influenzae 727 -11537704 7500881851 hi0770 cell division protein ftsx (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to sp:p10122 gb:u00039 gb:x04398 pid:41500) (le:12525) (re:13457) (di:direct) U32760 U32760 g1573778 Haemophilus influenzae Rd 71421 -11537704 5000694915 (de:(hi0770) (pn:cell division protein homolog:cell division membrane protein:ftsx) (gn:ftsx) (gtcfc:12.8) (ec:) (ftsx_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI0770 HI0770 Haemophilus influenzae 727 10015021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887738	15349	37505	216	71

Description

5000694916 cell filamentation protein:fic:sp:p20605:hypothetical protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI0977 HI0977 Haemophilus influenzae 727 -11537705 109338 hi0977 (de:hypothetical protein hi0977) (db:swissprot) Y977_HAEIN P44088 HAEMOPHILUS INFLUENZAE 727 -11537705 166589 hypothetical protein hi0977 (db:pir2.dat) G64017 G64017 Haemophilus influenzae 727 -11537705 7500895781 hi0977 cell filamentation protein fic (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:similar to gb:m28363 sp:p20605 pid:145955) (le:7436) (re:8011) (di:direct) U32778 U32778 g1574005 Haemophilus influenzae Rd 71421 -11537705 6500733847 cell filamentation protein:fic:sp:p20605:hypothetical protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI0977 HI0977 Haemophilus influenzae 727 -11537705

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887740	15350	37506	2226	741

Description

6500733848 mukb:pyrh:smba:hi1065 mukb suppressor protein:uridylate kinase:uk:uridine monophosphate kinase:ump kinase (gtcfc:12.8:10.2) (ec:2.7.4.-) (keggfc:14.1) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1065 HI1065 Haemophilus influenzae 727 -11537706 92645 pyrh:smba:hi1065 (ec:2.7.4.-) (de:(ump kinase)) (db:swissprot) PYRH_HAEIN P43890 HAEMOPHILUS INFLUENZAE 727 -11537706 167011 uridine 5-monophosphate kinase (cl:uridine 5'-monophosphate kinase) (ec:2.7.4.-) (db:pir2.dat) H64180 H64180 Haemophilus influenzae 727 -11537706 7500889181 hi1065 uridylate kinase pyrh (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to gb:d26562 sp:p29464 gb:d13334 gb:x78809) (le:11604) (re:12317) (di:direct) U32786 U32786 g1574616 Haemophilus influenzae Rd 71421 -11537706 5000694917 (de:(hi1065) (pn:uridylate kinase:uk:uridine monophosphate kinase:ump kinase:mukb suppressor protein:smba) (gn:pyrh:smba) (gtcfc:12.8) (ec:2.7.4.-) (pyrh_haein) (keggfc:11.1) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1065 HI1065 Haemophilus influenzae 727 10034677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887764	15351	37507	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887780	15352	37508	891	296

Description

6500733849 ftsl:hi1131 cell division protein:cell division protein homolog (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1131 HI1131 Haemophilus influenzae 727 -11537707 72460 ftsl:hi1131 (de:cell division protein ftsl homolog) (db:swissprot) FTSL_HAEIN P45058 HAEMOPHILUS INFLUENZAE 727 -11537707 166048 cell division protein ftsl homolog hi1131 (db:pir2.dat) F64184 F64184 Haemophilus influenzae 727 -11537707 7500881841 hi1131 cell division protein ftsl (db:genpept-bct1) (de:haemophilus influenzae rd section 108 of 163 of the completegenome.) (nt:similar to sp:p22187 gb:k00137 gb:s49802 gb:s49875) (le:1585) (re:1908) (di:direct) U32793 U32793 g1574686 Haemophilus influenzae Rd 71421 -11537707 5000694918 (de:(hi1131) (pn:cell division protein homolog:cell division protein:ftsl) (gn:ftsl) (gtcfc:12.8) (ec:) (ftsl_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1131 HI1131 Haemophilus influenzae 727 10015011

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887798	15353	37509	1152	383

Description

6500733850 ftsi:hi1132 penicillin-binding protein 3:pbp-3 (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1132 HI1132 Haemophilus influenzae 727 -11537708 88732 ftsi:hi1132 (de:penicillin-binding protein 3 (pbp-3)) (db:swissprot) PBP3_HAEIN P45059 HAEMOPHILUS INFLUENZAE 727 -11537708 153138 penicillin-binding protein 3 (cl:penicillin-binding protein 3) (db:pir2.dat) G64184 G64184 Haemophilus influenzae 727 -11537708 7500887695 hi1132 penicillin-binding protein 3 ftsi (db:genpept-bct1) (de:haemophilus influenzae rd section 108 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p04286 gb:k00137 gb:s49802) (le:1921) (re:3753) (di:direct) U32793 U32793 g1574687 Haemophilus influenzae Rd 71421 -11537708 5000694919 (de:(hi1132) (pn:pbp-3:penicillin-binding protein 3:ftsi) (gn:ftsi) (gtcfc:12.8) (ec:) (pbp3_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1132 HI1132 Haemophilus influenzae 727 10030859

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887805	15354	37510	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887812	15355	37511	825	274

Description

6500733851 ftsw:hi1137 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1137 HI1137 Haemophilus influenzae 727 -11537709 72468 ftsw:hi1137 (de:cell division protein ftsw) (db:swissprot) FTSW_HAEIN P45064 HAEMOPHILUS INFLUENZAE 727 -11537709 154882 ftsw cell division protein ftsw (cl:rod shape-determining protein) (db:pir2.dat) C64185 C64185 Haemophilus influenzae 727 -11537709 7500881847 hi1137 cell division protein ftsw (db:genpept-bct1) (de:haemophilus influenzae rd section 108 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p16457 gb:m30807 pid:146039) (le:9150) (re:10334) (di:direct) U32793 U32793 g1574692 Haemophilus influenzae Rd 71421 -11537709 5000694920 (de:(hi1137) (pn:cell division protein :cell division protein:ftsw) (gn:ftsw) (gtcfc:12.8) (ec:) (ftsw_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1137 HI1137 Haemophilus influenzae 727 10015019

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887813	15356	37512	510	169

Description

GTC ORF with score 366 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0600.) (nt:similar to saccharomyces cerevisiae hypothetical) (le:<1) (re:1026) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887815	15357	37513	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887859	15358	37514	816	272

Description

6500733852 ftsq:hi1141 cell division protein:cell division protein homolog (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1141 HI1141 Haemophilus influenzae 727 -11537710 72463 ftsq:hi1141 (de:cell division protein ftsq homolog) (db:swissprot) FTSQ_HAEIN P45067 HAEMOPHILUS INFLUENZAE 727 -11537710 166049 cell division protein ftsq homolog hi1141 (db:pir2.dat) G64185 G64185 Haemophilus influenzae 727 -11537710 7500881843 hi1141 cell division protein ftsq (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p06136 gb:k02668 gb:x02821) (le:2518) (re:3282) (di:direct) U32794 U32794 g1574697 Haemophilus influenzae Rd 71421 -11537710 5000694921 (de:(hi1141) (pn:cell division protein homolog:cell division protein:ftsq) (gn:ftsq) (gtcfc:12.8) (ec:) (ftsq_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1141 HI1141 Haemophilus influenzae 727 10015014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887860	15359	37515	543	180

Description

GTC ORF with score 288 to: (de:(yil003w) (pn:hypothetical 31:strong similarity to nbp35p and human nucleotide-binding protein) (gn:yia3w) (gtcfc:13.7) (ec:) (yia3_yeast) (keggfc:11.2) (sgdfc:13.0.0) (db:gtc-saccharomyces cerevisiae))

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887876	15360	37516	1323	440

Description

GTC ORF with score 108 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t28m21 genomic sequence,complete sequence.) (nt:unknown protein) (le:97328:98826:99416) (re:98518:98940:99530) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887878	15361	37517	285	94

Description

6500733853 ftsa:hi1142 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1142 HI1142 Haemophilus influenzae 727 -11537711 72442 ftsa:hi1142 (de:cell division protein ftsa) (db:swissprot) FTSA_HAEIN P45068 HAEMOPHILUS INFLUENZAE 727 -11537711 154439 ftsa cell division protein ftsa (cl:cell division protein ftsa) (db:pir2.dat) H64185 H64185 Haemophilus influenzae 727 -11537711 7500881804 hi1142 cell division protein ftsa (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p06137 gb:k02668 gb:m36531) (le:3301) (re:4578) (di:direct) U32794 U32794 g1574698 Haemophilus influenzae Rd 71421 -11537711 5000694922 (de:(hi1142) (pn:cell division protein :cell division protein:ftsa) (gn:ftsa) (gtcfc:12.8) (ec:) (ftsa_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1142 HI1142 Haemophilus influenzae 727 10014993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887879	15362	37518	183	60

Description

6500733854 ftsz:hi1143 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1143 HI1143 Haemophilus influenzae 727 -11537712 72481 ftsz:hi1143 (de:cell division protein ftsz) (db:swissprot) FTSZ_HAEIN P45069 HAEMOPHILUS INFLUENZAE 727 -11537712 131342 ftsz cell division protein ftsz (cl:cell division protein ftsz) (db:pir1.dat) I64185 I64185 Haemophilus influenzae 727 -11537712 7500881877 hi1143 cell division protein ftsz (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p06138 gb:x02821 pid:216509) (le:4662) (re:5927) (di:direct) U32794 U32794 g1574699 Haemophilus influenzae Rd 71421 -11537712 5000694923 (de:(hi1143) (pn:cell division protein :cell division protein:ftsz) (gn:ftsz) (gtcfc:12.8) (ec:) (ftsz_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1143 HI1143 Haemophilus influenzae 727 10015032

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887880	15363	37519	3240	1079

Description

6500733855 sula:hi1208 cell division inhibitor (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1208 HI1208 Haemophilus influenzae 727 -11537713 166043 cell division inhibitor homolog hi1208 (cl:cell division inhibitor yfhf) (db:pir2.dat) A64110 A64110 Haemophilus influenzae 727 -11537713 7500960648 hi1208 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 115 of 163 of the completegenome.) (nt:similar to gb:l42023 pid:1007092 pid:1221333) (le:4088) (re:4978) (di:complement) U32800 U32800 g1574138 Haemophilus influenzae Rd 71421 -11537713 5000694924 (de:(hi1208) (pn:cell division inhibitor:sula) (gn:sula) (gtcfc:12.8) (ec:) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1208 HI1208 Haemophilus influenzae 727 10088063

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887918	15364	37520	891	296

Description

GTC ORF with score 671 to: (db:genpept-pln2) (de:emericella nidulans negative-acting regulatory protein (qutr) gene,complete cds; and unknown gene.) (nt:repressor protein; coding region predicted from dna) (le:3826) (re:6531) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887919	15365	37521	282	93

Description

6500733856 ftsj:hi1334 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1334 HI1334 Haemophilus influenzae 727 -11537714 72454 ftsj:hi1334 (de:cell division protein ftsj) (db:swissprot) FTSJ_HAEIN P45162 HAEMOPHILUS INFLUENZAE 727 -11537714 166047 ftsj ftsj protein (cl:cell division protein j) (db:pir2.dat) C64117 C64117 Haemophilus influenzae 727 -11537714 7500881832 hi1334 cell division protein ftsj (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:similar to gb:m83138 sp:p28692 gb:u01376 pid:146027) (le:7403) (re:8032) (di:direct) U32812 U32812 g1574792 Haemophilus influenzae Rd 71421 -11537714 5000694925 (de:(hi1334) (pn:cell division protein :cell division protein:ftsj) (gn:ftsj) (gtcfc:12.8) (ec:) (ftsj_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1334 HI1334 Haemophilus influenzae 727 10015005

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887921	15366	37522	375	124

Description

6500733857 ftsh:hi1335 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1335 HI1335 Haemophilus influenzae 727 -11537715 1500685757 ftsh-a:hi1335 (ec:3.4.24.-) (de:cell division protein ftsh homolog 1,) (db:swissprot) FTH1_HAEIN P71377 HAEMOPHILUS INFLUENZAE 727 -11537715 7500881774 hi1335 cell division protein ftsh (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:similar to gb:m83138 sp:p28691 gb:u01376 pid:146028) (le:8123) (re:10030) (di:direct) U32812 U32812 g1574793 Haemophilus influenzae Rd 71421 -11537715 5000694926 (de:(hi1335) (pn:cell division protein:ftsh) (gn:ftsh) (gtcfc:12.8) (ec:) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1335 HI1335 Haemophilus influenzae 727 10059003

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887931	15367	37523	492	163

Description

6500733858 cafa:hi1353 cytoplasmic axial filament protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1353 HI1353 Haemophilus influenzae 727 -11537716 62451 cafa:hi1353 (de:cytoplasmic axial filament protein) (db:swissprot) CAFA_HAEIN P45175 HAEMOPHILUS INFLUENZAE 727 -11537716 166076 cytosolic axial filament protein (db:pir2.dat) F64118 F64118 Haemophilus influenzae 727 -11537716 7500878100 hi1353 cytoplasmic axial filament protein cafa (db:genpept-bct1) (de:haemophilus influenzae rd section 129 of 163 of the completegenome.) (nt:similar to sp:p25537 pid:48826 pid:606187 gb:u00096) (le:6236) (re:7711) (di:direct) U32814 U32814 g1574815 Haemophilus influenzae Rd 71421 -11537716 5000694927 (de:(hi1353) (pn:cytoplasmic axial filament protein:cafa) (gn:cafa) (gtcfc:12.8) (ec:) (cafa_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1353 HI1353 Haemophilus influenzae 727 10005149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887939	15368	37524	432	143

Description

GTC ORF with score 210 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c54d1.) (nt:similar to aldehyde dehydrogenase) (le:11836:12300:12475) (re:11964:12428:12585) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887940	15369	37525	579	192

Description

GTC ORF with score 424 to: (sr:human) (db:genpept-pri3) (de:homo sapiens dna sequence from pac 352a20 on chromosome6q24.1-25.1. contains a pseudogene similar to yeast, bacterial,worm and slime mold hypothetical genes, and a gene coding for analdehyde ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887946	15370	37526	471	156

Description

6500733859 mukb:hi1374 cell division protein:cell division protein homolog (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1374 HI1374 Haemophilus influenzae 727 -11537717 84671 mukb:hi1374 (de:cell division protein mukb homolog) (db:swissprot) MUKB_HAEIN P45187 HAEMOPHILUS INFLUENZAE 727 -11537717 166050 mukb cell division protein mukb (cl:escherichia coli mukb protein) (db:pir2.dat) D64120 D64120 Haemophilus influenzae 727 -11537717 7500886083 hi1374 cell division protein mukb (db:genpept-bct1) (de:haemophilus influenzae rd section 132 of 163 of the completegenome.) (nt:similar to sp:p22523 pid:146898 pid:42043) (le:6496) (re:11028) (di:direct) U32817 U32817 g1574208 Haemophilus influenzae Rd 71421 -11537717 5000694928 (de:(hi1374) (pn:cell division protein homolog:cell division protein:mukb) (gn:mukb) (gtcfc:12.8) (ec:) (mukb_haein) (keggfc:11.2) (tigrfc:4.1) (db:gtc-haemophilus influenzae)) HI1374 HI1374 Haemophilus influenzae 727 10026862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887955	15371	37527	216	71

Description

5000694929 ftsh:hflb:hi1465 cell division protein:ftsh:cell division protein ftsh homolog (gtcfc:12.8) (ec:3.4.24.-) (keggfc:14.1) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1465 HI1465 Haemophilus influenzae 727 -11537718 72448 ftsh-b:hi1465 (ec:3.4.24.-) (de:cell division protein ftsh homolog 2,) (db:swissprot) FTH2_HAEIN P45219 HAEMOPHILUS INFLUENZAE 727 -11537718 166045 ftsh protein homolog hi1465 (db:pir2.dat) B64125 B64125 Haemophilus influenzae 727 -11537718 7500881776 hi1465 cell division ftsh-related protein (db:genpept-bct1) (de:haemophilus influenzae rd section 139 of 163 of the completegenome.) (nt:similar to gb:m83138 sp:p28691 gb:u01376 pid:146028) (le:7448) (re:8593) (di:complement) U32824 U32824 g1574299 Haemophilus influenzae Rd 71421 -11537718 6500733860 ftsh:hflb cell division protein:ftsh:cell division protein ftsh homolog (gtcfc:12.8) (ec:3.4.24.-) (keggfc:14.1) (tigrfc:4.1) (db:gtc-haemophilus influenzae) HI1465 HI1465 Haemophilus influenzae 727 -11537718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887959	15372	37528	561	186

Description

GTC ORF with score 226 to: (sr:human) (db:genpept-pri3) (de:homo sapiens dna sequence from pac 352a20 on chromosome6q24.1-25.1. contains a pseudogene similar to yeast, bacterial,worm and slime mold hypothetical genes, and a gene coding for analdehyde ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887962	15373	37529	762	253

Description

6500733861 hfq:hi0411 host factor-i:host factor-i protein:hf-i (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI0411 HI0411 Haemophilus influenzae 727 -11537719 166204 host factor i (cl:host factor i) (db:pir2.dat) D64066 D64066 Haemophilus influenzae 727 -11537719 7500960657 hi0411 host factor-i protein hfq (db:genpept-bct1) (de:haemophilus influenzae rd section 39 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p25521 gb:d00743 gb:u00005) (le:5462) (re:5737) (di:complement) U32724 U32724 g1573384 Haemophilus influenzae Rd 71421 -11537719 5000694969 (de:(hi0411) (pn:host factor-i protein:host factor-i:hf-i:hfq) (gn:hfq) (gtcfc:13.6) (ec:) (hfq_haein) (keggfc:11.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae)) HI0411 HI0411 Haemophilus influenzae 727 10088106

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887968	15374	37530	1242	414

Description

5000694970 terminase subunit 1 (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1411 HI1411 Haemophilus influenzae 727 -11537720 5500686550 hi1411 (de:hypothetical protein hi1411) (db:swissprot) YE11_HAEIN Q57374 HAEMOPHILUS INFLUENZAE 727 -11537720 167186 hypothetical protein hi1411 (db:pir2.dat) C64122 C64122 Haemophilus influenzae 727 -11537720 7500922607 hi1411 terminase:small subunit (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:similar to sp:q38627 pid:522116 percent ident:) (le:103) (re:618) (di:complement) U32821 U32821 g1574249 Haemophilus influenzae Rd 71421 -11537720 6500733862 terminase subunit 1 (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1411 HI1411 Haemophilus influenzae 727 -11537720

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887970	15375	37531	471	156

Description

6500733863 mua:hi1478 transposase a (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1478 HI1478 Haemophilus influenzae 727 -11537721 167224 transposase homolog hi1478 (db:pir2.dat) B64126 B64126 Haemophilus influenzae 727 -11537721 7500960743 hi1478 transposase mua (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to sp:p07636 pid:15450 pid:15810 pid:215511) (le:10013) (re:12076) (di:direct) U32825 U32825 g1574318 Haemophilus influenzae Rd 71421 -11537721 5000694971 (de:(hi1478) (pn:transposase a:mua) (gn:mua) (gtcfc:13.6) (ec:) (keggfc:11.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae)) HI1478 HI1478 Haemophilus influenzae 727 10088314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887974	15376	37532	285	94

Description

6500733864 mub:hi1481 mub protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1481 HI1481 Haemophilus influenzae 727 -11537722 167009 gene b protein homolog (db:pir2.dat) C64126 C64126 Haemophilus influenzae 727 -11537722 7500960654 hi1481 dna transposition protein mub (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to sp:p03763 pid:15448 pid:215512) (le:12842) (re:13705) (di:direct) U32825 U32825 g1574320 Haemophilus influenzae Rd 71421 -11537722 5000694972 (de:(hi1481) (pn:mub protein:mub) (gn:mub) (gtcfc:13.6) (ec:) (keggfc:11.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae)) HI1481 HI1481 Haemophilus influenzae 727 10088254

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501887978	15377	37533	312	103

Description

5000694973 gam protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1483 HI1483 Haemophilus influenzae 727 -11537723 148297 dna-binding protein (cl:phage mu dna-binding protein) (db:pir2.dat) D64126 D64126 Haemophilus influenzae 727 -11537723 7500954784 hi1483 host-nuclease inhibitor protein gam (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:similar to sp:p06023 pid:15461 pid:215562 percent) (le:393) (re:902) (di:direct) U32826 U32826 g1574323 Haemophilus influenzae Rd 71421 -11537723 6500733865 gam protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1483 HI1483 Haemophilus influenzae 727 -11537723

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888028	15378	37534	876	291

Description

6500733866 mue16:hi1488 e16 protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1488 HI1488 Haemophilus influenzae 727 -11537724 166115 hypothetical protein hi1488 (db:pir2.dat) E64126 E64126 Haemophilus influenzae 727 -11537724 7500960689 hi1488 e16 protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:similar to pid:215574 percent ident: 29.53;) (le:2663) (re:3220) (di:direct) U32826 U32826 g1574324 Haemophilus influenzae Rd 71421 -11537724 5000694974 (de:(hi1488) (pn:e16 protein:mue16) (gn:mue16) (gtcfc:13.6) (ec:) (keggfc:11.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae)) HI1488 HI1488 Haemophilus influenzae 727 10088076

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888059	15379	37535	810	269

Description

6500733867 mug:hi1503 g protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1503 HI1503 Haemophilus influenzae 727 -11537725 166149 hypothetical protein hi1503 (db:pir2.dat) H64126 H64126 Haemophilus influenzae 727 -11537725 7500960690 hi1503 g protein mug-1 (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to sp:q01261 pid:215535 percent ident:) (le:1458) (re:1898) (di:direct) U32827 U32827 g1574345 Haemophilus influenzae Rd 71421 -11537725 5000694975 (de:(hi1503) (pn:g protein:mug) (gn:mug) (gtcfc:13.6) (ec:) (keggfc:11.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae)) HI1503 HI1503 Haemophilus influenzae 727 10088087

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888061	15380	37536	669	222

Description

6500733868 mui:hi1504 i protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1504 HI1504 Haemophilus influenzae 727 -11537726 166911 hypothetical protein hi1504 (db:pir2.dat) I64126 I64126 Haemophilus influenzae 727 -11537726 7500960691 hi1504 i protein mui (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to sp:q01267 pid:215536 percent ident:) (le:2129) (re:3196) (di:direct) U32827 U32827 g1574346 Haemophilus influenzae Rd 71421 -11537726 5000694976 (de:(hi1504) (pn:i protein:mui) (gn:mui) (gtcfc:13.6) (ec:) (keggfc:11.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae)) HI1504 HI1504 Haemophilus influenzae 727 10088194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888065	15381	37537	471	156

Description

6500733869 mun:hi1515 n protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1515 HI1515 Haemophilus influenzae 727 -11537727 7500976292 hi1515 64 kda virion protein mun (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to sp:p08557 pid:15105 percent ident:) (le:9974) (re:11341) (di:direct) U32827 U32827 g1574348 Haemophilus influenzae Rd 71421 -11537727 5000694977 (de:(hi1515) (pn:n protein:mun) (gn:mun) (gtcfc:13.6) (ec:) (keggfc:11.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae)) HI1515 HI1515 Haemophilus influenzae 727 10126721

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888091	15382	37538	678	225

Description

5000694978 g protein:mug:hypothetical protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1568 HI1568 Haemophilus influenzae 727 -11537728 111782 hi1568 (de:hypothetical protein hi1568) (db:swissprot) YF68_HAEIN P45255 HAEMOPHILUS INFLUENZAE 727 -11537728 166148 hypothetical protein hi1568 (db:pir2.dat) B64130 B64130 Haemophilus influenzae 727 -11537728 7500923284 hi1568 g protein mug-2 (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the completegenome.) (nt:similar to sp:q01261 pid:215535 percent ident:) (le:4728) (re:5144) (di:complement) U32831 U32831 g1574409 Haemophilus influenzae Rd 71421 -11537728 6500733870 g protein:mug:hypothetical protein (gtcfc:13.1) (keggfc:14.2) (tigrfc:14.4) (db:gtc-haemophilus influenzae) HI1568 HI1568 Haemophilus influenzae 727 -11537728

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888107	15383	37539	306	101

Description

GTC ORF with score 197 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 2.7 kb genomic dna, clone c1791.) (nt:similar to rattus norvegicus alpha-adaptin:) (le:<1) (re:1703) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888108	15384	37540	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888110	15385	37541	471	156

Description

5000694930 nucleotide binding protein:potg:hypothetical abc transporter atp-binding protein hi0099 (gtcfc:13.11) (keggfc:14.2) (tigrfc:5.4) (db:gtc-haemophilus influenzae) HI0099 HI0099 Haemophilus influenzae 727 -11537729 7500976238 hi0099 iron iii abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:similar to pid:1098689 percent identity: 50.87;) (le:6530) (re:7585) (di:direct) U32695 U32695 g1573050 Haemophilus influenzae Rd 71421 -11537729 6500733871 nucleotide binding protein:potg:hypothetical abc transporter atp-binding protein hi0099 (gtcfc:13.11) (keggfc:14.2) (tigrfc:5.4) (db:gtc-haemophilus influenzae) HI0099 HI0099 Haemophilus influenzae 727 -11537729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888111	15386	37542	792	263

Description

6500733872 comf:hi0434 transformation protein:competence protein f:dna transformation protein:protein com101a (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI0434 HI0434 Haemophilus influenzae 727 -11537730 65410 comf:hi0434 (de:com101a)) (db:swissprot) COMF_HAEIN P31773 HAEMOPHILUS INFLUENZAE 727 -11537730 167216 comf transformation competence-related protein comf:protein com101a (cl:transformation competence-related protein comf) (db:pir2.dat) JH0435 JH0435 Haemophilus influenzae 727 -11537730 241251 com101a (sr:h.influenzae dna) (db:genpept-bct1) (de:h.influenzae com101a gene, orf1, orf3 and orf1r, complete cds.) (nt:probable com101a gene) (le:1154) (re:1843) (di:direct) HEACOM101 M59751 g148876 Haemophilus influenzae 727 -11537730 241345 (sr:haemophilus influenzae rd dna) (db:genpept-bct1) (de:haemophilus influenzae transformation gene cluster dna.) (nt:a haemophilus strain carrying an insertion in orf f) (le:7350) (re:8039) (di:direct) HEATRANS M62809 g148999 Haemophilus influenzae 727 -11537730 7500879078 hi0434 competence protein f comf (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:m59751 sp:p31773 pid:1573409 percent) (le:9022) (re:9711) (di:complement) U32726 U32726 g1573409 Haemophilus influenzae Rd 71421 -11537730 5000694931 (de:(hi0434) (pn:competence protein f:dna transformation protein :protein com101a:transformation protein:comf) (gn:comf) (gtcfc:13.12) (ec:) (comf_haein) (keggfc:11.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae)) HI0434 HI0434 Haemophilus influenzae 727 10008058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888114	15387	37543	402	133

Description

6500733873 come:hi0435 transformation protein:competence protein e precursor:dna transformation protein come (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI0435 HI0435 Haemophilus influenzae 727 -11537731 65409 come:hi0435 (de:competence protein e precursor (dna transformation protein come)) (db:swissprot) COME_HAEIN P31772 HAEMOPHILUS INFLUENZAE 727 -11537731 167218 hypothetical protein hi0435 transformation locus:orfe protein (cl:hypothetical protein hi0435) (db:pir2.dat) H64067 H64067 Haemophilus influenzae 727 -11537731 7500879077 hi0435 competence protein e come (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:m62809 sp:p31772 pid:1573410 percent) (le:9720) (re:11057) (di:complement) U32726 U32726 g1573410 Haemophilus influenzae Rd 71421 -11537731 5000694932 (de:(hi0435) (pn:competence protein e precursor:dna transformation protein come:transformation protein:come) (gn:come) (gtcfc:13.12) (ec:) (come_haein) (keggfc:11.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae)) HI0435 HI0435 Haemophilus influenzae 727 10008057

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888116	15388	37544	405	134

Description

6500733874 comd:hi0436 transformation protein:competence protein d:dna transformation protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI0436 HI0436 Haemophilus influenzae 727 -11537732 65408 comd:hi0436 (de:competence protein d (dna transformation protein comd)) (db:swissprot) COMD_HAEIN P31771 HAEMOPHILUS INFLUENZAE 727 -11537732 167215 comd transformation competence-related protein comd (db:pir2.dat) JH0433 I64067 Haemophilus influenzae 727 -11537732 241342 (sr:haemophilus influenzae rd dna) (db:genpept-bct1) (de:haemophilus influenzae transformation gene cluster dna.) (nt:the predicted molecular weight and pi of orf d are) (le:5580) (re:5993) (di:direct) HEATRANS M62809 g148996 Haemophilus influenzae 727 -11537732 7500879076 hi0436 competence protein d comd (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:m62809 sp:p31771 pid:1573411 percent) (le:11067) (re:11480) (di:complement) U32726 U32726 g1573411 Haemophilus influenzae Rd 71421 -11537732 5000694933 (de:(hi0436) (pn:competence protein d:dna transformation protein :transformation protein:comd) (gn:comd) (gtcfc:13.12) (ec:) (comd_haein) (keggfc:11.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae)) HI0436 HI0436 Haemophilus influenzae 727 10008056

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888117	15389	37545	1062	353

Description

6500733875 comc:hi0437 transformation protein:competence protein c:dna transformation protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI0437 HI0437 Haemophilus influenzae 727 -11537733 65407 comc:hi0437 (de:competence protein c (dna transformation protein comc)) (db:swissprot) COMC_HAEIN P31770 HAEMOPHILUS INFLUENZAE 727 -11537733 167214 comc transformation competence-related protein comc (db:pir2.dat) JH0432 A64068 Haemophilus influenzae 727 -11537733 241341 (sr:haemophilus influenzae rd dna) (db:genpept-bct1) (de:haemophilus influenzae transformation gene cluster dna.) (nt:a haemophilus strain carrying a mini-tn10kan) (le:5062) (re:5583) (di:direct) HEATRANS M62809 g148995 Haemophilus influenzae 727 -11537733 7500879075 hi0437 competence protein c comc (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:m62809 sp:p31770 pid:1573412 percent) (le:11477) (re:11998) (di:complement) U32726 U32726 g1573412 Haemophilus influenzae Rd 71421 -11537733 5000694934 (de:(hi0437) (pn:competence protein c:dna transformation protein :transformation protein:comc) (gn:comc) (gtcfc:13.12) (ec:) (comc_haein) (keggfc:11.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae)) HI0437 HI0437 Haemophilus influenzae 727 10008055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888143	15390	37546	1056	351

Description

6500733876 comb:hi0438 transformation protein:competence protein b:dna transformation protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI0438 HI0438 Haemophilus influenzae 727 -11537734 65405 comb:hi0438 (de:competence protein b (dna transformation protein comb)) (db:swissprot) COMB_HAEIN P31769 HAEMOPHILUS INFLUENZAE 727 -11537734 167213 comb transformation competence-related protein comb (db:pir2.dat) JH0431 B64068 Haemophilus influenzae 727 -11537734 241340 (sr:haemophilus influenzae rd dna) (db:genpept-bct1) (de:haemophilus influenzae transformation gene cluster dna.) (nt:the predicted molecular weight and pi of orf b are) (le:4559) (re:5065) (di:direct) HEATRANS M62809 g148994 Haemophilus influenzae 727 -11537734 7500879074 hi0438 competence protein b comb (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:m62809 sp:p31769 pid:1573413 percent) (le:11995) (re:12501) (di:complement) U32726 U32726 g1573413 Haemophilus influenzae Rd 71421 -11537734 5000694935 (de:(hi0438) (pn:competence protein b:dna transformation protein :transformation protein:comb) (gn:comb) (gtcfc:13.12) (ec:) (comb_haein) (keggfc:11.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae)) HI0438 HI0438 Haemophilus influenzae 727 10008053

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888155	15391	37547	1071	356

Description

6500733877 coma:hi0439 transformation protein:competence protein a:dna transformation protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI0439 HI0439 Haemophilus influenzae 727 -11537735 65402 coma:hi0439 (de:competence protein a (dna transformation protein coma)) (db:swissprot) COMA_HAEIN P31768 HAEMOPHILUS INFLUENZAE 727 -11537735 167212 coma transformation competence-related protein coma (db:pir2.dat) JH0430 C64068 Haemophilus influenzae 727 -11537735 241339 (sr:haemophilus influenzae rd dna) (db:genpept-bct1) (de:haemophilus influenzae transformation gene cluster dna.) (nt:a haemophilus strain carrying a mini-tn10kan) (le:3761) (re:4558) (di:direct) HEATRANS M62809 g148993 Haemophilus influenzae 727 -11537735 7500879073 hi0439 competence protein a coma (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:m62809 sp:p31768 pid:1573414 percent) (le:12502) (re:13299) (di:complement) U32726 U32726 g1573414 Haemophilus influenzae Rd 71421 -11537735 5000694936 (de:(hi0439) (pn:competence protein a:dna transformation protein :transformation protein:coma) (gn:coma) (gtcfc:13.12) (ec:) (coma_haein) (keggfc:11.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae)) HI0439 HI0439 Haemophilus influenzae 727 10008050

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888158	15392	37548	339	112

Description

5000694937 tfox:sxy:hi0601 tfox protein:tfox:dna transformation protein tfox:competence activator:protein sxy (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI0601 HI0601 Haemophilus influenzae 727 -11537736 101142 tfox:sxy:hi0601 (de:dna transformation protein tfox (competence activator) (protein sxy)) (db:swissprot) TFOX_HAEIN P43779 HAEMOPHILUS INFLUENZAE 727 -11537736 167187 hypothetical protein hi0601 (db:pir2.dat) B64080 B64080 Haemophilus influenzae 727 -11537736 7500892983 hi0601 dna transformation protein tfox (db:genpept-bct1) (de:haemophilus influenzae rd section 56 of 163 of the complete genome.) (nt:similar to gb:u13205 pid:1573592 percent ident:) (le:7995) (re:8648) (di:direct) U32741 U32741 g1573592 Haemophilus influenzae Rd 71421 -11537736 6500733878 tfox:sxy tfox protein:tfox:dna transformation protein tfox:competence activator:protein sxy (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI0601 HI0601 Haemophilus influenzae 727 -11537736

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888175	15393	37549	582	193

Description

6500733879 come1:hi1008 competence locus e (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae) HI1008 HI1008 Haemophilus influenzae 727 -11537737 4000708174 hi1008 (de:hypothetical protein hi1008) (db:swissprot) YBAV_HAEIN Q57134 HAEMOPHILUS INFLUENZAE 727 -11537737 166063 hypothetical protein hi1008 (cl:hypothetical protein hi1008) (db:pir2.dat) I64107 I64107 Haemophilus influenzae 727 -11537737 7500896547 hi1008 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77415 pid:1580713) (le:9407) (re:9745) (di:direct) U32781 U32781 g1574038 Haemophilus influenzae Rd 71421 -11537737 5000694938 (de:(hi1008) (pn:competence locus e:come1) (gn:come1) (gtcfc:13.12) (ec:) (keggfc:11.2) (tigrfc:4.6) (db:gtc-haemophilus influenzae)) HI1008 HI1008 Haemophilus influenzae 727 10088067

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888177	15394	37550	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888190	15395	37551	852	283

Description

6500733880 grpe:hi0071 heat shock protein b253 (gtcfc:12.7) (keggfc:12.7) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0071 HI0071 Haemophilus influenzae 727 -11537738 74556 grpe:hi0071 (de:grpe protein) (db:swissprot) GRPE_HAEIN P43732 HAEMOPHILUS INFLUENZAE 727 -11537738 166180 heat shock protein b25.3 homolog (db:pir2.dat) I64046 I64046 Haemophilus influenzae 727 -11537738 7500882748 hi0071 heat shock protein grpe (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:similar to sp:p09372 gb:x07863 pid:41619 gb:u00096) (le:62) (re:766) (di:direct) U32693 U32693 g1573022 Haemophilus influenzae Rd 71421 -11537738 5000694939 (de:(hi0071) (pn:protein:heat shock protein b253:grpe) (gn:grpe) (gtcfc:13.2) (ec:) (grpe_haein) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0071 HI0071 Haemophilus influenzae 727 10017071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888191	15396	37552	2172	723

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888202	15397	37553	1038	345

Description

6500733881 vagc:hi0321 virulence plasmid protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0321 HI0321 Haemophilus influenzae 727 -11537739 4000708215 hi0321 (de:hypothetical protein hi0321) (db:swissprot) Y321_HAEIN Q57534 HAEMOPHILUS INFLUENZAE 727 -11537739 167269 virulence-associated protein vapb homolog hi0321 (cl:virulence-associated protein vagc homolog) (db:pir2.dat) F64061 F64061 Haemophilus influenzae 727 -11537739 7500895121 hi0321 virulence associated protein b vapb (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:l22308 gb:l31763 gb:m74565 pid:145069) (le:5454) (re:5690) (di:direct) U32717 U32717 g1573290 Haemophilus influenzae Rd 71421 -11537739 5000694940 (de:(hi0321) (pn:virulence plasmid protein:vagc) (gn:vagc) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0321 HI0321 Haemophilus influenzae 727 10088328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888205	15398	37554	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888206	15399	37555	381	126

Description

6500733882 vapc:hi0322 virulence associated protein c (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0322 HI0322 Haemophilus influenzae 727 -11537740 5500686296 hi0322 (de:hypothetical protein hi0322) (db:swissprot) Y322_HAEIN Q57122 HAEMOPHILUS INFLUENZAE 727 -11537740 167265 virulence-associated protein vapc homolog hi0322 (cl:virulence-associated protein vapc) (db:pir2.dat) G64061 G64061 Haemophilus influenzae 727 -11537740 7500895124 hi0322 virulence associated protein c:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:l22308 gb:l31763 gb:m74565 pid:145068) (le:5687) (re:6091) (di:direct) U32717 U32717 g1573291 Haemophilus influenzae Rd 71421 -11537740 5000694941 (de:(hi0322) (pn:virulence associated protein c:vapc) (gn:vapc) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0322 HI0322 Haemophilus influenzae 727 10088325

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888218	15400	37556	474	157

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888239	15401	37557	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888240	15402	37558	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888262	15403	37559	1029	342

Description

6500733883 vapd:hi0450 virulence associated protein d (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0450 HI0450 Haemophilus influenzae 727 -11537741 167266 virulence-associated protein vapd homolog hi0450 (cl:virulence-associated protein vapd) (db:pir2.dat) C64069 C64069 Haemophilus influenzae 727 -11537741 7500955359 hi0450 virulence associated protein d vapd (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to gb:l22307 gb:l31763 gb:m74565 pid:145067) (le:689) (re:964) (di:complement) U32728 U32728 g1573426 Haemophilus influenzae Rd 71421 -11537741 5000694942 (de:(hi0450) (pn:virulence associated protein d:vapd) (gn:vapd) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0450 HI0450 Haemophilus influenzae 727 10088326

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888270	15404	37560	1929	642

Description

6500733884 sura:hi0458 survival protein:survival protein homolog precursor (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0458 HI0458 Haemophilus influenzae 727 -11537742 99887 sura:hi0458 (de:survival protein sura homolog precursor) (db:swissprot) SURA_HAEIN P44721 HAEMOPHILUS INFLUENZAE 727 -11537742 167183 survival protein sura homolog (db:pir2.dat) F64069 F64069 Haemophilus influenzae 727 -11537742 7500892275 hi0458 stationary phase survival protein sura (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to sp:p21202 gb:m68521 pid:147119) (le:6715) (re:7656) (di:complement) U32728 U32728 g1573432 Haemophilus influenzae Rd 71421 -11537742 5000694943 (de:(hi0458) (pn:survival protein homolog precursor:survival protein:sura) (gn:sura) (gtcfc:13.2) (ec:) (sura_haein) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0458 HI0458 Haemophilus influenzae 727 10041742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888271	15405	37561	282	93

Description

6500733885 htpx:hi0720 heat shock protein homolog (gtcfc:12.7) (keggfc:12.7) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0720 HI0720 Haemophilus influenzae 727 -11537743 78026 htpx:hi0720 (de:heat shock protein htpx homolog) (db:swissprot) HTPX_HAEIN P44840 HAEMOPHILUS INFLUENZAE 727 -11537743 166178 htpx heat shock protein htpx (cl:heat-shock protein htpx) (db:pir2.dat) H64088 H64088 Haemophilus influenzae 727 -11537743 7500883604 hi0720 heat shock protein htpx (db:genpept-bct1) (de:haemophilus influenzae rd section 70 of 163 of the complete genome.) (nt:similar to gb:m58470 sp:p23894 pid:146412 gb:u00096) (le:114) (re:965) (di:direct) U32755 U32755 g1573723 Haemophilus influenzae Rd 71421 -11537743 5000694944 (de:(hi0720) (pn:heat shock protein homolog:heat shock protein:htpx) (gn:htpx) (gtcfc:13.2) (ec:) (htpx_haein) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0720 HI0720 Haemophilus influenzae 727 10020365

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888272	15406	37562	543	180

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888284	15407	37563	555	184

Description

6500733886 uspa:hi0815 universal stress protein:universal stress protein a homolog (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0815 HI0815 Haemophilus influenzae 727 -11537744 104012 uspa:hi0815 (de:universal stress protein a homolog) (db:swissprot) USPA_HAEIN P44880 HAEMOPHILUS INFLUENZAE 727 -11537744 167249 universal stress protein a (cl:universal stress protein a) (db:pir2.dat) A64096 A64096 Haemophilus influenzae 727 -11537744 7500893870 hi0815 universal stress protein a uspa (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to gb:u00039 sp:p28242 gb:x67639 pid:43280) (le:124) (re:549) (di:complement) U32764 U32764 g1573828 Haemophilus influenzae Rd 71421 -11537744 5000694945 (de:(hi0815) (pn:universal stress protein a homolog:universal stress protein:uspa) (gn:uspa) (gtcfc:13.2) (ec:) (uspa_haein) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0815 HI0815 Haemophilus influenzae 727 10045782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888293	15408	37564	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888303	15409	37565	1050	349

Description

6500733887 inva:hi0901 invasion protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0901 HI0901 Haemophilus influenzae 727 -11537745 4000708954 hi0901 (de:hypothetical protein hi0901) (db:swissprot) YGDP_HAEIN Q57045 HAEMOPHILUS INFLUENZAE 727 -11537745 166924 invasion protein (cl:invasion-associated protein:mutt domain homology) (db:pir2.dat) E64101 E64101 Haemophilus influenzae 727 -11537745 7500924092 hi0901 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to pid:882723 gb:u00096 sp:q46930) (le:1892) (re:2482) (di:direct) U32772 U32772 g1573921 Haemophilus influenzae Rd 71421 -11537745 5000694946 (de:(hi0901) (pn:invasion protein:inva) (gn:inva) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0901 HI0901 Haemophilus influenzae 727 10088201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888308	15410	37566	402	133

Description

5000694947 hhob:htrh:hi0945 htra-like protein:htrh:protease hhob precursor (gtcfc:13.2) (ec:3.4.21.-) (keggfc:14.1) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0945 HI0945 Haemophilus influenzae 727 -11537746 76965 degs:hhob:htrh:hi0945 (ec:3.4.21.-) (de:protease degs precursor,) (db:swissprot) DEGS_HAEIN P44947 HAEMOPHILUS INFLUENZAE 727 -11537746 166207 trypsin-like proteinase (ec:3.4.21.-) (db:pir2.dat) I64103 I64103 Haemophilus influenzae 727 -11537746 7500880153 hi0945 protease degs (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to sp:p31137 gb:u15661 gb:u00096) (le:16986) (re:18008) (di:direct) U32775 U32775 g1573965 Haemophilus influenzae Rd 71421 -11537746 6500733888 hhob:htrh htra-like protein:htrh:protease hhob precursor (gtcfc:13.2) (ec:3.4.21.-) (keggfc:14.1) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0945 HI0945 Haemophilus influenzae 727 -11537746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888315	15411	37567	570	189

Description

6500733889 vapc:hi0947 virulence associated protein c (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI0947 HI0947 Haemophilus influenzae 727 -11537747 5500686452 hi0947 (de:hypothetical protein hi0947) (db:swissprot) Y947_HAEIN P71363 HAEMOPHILUS INFLUENZAE 727 -11537747 167264 virulence-associated protein vapc homolog hi0947 (cl:virulence-associated protein vapc) (db:pir2.dat) B64104 B64104 Haemophilus influenzae 727 -11537747 7500895720 hi0947 virulence associated protein c vapc (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to gb:l22308 gb:l31763 gb:m74565 pid:145068) (le:2670) (re:3068) (di:complement) U32776 U32776 g1573972 Haemophilus influenzae Rd 71421 -11537747 5000694948 (de:(hi0947) (pn:virulence associated protein c:vapc) (gn:vapc) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI0947 HI0947 Haemophilus influenzae 727 10088324

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888320	15412	37568	183	60

Description

6500733890 vapa:hi1251 virulence associated protein a (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI1251 HI1251 Haemophilus influenzae 727 -11537748 4000708171 hi1251 (de:hypothetical protein hi1251) (db:swissprot) YBAQ_HAEIN Q57089 HAEMOPHILUS INFLUENZAE 727 -11537748 167263 virulence-associated protein vapa homolog hi1251 (cl:virulence-associated protein vapa) (db:pir2.dat) H64112 H64112 Haemophilus influenzae 727 -11537748 7500896543 hi1251 virulence associated protein a vapa (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:similar to pid:1002991 pid:563265 sp:q46560 percent) (le:2657) (re:2980) (di:direct) U32805 U32805 g1574183 Haemophilus influenzae Rd 71421 -11537748 5000694949 (de:(hi1251) (pn:virulence associated protein a:vapa) (gn:vapa) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI1251 HI1251 Haemophilus influenzae 727 10088323

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888321	15413	37569	1161	386

Description

6500733891 mlga:hi1307 virulence plasmid protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI1307 HI1307 Haemophilus influenzae 727 -11537749 5500686502 hi1307 (de:hypothetical protein hi1307) (db:swissprot) YD07_HAEIN Q57320 HAEMOPHILUS INFLUENZAE 727 -11537749 167268 hypothetical protein hi1307 (cl:hypothetical protein b1798) (db:pir2.dat) F64115 F64115 Haemophilus influenzae 727 -11537749 7500922052 hi1307 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75693 pid:1657525) (le:4147) (re:4779) (di:direct) U32810 U32810 g1574766 Haemophilus influenzae Rd 71421 -11537749 5000694950 (de:(hi1307) (pn:virulence plasmid protein:mlga) (gn:mlga) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI1307 HI1307 Haemophilus influenzae 727 10088327

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888326	15414	37570	282	93

Description

6500733892 aut:hi1526 autotrophic growth protein:otrophic growth protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI1526 HI1526 Haemophilus influenzae 727 -11537750 166025 adp-heptose synthase homolog (cl:hypothetical protein b3052) (db:pir2.dat) C64127 C64127 Haemophilus influenzae 727 -11537750 7500955790 hi1526 adp-heptose synthase rfae (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:similar to pid:882153 percent ident: 97.38;) (le:5432) (re:6862) (di:complement) U32828 U32828 g1574367 Haemophilus influenzae Rd 71421 -11537750 5000694951 (de:(hi1526) (pn:otrophic growth protein:autotrophic growth protein:aut) (gn:aut) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI1526 HI1526 Haemophilus influenzae 727 10088059

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888357	15415	37571	402	133

Description

6500733893 htrb:ibpb:hi1527 heat shock protein b (gtcfc:12.7) (keggfc:12.7) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI1527 HI1527 Haemophilus influenzae 727 -11537751 166179 htrb lipid a biosynthesis lauroyl acyltransferase::htrb protein (ec:2.3.1.-) (db:pir2.dat) D64127 D64127 Haemophilus influenzae 727 -11537751 78034 htrb:hi1527 (ec:2.3.1.-) (de:protein b)) (db:swissprot) HTRB_HAEIN P45239 HAEMOPHILUS INFLUENZAE 727 -11537751 7500883607 hi1527 lipid a biosynthesis lauroyl acyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:similar to sp:p24187 gb:x61000 pid:48957 gb:u00096) (le:6947) (re:7894) (di:direct) U32828 U32828 g1574368 Haemophilus influenzae Rd 71421 -11537751 5000694952 (de:(hi1527) (pn:heat shock protein b:ibpb) (gn:htrb) (gtcfc:13.2) (ec:) (htrb_haein) (keggfc:11.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae)) HI1527 HI1527 Haemophilus influenzae 727 10020373

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888362	15416	37572	804	267

Description

5000694953 nad:ph:menadione oxidoreductase:hypothetical nad:ph oxidoreductase hi1544 (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI1544 HI1544 Haemophilus influenzae 727 -11537752 111771 hi1544 (ec:1.6.99.-) (de:putative nad(p)h oxidoreductase hi1544,) (db:swissprot) YF44_HAEIN P45245 HAEMOPHILUS INFLUENZAE 727 -11537752 167027 nad p h dehydrogenase quinone homolog (db:pir2.dat) G64128 G64128 Haemophilus influenzae 727 -11537752 7500923243 hi1544 nad p h oxidoreductase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to sp:q64669 pid:595518 percent ident:) (le:10367) (re:10975) (di:complement) U32829 U32829 g1574386 Haemophilus influenzae Rd 71421 -11537752 6500733894 nad:ph:menadione oxidoreductase:hypothetical nad:ph oxidoreductase hi1544 (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-haemophilus influenzae) HI1544 HI1544 Haemophilus influenzae 727 -11537752

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888371	15417	37573	402	133

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888372	15418	37574	312	103

Description

6500733895 mdl:hi0036 multidrug resistance protein (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI0036 HI0036 Haemophilus influenzae 727 -11537753 5500686214 hi0036 (de:hypothetical abc transporter atp-binding protein hi0036) (db:swissprot) Y036_HAEIN Q57335 HAEMOPHILUS INFLUENZAE 727 -11537753 167015 hypothetical protein hi0036 (cl:atp-binding cassette homology) (db:pir2.dat) D64044 D64044 Haemophilus influenzae 727 -11537753 7500894561 hi0036 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to sp:q50614 pid:1483552 percent identity:) (le:1954) (re:3732) (di:direct) U32689 U32689 g1572982 Haemophilus influenzae Rd 71421 -11537753 5000694954 (de:(hi0036) (pn:multidrug resistance protein:mdl) (gn:mdl) (gtcfc:13.3) (ec:) (keggfc:11.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae)) HI0036 HI0036 Haemophilus influenzae 727 10088255

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888374	15419	37575	1008	335

Description

6500733896 ampd:hi0300 ampd signalling protein:protein homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI0300 HI0300 Haemophilus influenzae 727 -11537754 59362 ampd:hi0300 (de:ampd protein homolog) (db:swissprot) AMPD_HAEIN P44624 HAEMOPHILUS INFLUENZAE 727 -11537754 165996 ampd signalling protein ampd (db:pir2.dat) F64060 F64060 Haemophilus influenzae 727 -11537754 7500876835 hi0300 ampd signalling protein ampd (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to gb:d26562 sp:p13016 gb:l28105 gb:x15237) (le:88) (re:642) (di:direct) U32716 U32716 g1573269 Haemophilus influenzae Rd 71421 -11537754 5000694955 (de:(hi0300) (pn:protein homolog:ampd signalling protein:ampd) (gn:ampd) (gtcfc:13.3) (ec:) (ampd_haein) (keggfc:11.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae)) HI0300 HI0300 Haemophilus influenzae 727 10002099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888392	15420	37576	1158	385

Description

6500733897 teha:hi0511 tellurite resistance protein:tellurite resistance protein homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI0511 HI0511 Haemophilus influenzae 727 -11537755 100991 teha:hi0511 (de:tellurite resistance protein teha homolog) (db:swissprot) TEHA_HAEIN P44741 HAEMOPHILUS INFLUENZAE 727 -11537755 167184 tellurite resistance protein teha homolog (db:pir2.dat) D64073 D64073 Haemophilus influenzae 727 -11537755 7500892923 hi0511 tellurite resistance protein teha (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:m74072 sp:p25396 pid:149017 gb:u00096) (le:10444) (re:11430) (di:complement) U32732 U32732 g1573492 Haemophilus influenzae Rd 71421 -11537755 5000694956 (de:(hi0511) (pn:tellurite resistance protein homolog:tellurite resistance protein:teha) (gn:teha) (gtcfc:13.3) (ec:) (teha_haein) (keggfc:11.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae)) HI0511 HI0511 Haemophilus influenzae 727 10042835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888400	15421	37577	501	166

Description

GTC ORF with score 191 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k09h9.) (nt:contains similarity to human rna-binding protein) (le:22612:23125:23857) (re:23071:23648:23899) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888402	15422	37578	1590	529

Description

5000694957 mdab:mda66:hi0648 modulator of drug activity:mda66:modulator of drug activity b homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI0648 HI0648 Haemophilus influenzae 727 -11537756 166997 drug activity modulator b (db:pir2.dat) C64084 C64084 Haemophilus influenzae 727 -11537756 7500960651 hi0648 modulator of drug activity b mdab (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to sp:p40717 pid:609328 pid:882558) (le:1104) (re:1730) (di:complement) U32748 U32748 g1573647 Haemophilus influenzae Rd 71421 -11537756 6500733898 mdab:mda66 modulator of drug activity:mda66:modulator of drug activity b homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI0648 HI0648 Haemophilus influenzae 727 -11537756

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888415	15423	37579	1674	557

Description

GTC ORF with score 153 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c09d1.) (nt:c09d1.1; coded for by c. elegans cdna cm20d2) (le:10843:11579:11897:13440) (re:10892:11852:12033:13610) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888445	15424	37580	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888446	15425	37581	642	213

Description

6500733899 acrb:hi0895 acriflavine resistance protein (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI0895 HI0895 Haemophilus influenzae 727 -11537757 5500686444 hi0895 (de:hypothetical protein hi0895) (db:swissprot) Y895_HAEIN Q57124 HAEMOPHILUS INFLUENZAE 727 -11537757 165978 acriflavine resistance protein homolog (db:pir2.dat) H64100 H64100 Haemophilus influenzae 727 -11537757 7500895629 hi0895 acriflavine resistance protein acrb (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to gb:m94248 sp:p31224 gb:u00734 pid:290406) (le:5645) (re:8743) (di:direct) U32771 U32771 g1573914 Haemophilus influenzae Rd 71421 -11537757 5000694958 (de:(hi0895) (pn:acriflavine resistance protein:acrb) (gn:acrb) (gtcfc:13.3) (ec:) (keggfc:11.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae)) HI0895 HI0895 Haemophilus influenzae 727 10088049

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888461	15426	37582	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888462	15427	37583	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888467	15428	37584	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888470	15429	37585	873	290

Description

6500733900 emrb:hi0897 multidrug resistance protein:multidrug resistance protein b homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI0897 HI0897 Haemophilus influenzae 727 -11537758 70131 emrb:hi0897 (de:multidrug resistance protein b homolog) (db:swissprot) EMRB_HAEIN P44927 HAEMOPHILUS INFLUENZAE 727 -11537758 167013 emrb multidrug resistance protein emrb (db:pir2.dat) A64101 A64101 Haemophilus influenzae 727 -11537758 7500881005 hi0897 multidrug resistance protein b emrb (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to gb:m86657 sp:p27304 pid:145836 gb:u00096) (le:9764) (re:11296) (di:complement) U32771 U32771 g1573916 Haemophilus influenzae Rd 71421 -11537758 5000694959 (de:(hi0897) (pn:multidrug resistance protein b homolog:multidrug resistance protein:emrb) (gn:emrb) (gtcfc:13.3) (ec:) (emrb_haein) (keggfc:11.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae)) HI0897 HI0897 Haemophilus influenzae 727 10012708

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888473	15430	37586	339	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888490	15431	37587	1437	478

Description

6500733901 emra:hi0898 multidrug resistance protein:erma:multidrug resistance protein a homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI0898 HI0898 Haemophilus influenzae 727 -11537759 70129 emra:hi0898 (de:multidrug resistance protein a homolog) (db:swissprot) EMRA_HAEIN P44928 HAEMOPHILUS INFLUENZAE 727 -11537759 167014 multidrug resistance protein erma homolog (cl:multidrug resistance protein a:lipoyl/biotin-binding homology) (db:pir2.dat) B64101 B64101 Haemophilus influenzae 727 -11537759 7500881003 hi0898 multidrug resistance protein a emra (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to gb:m86657 sp:p27303 pid:145835 gb:u00096) (le:11306) (re:12478) (di:complement) U32771 U32771 g1573917 Haemophilus influenzae Rd 71421 -11537759 5000694960 (de:(hi0898) (pn:multidrug resistance protein a homolog:multidrug resistance protein:erma) (gn:emra) (gtcfc:13.3) (ec:) (emra_haein) (keggfc:11.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae)) HI0898 HI0898 Haemophilus influenzae 727 10012706

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888491	15432	37588	276	92

Description

6500733902 bcr:hi1242 bicyclomycin resistance protein:bicyclomycin resistance protein homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI1242 HI1242 Haemophilus influenzae 727 -11537760 61516 bcr:hi1242 (de:bicyclomycin resistance protein homolog) (db:swissprot) BCR_HAEIN P45123 HAEMOPHILUS INFLUENZAE 727 -11537760 166028 bicyclomycin resistance protein homolog (cl:bicyclomycin resistance protein) (db:pir2.dat) E64112 E64112 Haemophilus influenzae 727 -11537760 7500877730 hi1242 bicyclomycin resistance protein bcr (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the completegenome.) (nt:similar to sp:p28246 gb:x63703 pid:41065 pid:424052) (le:2936) (re:4132) (di:complement) U32804 U32804 g1574174 Haemophilus influenzae Rd 71421 -11537760 5000694961 (de:(hi1242) (pn:bicyclomycin resistance protein homolog:bicyclomycin resistance protein:bcr) (gn:bcr) (gtcfc:13.3) (ec:) (bcr_haein) (keggfc:11.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae)) HI1242 HI1242 Haemophilus influenzae 727 10004225

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888515	15433	37589	996	331

Description

6500733903 tehb:hi1275 tellurite resistance protein:tellurite resistance protein homolog (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI1275 HI1275 Haemophilus influenzae 727 -11537761 100993 tehb:hi1275 (de:tellurite resistance protein tehb homolog) (db:swissprot) TEHB_HAEIN P45134 HAEMOPHILUS INFLUENZAE 727 -11537761 167185 hemagglutinin hag1 homolog (cl:hemagglutinin hag1) (db:pir2.dat) H64113 H64113 Haemophilus influenzae 727 -11537761 7500892924 hi1275 tellurite resistance protein tehb (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:similar to gb:m74072 sp:p25397 pid:149018 gb:u00096) (le:3620) (re:4480) (di:complement) U32807 U32807 g1574730 Haemophilus influenzae Rd 71421 -11537761 5000694962 (de:(hi1275) (pn:tellurite resistance protein homolog:tellurite resistance protein:tehb) (gn:tehb) (gtcfc:13.3) (ec:) (tehb_haein) (keggfc:11.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae)) HI1275 HI1275 Haemophilus influenzae 727 10042837

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888522	15434	37590	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888523	15435	37591	378	125

Description

5000694963 nodulation protein t:nodt:hypothetical protein (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI1462 HI1462 Haemophilus influenzae 727 -11537762 111435 hi1462 (de:hypothetical protein hi1462) (db:swissprot) YE62_HAEIN P45217 HAEMOPHILUS INFLUENZAE 727 -11537762 167044 virion morphogenesis late i orf homolog (db:pir2.dat) I64124 I64124 Haemophilus influenzae 727 -11537762 7500922722 hi1462 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 139 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77211 pid:1778487) (le:2548) (re:3912) (di:direct) U32824 U32824 g1574302 Haemophilus influenzae Rd 71421 -11537762 6500733904 nodulation protein t:nodt:hypothetical protein (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI1462 HI1462 Haemophilus influenzae 727 -11537762

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888531	15436	37592	1212	403

Description

5000694964 mercury resistance regulatory protein:merr2:hypothetical transcriptional regulator hi1623 (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI1623 HI1623 Haemophilus influenzae 727 -11537763 112727 zntr:hi1623 (de:zn(ii)-responsive regulator homolog) (db:swissprot) ZNTR_HAEIN P45277 HAEMOPHILUS INFLUENZAE 727 -11537763 7500936843 hi1623 mercuric resistance operon regulatory protein (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:similar to gb:x57326 pid:48151 percent ident:) (le:9187) (re:9594) (di:direct) U32835 U32835 g1574465 Haemophilus influenzae Rd 71421 -11537763 6500733905 mercury resistance regulatory protein:merr2:hypothetical transcriptional regulator hi1623 (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-haemophilus influenzae) HI1623 HI1623 Haemophilus influenzae 727 -11537763

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888546	15437	37593	900	299

Description

GTC ORF with score 334 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c1020.) (nt:spcc1020.07, unknown, len:236aa, similar eg. to s.) (le:23174:23378:23486:23606) (re:23206:23420:23548:24177) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888556	15438	37594	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888581	15439	37595	2127	708

Description

6500733906 radc:hi0952 dna repair protein:dna repair protein homolog (gtcfc:13.4) (keggfc:14.2) (tigrfc:14.5) (db:gtc-haemophilus influenzae) HI0952 HI0952 Haemophilus influenzae 727 -11537764 92961 radc:hi0952 (de:dna repair protein radc homolog) (db:swissprot) RADC_HAEIN P44952 HAEMOPHILUS INFLUENZAE 727 -11537764 166109 hypothetical protein hi0952 (cl:dna repair protein radc) (db:pir2.dat) F64104 F64104 Haemophilus influenzae 727 -11537764 7500889343 hi0952 dna repair protein radc (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p25531 gb:x63366 gb:x63367) (le:5792) (re:6496) (di:complement) U32776 U32776 g1573977 Haemophilus influenzae Rd 71421 -11537764 5000694965 (de:(hi0952) (pn:dna repair protein homolog:dna repair protein:radc) (gn:radc) (gtcfc:13.4) (ec:) (radc_haein) (keggfc:11.2) (tigrfc:14.5) (db:gtc-haemophilus influenzae)) HI0952 HI0952 Haemophilus influenzae 727 10034978

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888582	15440	37596	756	252

Description

6500733907 is1016-v6:hi1018 is1016-v6 protein:protein (gtcfc:13.5) (keggfc:14.2) (tigrfc:14.6) (db:gtc-haemophilus influenzae) HI1018 HI1018 Haemophilus influenzae 727 -11537765 166927 protein v6:truncated (db:pir2.dat) E64108 E64108 Haemophilus influenzae 727 -11537765 5000694966 (de:(hi1018) (pn:protein:is1016-v6 protein:is1016-v6) (gn:is1016-v6) (gtcfc:13.5) (ec:) (keggfc:11.2) (tigrfc:14.6) (db:gtc-haemophilus influenzae)) HI1018 HI1018 Haemophilus influenzae 727 10088203

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888588	15441	37597	183	60

Description

6500733908 is1016-v6:hi1329 is1016-v6 protein:protein (gtcfc:13.5) (keggfc:14.2) (tigrfc:14.6) (db:gtc-haemophilus influenzae) HI1329 HI1329 Haemophilus influenzae 727 -11537766 5500686506 hi1329 (de:hypothetical protein hi1329) (db:swissprot) YD29_HAEIN Q57255 HAEMOPHILUS INFLUENZAE 727 -11537766 166929 hypothetical protein hi1329 (db:pir2.dat) I64116 I64116 Haemophilus influenzae 727 -11537766 7500922079 hi1329 is1016-v6 protein is1016-v6 (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:similar to gb:x59756 percent ident: 54.71;) (le:4496) (re:4807) (di:complement) U32812 U32812 g1574795 Haemophilus influenzae Rd 71421 -11537766 5000694967 (de:(hi1329) (pn:protein:is1016-v6 protein:is1016-v6) (gn:is1016-v6) (gtcfc:13.5) (ec:) (keggfc:11.2) (tigrfc:14.6) (db:gtc-haemophilus influenzae)) HI1329 HI1329 Haemophilus influenzae 727 10088205

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888590	15442	37598	567	188

Description

6500733909 is1016-v6:hi1577 is1016-v6 protein:protein (gtcfc:13.5) (keggfc:14.2) (tigrfc:14.6) (db:gtc-haemophilus influenzae) HI1577 HI1577 Haemophilus influenzae 727 -11537767 5500686576 hi1577 (de:hypothetical protein hi1577) (db:swissprot) YF77_HAEIN Q57070 HAEMOPHILUS INFLUENZAE 727 -11537767 166928 hypothetical protein hi1577 (db:pir2.dat) G64130 G64130 Haemophilus influenzae 727 -11537767 7500923293 hi1577 is1016-v6 protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to gb:x59756 percent ident: 43.95;) (le:67) (re:285) (di:direct) U32832 U32832 g1574429 Haemophilus influenzae Rd 71421 -11537767 5000694968 (de:(hi1577) (pn:protein:is1016-v6 protein:is1016-v6) (gn:is1016-v6) (gtcfc:13.5) (ec:) (keggfc:11.2) (tigrfc:14.6) (db:gtc-haemophilus influenzae)) HI1577 HI1577 Haemophilus influenzae 727 10088204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888598	15443	37599	510	169

Description

6500733910 bira:hi0220b bira bifunctional protein:biotin operon repressor:biotin-acetyl-coa-carboxylase synthetase (gtcfc:9.6:12.13) (ec:6.3.4.15) (keggfc:14.1) (db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:cell processes-metabolic regulators signal transduction--two component system senso... HI0220B HI0220B Haemophilus influenzae 727 -11537768 61753 bira:hi0220.1 (ec:6.3.4.15) (de:coa-carboxylase) synthetase), (biotin--protein ligase)) (db:swissprot) BIRA_HAEIN P46363 HAEMOPHILUS INFLUENZAE 727 -11537768 7500877841 hi0220.1 biotin operon repressor/biotin acetyl coenzyme a (db:genpept-bct1) (de:haemophilus influenzae rd section 23 of 163 of the complete genome.) (nt:similar to sp:p06709 gb:l14557 gb:m10123 gb:m15820) (le:2270) (re:3178) (di:complement) U32708 U32708 g1573184 Haemophilus influenzae Rd 71421 -11537768 5000695335 (de:(hi02201) (pn:bifunctional protein:biotin operon repressor:biotin--) (gn:bira) (gtcfc:13.7) (ec:6.3.4.15) (bira_haein) (keggfc:11.1) (db:gtc-haemophilus influenzae)) HI02201 HI02201 Haemophilus influenzae 727 10004461

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888611	15444	37600	294	97

Description

6500733911 pbpg:hi0364 penicillin-binding protein 7 homolog precursor:pbp-7:d-alanyl-d-alanine-endopeptidase:dd-endopeptidase (gtcfc:11.4:13.3) (ec:3.4.99.-) (keggfc:14.1) (db:gtc-haemophilus influenzae) HI0364 HI0364 Haemophilus influenzae 727 -11537769 88739 pbpg:hi0364 (ec:3.4.99.-) (de:alanine-endopeptidase), (dd-endopeptidase)) (db:swissprot) PBP7_HAEIN P44664 HAEMOPHILUS INFLUENZAE 727 -11537769 166380 hypothetical protein hi0364 (db:pir2.dat) H64149 H64149 Haemophilus influenzae 727 -11537769 7500887699 hi0364 penicillin-binding protein 7:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to sp:p33364 gb:x01067 pid:405864) (le:8533) (re:9411) (di:complement) U32720 U32720 g1573331 Haemophilus influenzae Rd 71421 -11537769 5000695336 (de:(hi0364) (pn:penicillin-binding protein 7 homolog precursor:pbp-7:d-alanyl-d-alanine-endopeptidase:dd-endopeptidase) (gn:pbpg) (gtcfc:13.7) (ec:3.4.99.-) (pbp7_haein) (keggfc:11.1) (db:gtc-haemophilus influenzae)) HI0364 HI0364 Haemophilus influenzae 727 10030866

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888647	15445	37601	849	283

Description

6500733912 meng:hi0508 s-adenosylmethionine:2-demethylmenaquinone methyltransferase (gtcfc:9.12) (ec:2.1.-.-) (keggfc:14.1) (db:gtc-haemophilus influenzae) HI0508 HI0508 Haemophilus influenzae 727 -11537770 83454 meng:hi0508 (ec:2.1.-.-) (de:(ec 2.1.-.-)) (db:swissprot) MENG_HAEIN P44738 HAEMOPHILUS INFLUENZAE 727 -11537770 166435 hypothetical protein hi0508 (db:pir2.dat) G64153 G64153 Haemophilus influenzae 727 -11537770 7500885498 hi0508 s-adenosylmethion:2-demethylmenaquinone (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32165 pid:305032 gb:u00096) (le:8159) (re:8647) (di:complement) U32732 U32732 g1573489 Haemophilus influenzae Rd 71421 -11537770 5000695337 (de:(hi0508) (pn:s-adenosylmethionine:2-demethylmenaquinone methyltransferase) (gn:meng) (gtcfc:13.7) (ec:2.1.-.-) (meng_haein) (keggfc:11.1) (db:gtc-haemophilus influenzae)) HI0508 HI0508 Haemophilus influenzae 727 10025668

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888660	15446	37602	507	168

Description

6500733913 nrdg:hi1155 anaerobic ribonucleoside-triphosphate reductase activating protein (gtcfc:14.1) (ec:1.97.1.-) (keggfc:14.1) (db:gtc-haemophilus influenzae) HI1155 HI1155 Haemophilus influenzae 727 -11537771 86498 nrdg:hi1155 (ec:1.97.1.-) (de:(ec 1.97.1.-)) (db:swissprot) NRDG_HAEIN P45080 HAEMOPHILUS INFLUENZAE 727 -11537771 166661 anaerobic ribonucleotide reductase activase (ec:1.97.1.-) (db:pir2.dat) E64168 E64168 Haemophilus influenzae 727 -11537771 7500886577 hi1155 anaerobic ribonucleoside-triphosphate reductase (db:genpept-bct1) (de:haemophilus influenzae rd section 110 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p39329 gb:z46865 pid:537079) (le:3908) (re:4375) (di:complement) U32795 U32795 g1574712 Haemophilus influenzae Rd 71421 -11537771 5000695338 (de:(hi1155) (pn:anaerobic ribonucleoside-triphosphate reductase activating protein) (gn:nrdg) (gtcfc:13.7) (ec:1.97.1.-) (nrdg_haein) (keggfc:11.1) (db:gtc-haemophilus influenzae)) HI1155 HI1155 Haemophilus influenzae 727 10028663

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888690	15447	37603	2124	707

Description

6500733914 xseb:hi1437 exodeoxyribonuclease small subunit:exonuclease vii small subunit (gtcfc:14.1) (ec:3.1.11.6) (keggfc:14.1) (db:gtc-haemophilus influenzae) HI1437 HI1437 Haemophilus influenzae 727 -11537772 70785 xseb:hi1437 (ec:3.1.11.6) (de:small subunit)) (db:swissprot) EX7S_HAEIN P43914 HAEMOPHILUS INFLUENZAE 727 -11537772 166772 xseb exodeoxyribonuclease vii:small chain (cl:exodeoxyribonuclease vii small chain) (ec:3.1.11.6) (db:pir2.dat) A64172 A64172 Haemophilus influenzae 727 -11537772 7500881228 hi1437 exodeoxyribonuclease:small subunit xseb (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to gb:d00694 sp:p22938 pid:216583 gb:u00096) (le:9723) (re:9977) (di:direct) U32822 U32822 g1574276 Haemophilus influenzae Rd 71421 -11537772 5000695340 (de:(hi1437) (pn:exodeoxyribonuclease small subunit:exonuclease vii small subunit) (gn:xseb) (gtcfc:13.7) (ec:3.1.11.6) (ex7s_haein) (keggfc:11.1) (db:gtc-haemophilus influenzae)) HI1437 HI1437 Haemophilus influenzae 727 10013360

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888691	15448	37604	477	159

Description

5000695341 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0040 HI0040 Haemophilus influenzae 727 -11537773 108489 hi0040 (de:hypothetical protein hi0040) (db:swissprot) Y040_HAEIN P43929 HAEMOPHILUS INFLUENZAE 727 -11537773 166244 hypothetical protein hi0040 (db:pir2.dat) A64000 A64000 Haemophilus influenzae 727 -11537773 7500894571 hi0040 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to pid:1944176 percent identity: 47.58;) (le:6591) (re:7367) (di:complement) U32689 U32689 g1572986 Haemophilus influenzae Rd 71421 -11537773 6500733915 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0040 HI0040 Haemophilus influenzae 727 -11537773

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888696	15449	37605	447	148

Description

5000695342 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0043 HI0043 Haemophilus influenzae 727 -11537774 110833 hi0043 (de:hypothetical protein hi0043) (db:swissprot) YCJF_HAEIN P43931 HAEMOPHILUS INFLUENZAE 727 -11537774 166246 hypothetical protein hi0043 (cl:hypothetical protein hi0043) (db:pir2.dat) C64000 C64000 Haemophilus influenzae 727 -11537774 7500921847 hi0043 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to sp:p45525 gb:u00096 pid:1787582 percent) (le:8902) (re:9966) (di:complement) U32689 U32689 g1572989 Haemophilus influenzae Rd 71421 -11537774 6500733916 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0043 HI0043 Haemophilus influenzae 727 -11537774

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888713	15450	37606	612	203

Description

6500733917 phna:hi0046 protein homolog (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0046 HI0046 Haemophilus influenzae 727 -11537775 89588 phna:hi0046 (de:phna protein homolog) (db:swissprot) PHNA_HAEIN P44479 HAEMOPHILUS INFLUENZAE 727 -11537775 165994 alkylphosphonate uptake protein (db:pir2.dat) I64044 I64044 Haemophilus influenzae 727 -11537775 7500888023 hi0046 alkylphosphonate uptake protein phna (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to sp:p16680 gb:u14003 pid:147194) (le:888) (re:1250) (di:direct) U32690 U32690 g1572993 Haemophilus influenzae Rd 71421 -11537775 5000695343 (de:(hi0046) (pn:protein homolog) (gn:phna) (gtcfc:13.7) (ec:) (phna_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0046 HI0046 Haemophilus influenzae 727 10031710

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888715	15451	37607	702	233

Description

5000695344 sorbitol dehydrogenase (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0053 HI0053 Haemophilus influenzae 727 -11537776 4000707543 hi0053 (de:hypothetical zinc-type alcohol dehydrogenase-like protein hi0053) (db:swissprot) Y053_HAEIN Q57517 HAEMOPHILUS INFLUENZAE 727 -11537776 166252 probable l-iditol 2-dehydrogenase:hi0053:sorbitol dehydrogenase (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.14) (db:pir1.dat) F64141 F64141 Haemophilus influenzae 727 -11537776 7500894595 hi0053 zinc-type alcohol dehydrogenase (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to gb:m96947 sp:q06004 pid:304153) (le:6610) (re:7638) (di:complement) U32690 U32690 g1573000 Haemophilus influenzae Rd 71421 -11537776 6500733918 sorbitol dehydrogenase (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0053 HI0053 Haemophilus influenzae 727 -11537776

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888720	15452	37608	393	130

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888727	15453	37609	1296	432

Description

GTC ORF with score 101 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f53f10.) (nt:similar to nucleoporins; coded for by c. elegans) (le:2756:2915:3079:4609) (re:2867:3007:4558:5079) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888738	15454	37610	564	187

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888739	15455	37611	651	216

Description

5000695345 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0073 HI0073 Haemophilus influenzae 727 -11537777 108627 hi0073 (de:hypothetical protein hi0073) (db:swissprot) Y073_HAEIN P43933 HAEMOPHILUS INFLUENZAE 727 -11537777 166257 hypothetical protein hi0073 (db:pir2.dat) E64000 E64000 Haemophilus influenzae 727 -11537777 7500894634 hi0073 h. influenzae predicted coding region hi0073 (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:779) (re:1123) (di:complement) U32693 U32693 g1573023 Haemophilus influenzae Rd 71421 -11537777 6500733919 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0073 HI0073 Haemophilus influenzae 727 -11537777

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888741	15456	37612	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888745	15457	37613	564	187

Description

5000695346 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0074 HI0074 Haemophilus influenzae 727 -11537778 108629 hi0074 (de:hypothetical protein hi0074) (db:swissprot) Y074_HAEIN P43934 HAEMOPHILUS INFLUENZAE 727 -11537778 166258 hypothetical protein hi0074 (db:pir2.dat) F64000 F64000 Haemophilus influenzae 727 -11537778 7500894635 hi0074 h. influenzae predicted coding region hi0074 (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1116) (re:1556) (di:complement) U32693 U32693 g1573031 Haemophilus influenzae Rd 71421 -11537778 6500733920 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0074 HI0074 Haemophilus influenzae 727 -11537778

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888749	15458	37614	498	165

Description

5000695347 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0077 HI0077 Haemophilus influenzae 727 -11537779 108638 hi0077 (de:hypothetical protein hi0077) (db:swissprot) Y077_HAEIN P43935 HAEMOPHILUS INFLUENZAE 727 -11537779 166259 hypothetical protein hi0077 (db:pir2.dat) G64000 G64000 Haemophilus influenzae 727 -11537779 7500894654 hi0077 h. influenzae predicted coding region hi0077 (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4949) (re:5815) (di:direct) U32693 U32693 g1573032 Haemophilus influenzae Rd 71421 -11537779 6500733921 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0077 HI0077 Haemophilus influenzae 727 -11537779

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888761	15459	37615	426	141

Description

5000695348 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0080 HI0080 Haemophilus influenzae 727 -11537780 108672 hi0080 (de:hypothetical protein hi0080) (db:swissprot) YIFN_HAEIN P43936 HAEMOPHILUS INFLUENZAE 727 -11537780 166260 hypothetical protein hi0080 (db:pir2.dat) H64000 H64000 Haemophilus influenzae 727 -11537780 7500937430 hi0080 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:2367279 percent identity:) (le:7886) (re:8317) (di:direct) U32693 U32693 g1573028 Haemophilus influenzae Rd 71421 -11537780 6500733922 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0080 HI0080 Haemophilus influenzae 727 -11537780

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888763	15460	37616	594	197

Description

5000695349 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0082 HI0082 Haemophilus influenzae 727 -11537781 108675 hi0082 (de:hypothetical protein hi0082 precursor) (db:swissprot) Y082_HAEIN P43937 HAEMOPHILUS INFLUENZAE 727 -11537781 166262 hypothetical protein hi0082 (db:pir2.dat) I64000 I64000 Haemophilus influenzae 727 -11537781 7500894657 hi0082 h. influenzae predicted coding region hi0082 (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9504) (re:9770) (di:direct) U32693 U32693 g1573033 Haemophilus influenzae Rd 71421 -11537781 6500733923 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0082 HI0082 Haemophilus influenzae 727 -11537781

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888766	15461	37617	441	146

Description

5000695350 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0083 HI0083 Haemophilus influenzae 727 -11537782 108678 hi0083 (de:hypothetical protein hi0083 precursor) (db:swissprot) Y083_HAEIN P43938 HAEMOPHILUS INFLUENZAE 727 -11537782 166263 hypothetical protein hi0083 (db:pir2.dat) A64001 A64001 Haemophilus influenzae 727 -11537782 7500894659 hi0083 h. influenzae predicted coding region hi0083 (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9785) (re:10000) (di:direct) U32693 U32693 g1573034 Haemophilus influenzae Rd 71421 -11537782 6500733924 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0083 HI0083 Haemophilus influenzae 727 -11537782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888769	15462	37618	585	194

Description

5000695351 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0094 HI0094 Haemophilus influenzae 727 -11537783 108709 hi0094 (de:hypothetical protein hi0094) (db:swissprot) Y094_HAEIN P43939 HAEMOPHILUS INFLUENZAE 727 -11537783 166268 hypothetical protein hi0094 (db:pir2.dat) B64001 B64001 Haemophilus influenzae 727 -11537783 7500894671 hi0094 h. influenzae predicted coding region hi0094 (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1399) (re:1719) (di:complement) U32695 U32695 g1573046 Haemophilus influenzae Rd 71421 -11537783 6500733925 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0094 HI0094 Haemophilus influenzae 727 -11537783

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888787	15463	37619	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888812	15464	37620	1329	442

Description

5000695352 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0096 HI0096 Haemophilus influenzae 727 -11537784 108712 hi0096 (de:hypothetical protein hi0096) (db:swissprot) Y096_HAEIN P43940 HAEMOPHILUS INFLUENZAE 727 -11537784 166269 hypothetical protein hi0096 (db:pir2.dat) C64001 C64001 Haemophilus influenzae 727 -11537784 7500894679 hi0096 h. influenzae predicted coding region hi0096 (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3158) (re:3733) (di:direct) U32695 U32695 g1573054 Haemophilus influenzae Rd 71421 -11537784 6500733926 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0096 HI0096 Haemophilus influenzae 727 -11537784

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888825	15465	37621	984	327

Description

5000695353 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0100 HI0100 Haemophilus influenzae 727 -11537785 108720 hi0100 (de:hypothetical protein hi0100) (db:swissprot) Y100_HAEIN P43941 HAEMOPHILUS INFLUENZAE 727 -11537785 166270 hypothetical protein hi0100 (db:pir2.dat) D64001 D64001 Haemophilus influenzae 727 -11537785 7500894694 hi0100 h. influenzae predicted coding region hi0100 (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7620) (re:8015) (di:complement) U32695 U32695 g1573055 Haemophilus influenzae Rd 71421 -11537785 6500733927 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0100 HI0100 Haemophilus influenzae 727 -11537785

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888838	15466	37622	636	211

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888846	15467	37623	504	167

Description

5000695354 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0101 HI0101 Haemophilus influenzae 727 -11537786 108723 hi0101 (de:hypothetical protein hi0101) (db:swissprot) Y101_HAEIN P43942 HAEMOPHILUS INFLUENZAE 727 -11537786 166271 hypothetical protein hi0101 (db:pir2.dat) E64001 E64001 Haemophilus influenzae 727 -11537786 7500894698 hi0101 h. influenzae predicted coding region hi0101 (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7859) (re:8299) (di:complement) U32695 U32695 g1573056 Haemophilus influenzae Rd 71421 -11537786 6500733928 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0101 HI0101 Haemophilus influenzae 727 -11537786

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888847	15468	37624	750	249

Description

GTC ORF with score 163 to: (sr:autographa californica nuclear polyhedrosis virus (clone: c6) dna) (db:genpept-vrl) (de:autographa californica nuclear polyhedrosis virus (clone c6)complete genome.) (nt:grail score: null; cap site and late promoter) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888848	15469	37625	231	76

Description

5000695355 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0109 HI0109 Haemophilus influenzae 727 -11537787 108742 hi0109 (de:hypothetical protein hi0109 precursor) (db:swissprot) Y109_HAEIN P43943 HAEMOPHILUS INFLUENZAE 727 -11537787 166276 hypothetical protein hi0109 (db:pir2.dat) F64001 F64001 Haemophilus influenzae 727 -11537787 7500894715 hi0109 h. influenzae predicted coding region hi0109 (db:genpept-bct1) (de:haemophilus influenzae rd section 11 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5077) (re:5418) (di:complement) U32696 U32696 g1573066 Haemophilus influenzae Rd 71421 -11537787 6500733929 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0109 HI0109 Haemophilus influenzae 727 -11537787

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888849	15470	37626	996	331

Description

5000695356 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0114 HI0114 Haemophilus influenzae 727 -11537788 108760 hi0114 (de:hypothetical protein hi0114) (db:swissprot) Y114_HAEIN P43944 HAEMOPHILUS INFLUENZAE 727 -11537788 166278 hypothetical protein hi0114 (db:pir2.dat) G64001 G64001 Haemophilus influenzae 727 -11537788 7500894725 hi0114 h. influenzae predicted coding region hi0114 (db:genpept-bct1) (de:haemophilus influenzae rd section 12 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:143) (re:259) (di:complement) U32697 U32697 g1573070 Haemophilus influenzae Rd 71421 -11537788 6500733930 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0114 HI0114 Haemophilus influenzae 727 -11537788

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888855	15471	37627	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888864	15472	37628	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888881	15473	37629	189	62

Description

5000695357 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0116 HI0116 Haemophilus influenzae 727 -11537789 166280 hypothetical protein hi0116 (db:pir2.dat) H64001 H64001 Haemophilus influenzae 727 -11537789 6500733931 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0116 HI0116 Haemophilus influenzae 727 -11537789 108768 y116_haein (de:hypothetical protein hi0116.) P43945 P43945 Haemophilus influenzae 727 -11537789

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888885	15474	37630	531	176

Description

5000695358 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0117 HI0117 Haemophilus influenzae 727 -11537790 108772 hi0117 (de:hypothetical protein hi0117) (db:swissprot) Y117_HAEIN P43946 HAEMOPHILUS INFLUENZAE 727 -11537790 166281 hypothetical protein hi0117 (db:pir2.dat) I64001 I64001 Haemophilus influenzae 727 -11537790 6500733932 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0117 HI0117 Haemophilus influenzae 727 -11537790

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888890	15475	37631	864	287

Description

5000695359 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0120 HI0120 Haemophilus influenzae 727 -11537791 108789 hi0120 (de:hypothetical protein hi0120) (db:swissprot) Y120_HAEIN P43947 HAEMOPHILUS INFLUENZAE 727 -11537791 166282 hypothetical protein hi0120 (cl:hypothetical protein hi1205) (db:pir2.dat) A64002 A64002 Haemophilus influenzae 727 -11537791 7500894738 hi0120 h. influenzae predicted coding region hi0120 (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3231) (re:3737) (di:complement) U32698 U32698 g1573075 Haemophilus influenzae Rd 71421 -11537791 6500733933 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0120 HI0120 Haemophilus influenzae 727 -11537791

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888894	15476	37632	495	164

Description

5000695360 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0127 HI0127 Haemophilus influenzae 727 -11537792 108802 hi0127 (de:hypothetical protein hi0127) (db:swissprot) Y127_HAEIN P43949 HAEMOPHILUS INFLUENZAE 727 -11537792 166286 hypothetical protein hi0127 (db:pir2.dat) C64002 C64002 Haemophilus influenzae 727 -11537792 6500733934 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0127 HI0127 Haemophilus influenzae 727 -11537792

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888903	15477	37633	309	102

Description

5000695361 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0130 HI0130 Haemophilus influenzae 727 -11537793 108834 hi0130 (de:hypothetical protein hi0130) (db:swissprot) Y130_HAEIN P43950 HAEMOPHILUS INFLUENZAE 727 -11537793 166287 hypothetical protein hi0130 (db:pir2.dat) D64002 D64002 Haemophilus influenzae 727 -11537793 6500733935 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0130 HI0130 Haemophilus influenzae 727 -11537793

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888907	15478	37634	192	63

Description

5000695362 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0131 HI0131 Haemophilus influenzae 727 -11537794 108836 hi0131 (de:hypothetical protein hi0131 precursor) (db:swissprot) Y131_HAEIN P43951 HAEMOPHILUS INFLUENZAE 727 -11537794 166288 hypothetical protein hi0131 (db:pir2.dat) E64002 E64002 Haemophilus influenzae 727 -11537794 7500894761 hi0131 afua protein (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:similar to pid:1469286 pid:1477455 percent) (le:301) (re:1341) (di:complement) U32699 U32699 g1573085 Haemophilus influenzae Rd 71421 -11537794 6500733936 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0131 HI0131 Haemophilus influenzae 727 -11537794

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888908	15479	37635	474	157

Description

GTC ORF with score 113 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888909	15480	37636	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888911	15481	37637	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888922	15482	37638	279	92

Description

5000695363 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0134 HI0134 Haemophilus influenzae 727 -11537795 108841 hi0134 (de:hypothetical protein hi0134) (db:swissprot) Y134_HAEIN P43952 HAEMOPHILUS INFLUENZAE 727 -11537795 166289 hypothetical protein hi0134 (db:pir2.dat) F64002 F64002 Haemophilus influenzae 727 -11537795 7500894764 hi0134 h. influenzae predicted coding region hi0134 (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2748) (re:3923) (di:direct) U32699 U32699 g1573094 Haemophilus influenzae Rd 71421 -11537795 6500733937 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0134 HI0134 Haemophilus influenzae 727 -11537795

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888924	15483	37639	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888929	15484	37640	1077	358

Description

6500733938 hi0145:hin_143 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_143 HIN_143 Haemophilus influenzae 727 -11537796 4000708212 hi0145 (de:hypothetical protein hi0145) (db:swissprot) YHCJ_HAEIN P71340 HAEMOPHILUS INFLUENZAE 727 -11537796 7500936816 hi0145 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the complete genome.) (nt:similar to sp:p45426 pid:606162 gb:u00096) (le:5340) (re:6026) (di:complement) U32700 U32700 g1573101 Haemophilus influenzae Rd 71421 -11537796 5000695364 (de:(hin14311) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN14311 HIN14311 Haemophilus influenzae 727 10126674

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888931	15485	37641	687	228

Description

5000695365 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0149 HI0149 Haemophilus influenzae 727 -11537797 108882 hi0149 (de:hypothetical protein hi0149 precursor) (db:swissprot) Y149_HAEIN P43953 HAEMOPHILUS INFLUENZAE 727 -11537797 166296 hypothetical protein hi0149 (db:pir2.dat) G64002 G64002 Haemophilus influenzae 727 -11537797 7500894795 hi0149 h. influenzae predicted coding region hi0149 (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:332) (re:523) (di:direct) U32701 U32701 g1573106 Haemophilus influenzae Rd 71421 -11537797 6500733939 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0149 HI0149 Haemophilus influenzae 727 -11537797

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888934	15486	37642	321	106

Description

5000695366 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0152 HI0152 Haemophilus influenzae 727 -11537798 108896 hi0152 (de:hypothetical protein hi0152) (db:swissprot) Y152_HAEIN P43954 HAEMOPHILUS INFLUENZAE 727 -11537798 166297 hypothetical protein hi0152 (db:pir2.dat) H64002 H64002 Haemophilus influenzae 727 -11537798 7500894798 hi0152 h. influenzae predicted coding region hi0152 (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2795) (re:3502) (di:complement) U32701 U32701 g1573109 Haemophilus influenzae Rd 71421 -11537798 6500733940 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0152 HI0152 Haemophilus influenzae 727 -11537798

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888938	15487	37643	804	267

Description

5000695367 nadh:ubiquinone oxidoreducatase subunit a:gp:z37111_2 (gtcfc:9.12) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0164 HI0164 Haemophilus influenzae 727 -11537799 108909 hi0164/165 (de:hypothetical protein hi0164/165) (db:swissprot) Y164_HAEIN P43955 HAEMOPHILUS INFLUENZAE 727 -11537799 7500894810 hi0164 nadh:ubiquinone oxidoreducatase subunit a:na (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to pid:663269 pid:663270 percent identity:) (le:2966) (re:4309) (di:direct) U32702 U32702 g1573122 Haemophilus influenzae Rd 71421 -11537799 6500733941 nadh:ubiquinone oxidoreducatase subunit a:gp:z37111_2 (gtcfc:9.12) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0164 HI0164 Haemophilus influenzae 727 -11537799

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888943	15488	37644	183	60

Description

5000695368 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0167 HI0167 Haemophilus influenzae 727 -11537800 108912 hi0167 (de:hypothetical protein hi0167) (db:swissprot) Y167_HAEIN P43957 HAEMOPHILUS INFLUENZAE 727 -11537800 166301 hypothetical protein hi0167 (db:pir2.dat) B64003 B64003 Haemophilus influenzae 727 -11537800 7500894811 hi0167 nadh:ubiquinone oxidoreductase:na (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to pid:663269 pid:663272 pid:893413 percent) (le:5540) (re:6274) (di:direct) U32702 U32702 g1573124 Haemophilus influenzae Rd 71421 -11537800 6500733942 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0167 HI0167 Haemophilus influenzae 727 -11537800

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888952	15489	37645	504	167

Description

5000695369 nadh:ubiquinone oxidoreductase:gp:z37111_5 (gtcfc:9.12) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0168 HI0168 Haemophilus influenzae 727 -11537801 108914 hi0168/169 (de:hypothetical protein hi0168/169) (db:swissprot) Y168_HAEIN P43958 HAEMOPHILUS INFLUENZAE 727 -11537801 7500894812 hi0168 nadh:ubiquinone oxidoreductase:na (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to pid:663269 pid:663273 pid:893414 percent) (le:6274) (re:6900) (di:direct) U32702 U32702 g1573125 Haemophilus influenzae Rd 71421 -11537801 6500733943 nadh:ubiquinone oxidoreductase:gp:z37111_5 (gtcfc:9.12) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0168 HI0168 Haemophilus influenzae 727 -11537801

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888972	15490	37646	2601	867

Description

6500733944 hi0170:hin_166 nadh:ubiquinone oxidoreductase:gb:z37111_6 (gtcfc:9.12) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_166 HIN_166 Haemophilus influenzae 727 -11537802 7500976241 hi0170 nadh:ubiquinone oxidoreductase:na (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to pid:893416 pid:893415 percent identity:) (le:6904) (re:7500) (di:direct) U32702 U32702 g1573126 Haemophilus influenzae Rd 71421 -11537802 5000695370 (de:(hin16611) (pn:nadh:ubiquinone oxidoreductase:gb:z37111_6) (gn:hi0170) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN16611 HIN16611 Haemophilus influenzae 727 10126677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888973	15491	37647	471	156

Description

5000695371 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0173 HI0173 Haemophilus influenzae 727 -11537803 108940 hi0173 (de:hypothetical protein hi0173) (db:swissprot) Y173_HAEIN P43960 HAEMOPHILUS INFLUENZAE 727 -11537803 166305 hypothetical protein hi0173 (db:pir2.dat) E64003 E64003 Haemophilus influenzae 727 -11537803 7500894818 hi0173 h. influenzae predicted coding region hi0173 (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9935) (re:10195) (di:direct) U32702 U32702 g1573132 Haemophilus influenzae Rd 71421 -11537803 6500733945 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0173 HI0173 Haemophilus influenzae 727 -11537803

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501888982	15492	37648	1518	505

Description

5000695372 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0178 HI0178 Haemophilus influenzae 727 -11537804 108943 hi0178 (de:hypothetical protein hi0178 precursor) (db:swissprot) Y178_HAEIN P43961 HAEMOPHILUS INFLUENZAE 727 -11537804 166310 hypothetical protein hi0178 (db:pir2.dat) F64003 F64003 Haemophilus influenzae 727 -11537804 7500894824 hi0178 h. influenzae predicted coding region hi0178 (db:genpept-bct1) (de:haemophilus influenzae rd section 18 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:952) (re:1434) (di:complement) U32703 U32703 g1573142 Haemophilus influenzae Rd 71421 -11537804 6500733946 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0178 HI0178 Haemophilus influenzae 727 -11537804

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889005	15493	37649	1857	618

Description

5000695373 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0182 HI0182 Haemophilus influenzae 727 -11537805 109809 hi0182 (de:hypothetical protein hi0182) (db:swissprot) YAJF_HAEIN P44554 HAEMOPHILUS INFLUENZAE 727 -11537805 166311 hypothetical protein hi0182 (cl:conserved hypothetical protein hi0182:glucose kinase homology) (db:pir2.dat) H64144 H64144 Haemophilus influenzae 727 -11537805 7500896232 hi0182 sugar kinase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 18 of 163 of the complete genome.) (nt:similar to gb:x65932 sp:p40184 pid:46851 percent) (le:6014) (re:6955) (di:direct) U32703 U32703 g1573138 Haemophilus influenzae Rd 71421 -11537805 6500733947 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0182 HI0182 Haemophilus influenzae 727 -11537805

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889006	15494	37650	525	175

Description

5000695374 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0184 HI0184 Haemophilus influenzae 727 -11537806 109787 hi0184 (de:hypothetical protein hi1084) (db:swissprot) YAIM_HAEIN P44556 HAEMOPHILUS INFLUENZAE 727 -11537806 166313 hypothetical protein hi0184 (cl:conserved hypothetical protein yjl068c) (db:pir2.dat) A64145 A64145 Haemophilus influenzae 727 -11537806 7500896203 hi0184 esterase (db:genpept-bct1) (de:haemophilus influenzae rd section 18 of 163 of the complete genome.) (nt:similar to sp:p10768 percent identity: 54.64;) (le:8764) (re:9591) (di:complement) U32703 U32703 g1573140 Haemophilus influenzae Rd 71421 -11537806 6500733948 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0184 HI0184 Haemophilus influenzae 727 -11537806

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889007	15495	37651	1077	358

Description

6500733949 hi0195:hin_191 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_191 HIN_191 Haemophilus influenzae 727 -11537807 121744 hi0195.1 (de:hypothetical protein hi0195.1 precursor) (db:swissprot) YJEP_HAEIN Q57362 HAEMOPHILUS INFLUENZAE 727 -11537807 7500937968 hi0195.1 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 19 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77338 pid:1707458) (le:8031) (re:11366) (di:direct) U32704 U32704 g1573153 Haemophilus influenzae Rd 71421 -11537807 5000695375 (de:(hin19111) (pn:hypothetical) (gn:hi0195) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN19111 HIN19111 Haemophilus influenzae 727 10065212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889014	15496	37652	663	220

Description

5000695376 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0195 HI0195 Haemophilus influenzae 727 -11537808 108967 hi0195 (de:hypothetical protein hi0195) (db:swissprot) Y195_HAEIN P43962 HAEMOPHILUS INFLUENZAE 727 -11537808 166316 hypothetical protein hi0195 (db:pir2.dat) G64003 G64003 Haemophilus influenzae 727 -11537808 6500733950 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0195 HI0195 Haemophilus influenzae 727 -11537808

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889027	15497	37653	2631	876

Description

5000695377 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0205 HI0205 Haemophilus influenzae 727 -11537809 108975 hi0205 (de:hypothetical protein hi0205 precursor) (db:swissprot) Y205_HAEIN P43963 HAEMOPHILUS INFLUENZAE 727 -11537809 166318 hypothetical protein hi0205 (db:pir2.dat) H64003 H64003 Haemophilus influenzae 727 -11537809 7500894878 hi0205 h. influenzae predicted coding region hi0205 (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6206) (re:6979) (di:direct) U32705 U32705 g1573169 Haemophilus influenzae Rd 71421 -11537809 6500733951 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0205 HI0205 Haemophilus influenzae 727 -11537809

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889028	15498	37654	1863	620

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889030	15499	37655	1359	453

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889034	15500	37656	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889047	15501	37657	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889049	15502	37658	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889059	15503	37659	240	79

Description

5000695378 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0210 HI0210 Haemophilus influenzae 727 -11537810 108982 hi0210 (de:hypothetical protein hi0210) (db:swissprot) Y210_HAEIN P43964 HAEMOPHILUS INFLUENZAE 727 -11537810 166319 hypothetical protein hi0210 (db:pir2.dat) I64003 I64003 Haemophilus influenzae 727 -11537810 7500894884 hi0210 h. influenzae predicted coding region hi0210 (db:genpept-bct1) (de:haemophilus influenzae rd section 21 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:518) (re:625) (di:direct) U32706 U32706 g1573177 Haemophilus influenzae Rd 71421 -11537810 6500733952 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0210 HI0210 Haemophilus influenzae 727 -11537810

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889067	15504	37660	366	121

Description

GTC ORF with score 191 to: (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889073	15505	37661	288	95

Description

GTC ORF with score 110 to: (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889080	15506	37662	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889081	15507	37663	414	137

Description

5000695379 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0217 HI0217 Haemophilus influenzae 727 -11537811 108988 hi0217 (de:hypothetical protein hi0217) (db:swissprot) YAFM_HAEIN P43965 HAEMOPHILUS INFLUENZAE 727 -11537811 166320 hypothetical protein hi0217 (cl:hypothetical protein hi0217) (db:pir2.dat) A64004 A64004 Haemophilus influenzae 727 -11537811 7500896131 hi0217 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 21 of 163 of the complete genome.) (nt:similar to pid:984584 gb:u00096 sp:q47152) (le:9593) (re:10123) (di:direct) U32706 U32706 g1573176 Haemophilus influenzae Rd 71421 -11537811 6500733953 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0217 HI0217 Haemophilus influenzae 727 -11537811

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889082	15508	37664	333	110

Description

5000695380 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0228 HI0228 Haemophilus influenzae 727 -11537812 109000 hi0228 (de:hypothetical protein hi0228) (db:swissprot) Y228_HAEIN P43966 HAEMOPHILUS INFLUENZAE 727 -11537812 166323 hypothetical protein hi0228 (db:pir2.dat) B64004 B64004 Haemophilus influenzae 727 -11537812 7500894918 hi0228 h. influenzae predicted coding region hi0228 (db:genpept-bct1) (de:haemophilus influenzae rd section 24 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2085) (re:2459) (di:complement) U32709 U32709 g1573197 Haemophilus influenzae Rd 71421 -11537812 6500733954 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0228 HI0228 Haemophilus influenzae 727 -11537812

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889089	15509	37665	396	131

Description

5000695381 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0233 HI0233 Haemophilus influenzae 727 -11537813 109002 hi0233 (de:hypothetical protein hi0233) (db:swissprot) Y233_HAEIN P43967 HAEMOPHILUS INFLUENZAE 727 -11537813 166326 hypothetical protein hi0233 (db:pir2.dat) C64004 C64004 Haemophilus influenzae 727 -11537813 7500894932 hi0233 h. influenzae predicted coding region hi0233 (db:genpept-bct1) (de:haemophilus influenzae rd section 24 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9446) (re:9598) (di:direct) U32709 U32709 g1573198 Haemophilus influenzae Rd 71421 -11537813 6500733955 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0233 HI0233 Haemophilus influenzae 727 -11537813

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889091	15510	37666	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889093	15511	37667	399	133

Description

5000695382 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0234 HI0234 Haemophilus influenzae 727 -11537814 109004 hi0234 (de:hypothetical protein hi0234) (db:swissprot) Y234_HAEIN P43968 HAEMOPHILUS INFLUENZAE 727 -11537814 166327 hypothetical protein hi0234 (db:pir2.dat) D64004 D64004 Haemophilus influenzae 727 -11537814 7500894935 hi0234 h. influenzae predicted coding region hi0234 (db:genpept-bct1) (de:haemophilus influenzae rd section 24 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9732) (re:9878) (di:complement) U32709 U32709 g1573199 Haemophilus influenzae Rd 71421 -11537814 6500733956 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0234 HI0234 Haemophilus influenzae 727 -11537814

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889096	15512	37668	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889098	15513	37669	312	103

Description

5000695383 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0237 HI0237 Haemophilus influenzae 727 -11537815 166329 hypothetical protein hi0237 (db:pir2.dat) E64004 E64004 Haemophilus influenzae 727 -11537815 6500733957 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0237 HI0237 Haemophilus influenzae 727 -11537815

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889099	15514	37670	312	103

Description

5000695384 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0238 HI0238 Haemophilus influenzae 727 -11537816 166330 hypothetical protein hi0238 (db:pir2.dat) F64004 F64004 Haemophilus influenzae 727 -11537816 6500733958 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0238 HI0238 Haemophilus influenzae 727 -11537816 109008 y238_haein (de:hypothetical protein hi0238.) P43970 P43970 Haemophilus influenzae 727 -11537816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889120	15515	37671	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889122	15516	37672	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889134	15517	37673	654	217

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889135	15518	37674	672	223

Description

5000695385 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0243 HI0243 Haemophilus influenzae 727 -11537817 109013 hi0243 (de:hypothetical protein hi0243) (db:swissprot) Y243_HAEIN P43971 HAEMOPHILUS INFLUENZAE 727 -11537817 166333 hypothetical protein hi0243 (db:pir2.dat) G64004 G64004 Haemophilus influenzae 727 -11537817 7500894950 hi0243 h. influenzae predicted coding region hi0243 (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5527) (re:6045) (di:complement) U32710 U32710 g1573208 Haemophilus influenzae Rd 71421 -11537817 6500733959 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0243 HI0243 Haemophilus influenzae 727 -11537817

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889147	15519	37675	297	98

Description

5000695386 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0246 HI0246 Haemophilus influenzae 727 -11537818 109017 hi0246 (de:hypothetical protein hi0246 precursor) (db:swissprot) Y246_HAEIN P43972 HAEMOPHILUS INFLUENZAE 727 -11537818 166334 hypothetical protein hi0246 (db:pir2.dat) H64004 H64004 Haemophilus influenzae 727 -11537818 7500894959 hi0246 h. influenzae predicted coding region hi0246 (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8817) (re:9263) (di:complement) U32710 U32710 g1573213 Haemophilus influenzae Rd 71421 -11537818 6500733960 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0246 HI0246 Haemophilus influenzae 727 -11537818

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889148	15520	37676	663	220

Description

6500733961 hi0257:hin_254 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_254 HIN_254 Haemophilus influenzae 727 -11537819 7500976246 hi0257 sigma 54 modulation protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to sp:p17160 gb:x05888 gb:x16334 pid:39270) (le:8140) (re:8463) (di:direct) U32711 U32711 g1573223 Haemophilus influenzae Rd 71421 -11537819 5000695387 (de:(hin25411) (pn:hypothetical) (gn:hi0257) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN25411 HIN25411 Haemophilus influenzae 727 10126679

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889149	15521	37677	312	103

Description

5000695388 glycosyl transferase lgtc:gp:u14554_4 (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0258 HI0258 Haemophilus influenzae 727 -11537820 109030 hi0258/259 (de:hypothetical protein hi0258/259) (db:swissprot) Y258_HAEIN P43974 HAEMOPHILUS INFLUENZAE 727 -11537820 7500894983 hi0258 glycosyl transferase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the complete genome.) (nt:similar to pid:1857120 percent identity: 38.06;) (le:9192) (re:10184) (di:complement) U32711 U32711 g1573224 Haemophilus influenzae Rd 71421 -11537820 6500733962 glycosyl transferase lgtc:gp:u14554_4 (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0258 HI0258 Haemophilus influenzae 727 -11537820

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889169	15522	37678	1467	488

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889171	15523	37679	333	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889179	15524	37680	621	206

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889190	15525	37681	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889195	15526	37682	2370	789

Description

5000695389 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0275 HI0275 Haemophilus influenzae 727 -11537821 109040 hi0275 (de:hypothetical protein hi0275) (db:swissprot) Y275_HAEIN P43975 HAEMOPHILUS INFLUENZAE 727 -11537821 166342 hypothetical protein hi0275 (db:pir2.dat) B64005 B64005 Haemophilus influenzae 727 -11537821 7500895047 hi0275 h. influenzae predicted coding region hi0275 (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:94) (re:1749) (di:direct) U32714 U32714 g1573251 Haemophilus influenzae Rd 71421 -11537821 6500733963 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0275 HI0275 Haemophilus influenzae 727 -11537821

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889197	15527	37683	954	317

Description

5000695390 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0278 HI0278 Haemophilus influenzae 727 -11537822 166345 hypothetical protein hi0278 (cl:hypothetical protein hi0278) (db:pir2.dat) C64005 C64005 Haemophilus influenzae 727 -11537822 7500955827 hi0278 h. influenzae predicted coding region hi0278 (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3063) (re:3479) (di:complement) U32714 U32714 g1573244 Haemophilus influenzae Rd 71421 -11537822 6500733964 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0278 HI0278 Haemophilus influenzae 727 -11537822

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889220	15528	37684	273	90

Description

5000695391 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0279 HI0279 Haemophilus influenzae 727 -11537823 109041 hi0279 (de:hypothetical protein hi0279) (db:swissprot) Y279_HAEIN P43977 HAEMOPHILUS INFLUENZAE 727 -11537823 166346 hypothetical protein hi0279 (db:pir2.dat) D64005 D64005 Haemophilus influenzae 727 -11537823 7500895056 hi0279 h. influenzae predicted coding region hi0279 (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3430) (re:3726) (di:complement) U32714 U32714 g1573252 Haemophilus influenzae Rd 71421 -11537823 6500733965 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0279 HI0279 Haemophilus influenzae 727 -11537823

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889225	15529	37685	2178	725

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889247	15530	37686	606	201

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889248	15531	37687	792	264

Description

5000695392 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0284 HI0284 Haemophilus influenzae 727 -11537824 109047 hi0284 (de:hypothetical protein hi0284) (db:swissprot) Y284_HAEIN P43978 HAEMOPHILUS INFLUENZAE 727 -11537824 166349 hypothetical protein hi0284 (db:pir2.dat) E64005 E64005 Haemophilus influenzae 727 -11537824 6500733966 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0284 HI0284 Haemophilus influenzae 727 -11537824

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889255	15532	37688	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889262	15533	37689	459	152

Description

6500733967 hi0286:hin_281 aspartate aminotransferase:aspc (gtcfc:5.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_281 HIN_281 Haemophilus influenzae 727 -11537825 7500976248 hi0286 aminotransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:similar to pid:2276334 percent identity: 59.65;) (le:10271) (re:11485) (di:direct) U32714 U32714 g1573250 Haemophilus influenzae Rd 71421 -11537825 5000695393 (de:(hin28111) (pn:aspartate aminotransferase:aspc) (gn:hi0286) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN28111 HIN28111 Haemophilus influenzae 727 10126681

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889263	15534	37690	1572	523

Description

GTC ORF with score 188 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889268	15535	37691	1014	337

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889285	15536	37692	279	92

Description

6500733968 hi0288:hin_283 l-serine deaminase:sdaa (gtcfc:5.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_283 HIN_283 Haemophilus influenzae 727 -11537826 5500685961 sdaa:hi0288 (ec:4.2.1.13) (de:l-serine dehydratase, (l-serine deaminase) (sdh) (l-sd)) (db:swissprot) SDHL_HAEIN P71349 HAEMOPHILUS INFLUENZAE 727 -11537826 7500891422 hi0288 l-serine deaminase sdaa (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:m28695 sp:p16095 pid:290464 gb:u00096) (le:1454) (re:2821) (di:complement) U32715 U32715 g1573256 Haemophilus influenzae Rd 71421 -11537826 5000695394 (de:(hin28311) (pn:l-serine deaminase:sdaa) (gn:hi0288) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN28311 HIN28311 Haemophilus influenzae 727 10126682

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889286	15537	37693	897	298

Description

6500733969 hi0290:hin_285 potassium/copper-transporting atpase a:copa (gtcfc:12.6) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_285 HIN_285 Haemophilus influenzae 727 -11537827 4000707593 hi0290 (ec:3.6.1.-) (de:probable cation-transporting atpase hi0290,) (db:swissprot) Y290_HAEIN P77868 HAEMOPHILUS INFLUENZAE 727 -11537827 7500895079 hi0290 potassium/copper-transporting atpase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:al009126 percent identity: 39.57;) (le:4317) (re:6485) (di:complement) U32715 U32715 g1573258 Haemophilus influenzae Rd 71421 -11537827 5000695395 (de:(hin28511) (pn:potassium) (gn:hi0290) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN28511 HIN28511 Haemophilus influenzae 727 10126683

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889287	15538	37694	1110	369

Description

5000695396 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0291 HI0291 Haemophilus influenzae 727 -11537828 109055 hi0291 (de:hypothetical protein hi0291) (db:swissprot) Y291_HAEIN P43979 HAEMOPHILUS INFLUENZAE 727 -11537828 166350 probable mercuric ion-binding protein hi0291:periplasmic mercuric ion-binding protein merp homolog (cl:mercuric resistance operon regulatory protein:heavy-metal-associated homology) (db:pir1.dat) F64005 F64005 Haemophilus influenzae 727 -11537828 7500895080 hi0291 h. influenzae predicted coding region hi0291 (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6460) (re:6666) (di:complement) U32715 U32715 g1573259 Haemophilus influenzae Rd 71421 -11537828 6500733970 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0291 HI0291 Haemophilus influenzae 727 -11537828

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889293	15539	37695	1677	558

Description

6500733971 ppdd:hi0299 prepilin peptidase dependent protein d homolog precursor (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0299 HI0299 Haemophilus influenzae 727 -11537829 90764 ppdd:hi0299 (de:prepilin peptidase dependent protein d homolog precursor) (db:swissprot) PPDD_HAEIN P44623 HAEMOPHILUS INFLUENZAE 727 -11537829 166351 hypothetical protein hi0299 (cl:gonococcal fimbrial protein) (db:pir2.dat) C64147 C64147 Haemophilus influenzae 727 -11537829 7500888358 hi0299 prepilin peptidase dependent protein d (db:genpept-bct1) (de:haemophilus influenzae rd section 30 of 163 of the complete genome.) (nt:similar to gb:d26562 sp:p36647 gb:128105 pid:473777) (le:12601) (re:13050) (di:complement) U32715 U32715 g1573267 Haemophilus influenzae Rd 71421 -11537829 5000695397 (de:(hi0299) (pn:prepilin peptidase dependent protein d homolog precursor) (gn:ppdd) (gtcfc:13.7) (ec:) (ppdd_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0299 HI0299 Haemophilus influenzae 727 10032879

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889295	15540	37696	342	114

Description

5000695398 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0304 HI0304 Haemophilus influenzae 727 -11537830 115899 hi0304 (de:hypothetical protein hi0304) (db:swissprot) YQGE_HAEIN P43980 HAEMOPHILUS INFLUENZAE 727 -11537830 166353 hypothetical protein hi0304 (cl:hypothetical protein hi0304) (db:pir2.dat) G64005 G64005 Haemophilus influenzae 727 -11537830 7500952442 hi0304 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to pid:882477 sp:p52049 gb:u00096) (le:4510) (re:5070) (di:direct) U32716 U32716 g1573273 Haemophilus influenzae Rd 71421 -11537830 6500733972 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0304 HI0304 Haemophilus influenzae 727 -11537830

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889296	15541	37697	759	252

Description

5000695399 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0305 HI0305 Haemophilus influenzae 727 -11537831 115902 hi0305 (de:hypothetical protein hi0305) (db:swissprot) YQGF_HAEIN P43981 HAEMOPHILUS INFLUENZAE 727 -11537831 166354 conserved hypothetical protein hi0305 (cl:haemophilus influenzae conserved hypothetical protein hi0305) (db:pir2.dat) H64005 H64005 Haemophilus influenzae 727 -11537831 7500952445 hi0305 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to pid:882478 sp:p52050 gb:u00096) (le:5070) (re:5489) (di:direct) U32716 U32716 g1573274 Haemophilus influenzae Rd 71421 -11537831 6500733973 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0305 HI0305 Haemophilus influenzae 727 -11537831

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889297	15542	37698	1083	360

Description

5000695400 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0311 HI0311 Haemophilus influenzae 727 -11537832 109072 hi0311 (de:hypothetical protein hi0311) (db:swissprot) Y311_HAEIN P43983 HAEMOPHILUS INFLUENZAE 727 -11537832 166358 hypothetical protein hi0311 (db:pir2.dat) A64006 A64006 Haemophilus influenzae 727 -11537832 6500733974 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0311 HI0311 Haemophilus influenzae 727 -11537832

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889298	15543	37699	429	142

Description

5000695401 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0310 HI0310 Haemophilus influenzae 727 -11537833 109071 hi0310 (de:hypothetical protein hi0310 precursor) (db:swissprot) Y310_HAEIN P43982 HAEMOPHILUS INFLUENZAE 727 -11537833 166357 hypothetical protein hi0310 (db:pir2.dat) I64005 I64005 Haemophilus influenzae 727 -11537833 7500895106 hi0310 h. influenzae predicted coding region hi0310 (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9591) (re:9878) (di:direct) U32716 U32716 g1573281 Haemophilus influenzae Rd 71421 -11537833 6500733975 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0310 HI0310 Haemophilus influenzae 727 -11537833

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889311	15544	37700	1722	573

Description

5000695402 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0318 HI0318 Haemophilus influenzae 727 -11537834 109075 hi0318 (de:hypothetical protein hi0318) (db:swissprot) Y318_HAEIN P43984 HAEMOPHILUS INFLUENZAE 727 -11537834 166361 hypothetical protein hi0318 (db:pir2.dat) B64006 B64006 Haemophilus influenzae 727 -11537834 7500895116 hi0318 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to sp:p54158 pid:1256620 gb:al009126) (le:4064) (re:4582) (di:direct) U32717 U32717 g1573288 Haemophilus influenzae Rd 71421 -11537834 6500733976 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0318 HI0318 Haemophilus influenzae 727 -11537834

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889312	15545	37701	807	268

Description

5000695403 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0319 HI0319 Haemophilus influenzae 727 -11537835 109076 hi0319/320 (de:hypothetical protein hi0319/320) (db:swissprot) YECO_HAEIN P43985 HAEMOPHILUS INFLUENZAE 727 -11537835 166362 hypothetical protein hi0319 (cl:conserved hypothetical protein hi0319) (db:pir2.dat) C64006 C64006 Haemophilus influenzae 727 -11537835 7500922949 hi0319 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788177 percent identity:) (le:4635) (re:5360) (di:direct) U32717 U32717 g1573289 Haemophilus influenzae Rd 71421 -11537835 6500733977 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0319 HI0319 Haemophilus influenzae 727 -11537835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889313	15546	37702	813	270

Description

5000695404 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0320 HI0320 Haemophilus influenzae 727 -11537836 6500733978 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0320 HI0320 Haemophilus influenzae 727 -11537836 109080 y320_haein (de:hypothetical protein hi0320.) P43986 P43986 Haemophilus influenzae 727 -11537836

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889314	15547	37703	417	138

Description

5000695405 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0326 HI0326 Haemophilus influenzae 727 -11537837 109087 hi0326 (de:hypothetical protein hi0326) (db:swissprot) Y326_HAEIN P43987 HAEMOPHILUS INFLUENZAE 727 -11537837 166365 hypothetical protein hi0326 (db:pir2.dat) E64006 E64006 Haemophilus influenzae 727 -11537837 7500895130 hi0326 h. influenzae predicted coding region hi0326 (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9027) (re:9290) (di:direct) U32717 U32717 g1573298 Haemophilus influenzae Rd 71421 -11537837 6500733979 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0326 HI0326 Haemophilus influenzae 727 -11537837

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889315	15548	37704	888	295

Description

6500733980 napb:hi0347 cytochrome c-type protein precursor (gtcfc:2.8) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0347 HI0347 Haemophilus influenzae 727 -11537838 85222 napb:hi0347 (de:cytochrome c-type protein napb precursor) (db:swissprot) NAPB_HAEIN P44654 HAEMOPHILUS INFLUENZAE 727 -11537838 167107 cytochrome c-type protein napb homolog:hypothetical protein hi0347 (cl:cytochrome c-type protein napb) (db:pir2.dat) C64149 C64149 Haemophilus influenzae 727 -11537838 7500886289 hi0347 periplasmic nitrate reductase napb (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p33933 pid:405928 gb:u00096) (le:6525) (re:6977) (di:direct) U32719 U32719 g1573317 Haemophilus influenzae Rd 71421 -11537838 5000695406 (de:(hi0347) (pn:cytochrome c-type protein precursor) (gn:napb) (gtcfc:13.7) (ec:) (napb_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0347 HI0347 Haemophilus influenzae 727 10027403

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889324	15549	37705	609	202

Description

5000695407 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0366 HI0366 Haemophilus influenzae 727 -11537839 109118 hi0366 (de:hypothetical protein hi0366 precursor) (db:swissprot) Y366_HAEIN P43988 HAEMOPHILUS INFLUENZAE 727 -11537839 166382 hypothetical protein hi0366 (cl:hypothetical protein hi0366:tetratricopeptide repeat homology) (db:pir2.dat) F64006 F64006 Haemophilus influenzae 727 -11537839 7500895194 hi0366 fimbrial biogenesis and twitching motility (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to pid:1162960 percent identity: 33.59;) (le:81) (re:620) (di:direct) U32721 U32721 g1573335 Haemophilus influenzae Rd 71421 -11537839 6500733981 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0366 HI0366 Haemophilus influenzae 727 -11537839

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889348	15550	37706	348	115

Description

5000695408 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0370 HI0370 Haemophilus influenzae 727 -11537840 109122 hi0370 (de:hypothetical protein hi0370) (db:swissprot) Y370_HAEIN P43989 HAEMOPHILUS INFLUENZAE 727 -11537840 166384 hypothetical protein hi0370 (cl:hypothetical protein hi0370) (db:pir2.dat) G64006 G64006 Haemophilus influenzae 727 -11537840 7500895200 hi0370 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788860 percent identity:) (le:4017) (re:4631) (di:direct) U32721 U32721 g1573339 Haemophilus influenzae Rd 71421 -11537840 6500733982 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0370 HI0370 Haemophilus influenzae 727 -11537840

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889356	15551	37707	354	117

Description

5000695409 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0388 HI0388 Haemophilus influenzae 727 -11537841 109134 hi0388 (de:hypothetical protein hi0388 precursor) (db:swissprot) YEAZ_HAEIN P43990 HAEMOPHILUS INFLUENZAE 727 -11537841 166391 hypothetical protein hi0388 (cl:hypothetical protein hi0388) (db:pir2.dat) H64006 H64006 Haemophilus influenzae 727 -11537841 7500922896 hi0388 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p76256 pid:1736440) (le:8541) (re:9251) (di:direct) U32722 U32722 g1573358 Haemophilus influenzae Rd 71421 -11537841 6500733983 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0388 HI0388 Haemophilus influenzae 727 -11537841

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889357	15552	37708	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889367	15553	37709	669	222

Description

GTC ORF with score 98 to: (db:genpept-bct2) (de:pseudomonas aeruginosa putative cytoplasmic membrane-associatedprotein, putative cytoplasmic membrane protein, and putative ecfsigma factor x (sigx) genes, complete cds; and major outer membraneprotein ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889368	15554	37710	2049	682

Description

GTC ORF with score 188 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k07e12.) (nt:similar to cell adhesion molecule, especially) (le:12633:12861:13021:13416) (re:12770:12976:13367:13647) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889372	15555	37711	618	205

Description

5000695410 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0389 HI0389 Haemophilus influenzae 727 -11537842 109136 hi0389 (de:hypothetical protein hi0389) (db:swissprot) Y389_HAEIN P43991 HAEMOPHILUS INFLUENZAE 727 -11537842 166392 hypothetical protein hi0389 (db:pir2.dat) I64006 I64006 Haemophilus influenzae 727 -11537842 7500895227 hi0389 outer membrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to gb:u00039 sp:p37194 gb:l23635 pid:387932) (le:9276) (re:9827) (di:direct) U32722 U32722 g1573359 Haemophilus influenzae Rd 71421 -11537842 6500733984 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0389 HI0389 Haemophilus influenzae 727 -11537842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889391	15556	37712	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889411	15557	37713	426	141

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889424	15558	37714	207	68

Description

5000695411 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0391 HI0391 Haemophilus influenzae 727 -11537843 109140 hi0391 (de:hypothetical protein hi0391) (db:swissprot) Y391_HAEIN P43992 HAEMOPHILUS INFLUENZAE 727 -11537843 166393 hypothetical protein hi0391 (db:pir2.dat) A64007 A64007 Haemophilus influenzae 727 -11537843 7500895232 hi0391 h. influenzae predicted coding region hi0391 (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12800) (re:13348) (di:complement) U32722 U32722 g1573362 Haemophilus influenzae Rd 71421 -11537843 6500733985 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0391 HI0391 Haemophilus influenzae 727 -11537843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889435	15559	37715	1512	503

Description

5000695412 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0392 HI0392 Haemophilus influenzae 727 -11537844 109141 hi0392 (de:hypothetical protein hi0392) (db:swissprot) Y392_HAEIN P43993 HAEMOPHILUS INFLUENZAE 727 -11537844 166394 hypothetical protein hi0392 (db:pir2.dat) B64007 B64007 Haemophilus influenzae 727 -11537844 7500895235 hi0392 o-antigen acetylase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to gp:1518853 percent ident: 31.46;) (le:275) (re:1012) (di:complement) U32723 U32723 g1573364 Haemophilus influenzae Rd 71421 -11537844 6500733986 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0392 HI0392 Haemophilus influenzae 727 -11537844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889444	15560	37716	366	121

Description

GTC ORF with score 101 to: (sr:saccharomyces cerevisiae cdna to mrna) (db:genpept-pln1) (de:saccharomyces cerevisiae antiviral protein ski2p (ski) mrna,complete cds.) (nt:with local similarity to fsn (fly) and ring3;) (le:184) (re:834) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889462	15561	37717	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889463	15562	37718	1689	562

Description

5000695413 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0395 HI0395 Haemophilus influenzae 727 -11537845 111975 hi0395 (de:hypothetical protein hi0395) (db:swissprot) YFJF_HAEIN P43994 HAEMOPHILUS INFLUENZAE 727 -11537845 166396 hypothetical protein hi0395 (db:pir2.dat) C64007 C64007 Haemophilus influenzae 727 -11537845 7500923547 hi0395 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to pid:1033114 sp:p52119 gb:u00096) (le:3086) (re:3394) (di:direct) U32723 U32723 g1573377 Haemophilus influenzae Rd 71421 -11537845 6500733987 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0395 HI0395 Haemophilus influenzae 727 -11537845

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889484	15563	37719	501	166

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889495	15564	37720	192	63

Description

5000695414 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0420 HI0420 Haemophilus influenzae 727 -11537846 109158 hi0420 (de:hypothetical protein hi0420) (db:swissprot) Y420_HAEIN P43995 HAEMOPHILUS INFLUENZAE 727 -11537846 166408 hypothetical protein hi0420 (db:pir2.dat) D64007 D64007 Haemophilus influenzae 727 -11537846 7500895268 hi0420 h. influenzae predicted coding region hi0420 (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5953) (re:6252) (di:direct) U32725 U32725 g1573397 Haemophilus influenzae Rd 71421 -11537846 6500733988 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0420 HI0420 Haemophilus influenzae 727 -11537846

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889500	15565	37721	792	263

Description

5000695415 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0421 HI0421 Haemophilus influenzae 727 -11537847 109159 hi0421 (de:hypothetical protein hi0421) (db:swissprot) Y421_HAEIN P43996 HAEMOPHILUS INFLUENZAE 727 -11537847 166409 hypothetical protein hi0421 (db:pir2.dat) E64007 E64007 Haemophilus influenzae 727 -11537847 7500895269 hi0421 h. influenzae predicted coding region hi0421 (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6432) (re:6596) (di:complement) U32725 U32725 g1573398 Haemophilus influenzae Rd 71421 -11537847 6500733989 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0421 HI0421 Haemophilus influenzae 727 -11537847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889518	15566	37722	1263	420

Description

5000695416 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0449 HI0449 Haemophilus influenzae 727 -11537848 109175 hi0449 (de:hypothetical protein hi0449 precursor) (db:swissprot) Y449_HAEIN P43997 HAEMOPHILUS INFLUENZAE 727 -11537848 166414 hypothetical protein hi0449 (db:pir2.dat) F64007 F64007 Haemophilus influenzae 727 -11537848 7500895314 hi0449 h. influenzae predicted coding region hi0449 (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:66) (re:602) (di:complement) U32728 U32728 g1573436 Haemophilus influenzae Rd 71421 -11537848 6500733990 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0449 HI0449 Haemophilus influenzae 727 -11537848

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889521	15567	37723	585	194

Description

5000695417 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0451 HI0451 Haemophilus influenzae 727 -11537849 109178 hi0451 (de:hypothetical protein hi0451) (db:swissprot) Y451_HAEIN P43998 HAEMOPHILUS INFLUENZAE 727 -11537849 166415 hypothetical protein hi0451 (db:pir2.dat) G64007 G64007 Haemophilus influenzae 727 -11537849 7500895321 hi0451 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to pid:1196479 percent ident: 56.67;) (le:973) (re:1164) (di:complement) U32728 U32728 g1573437 Haemophilus influenzae Rd 71421 -11537849 6500733991 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0451 HI0451 Haemophilus influenzae 727 -11537849

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889522	15568	37724	627	208

Description

GTC ORF with score 129 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889526	15569	37725	474	157

Description

5000695418 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0453 HI0453 Haemophilus influenzae 727 -11537850 109180 hi0453 (de:hypothetical protein hi0453) (db:swissprot) Y453_HAEIN P43999 HAEMOPHILUS INFLUENZAE 727 -11537850 166417 hypothetical protein hi0453 (cl:conserved hypothetical protein hi0453) (db:pir2.dat) H64007 H64007 Haemophilus influenzae 727 -11537850 7500895325 hi0453 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to gb:ae000511 pid:2313105 percent) (le:2585) (re:3109) (di:complement) U32728 U32728 g1573438 Haemophilus influenzae Rd 71421 -11537850 6500733992 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0453 HI0453 Haemophilus influenzae 727 -11537850

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889527	15570	37726	615	204

Description

5000695419 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0466 HI0466 Haemophilus influenzae 727 -11537851 109187 hi0466 (de:hypothetical protein hi0466) (db:swissprot) Y466_HAEIN P44000 HAEMOPHILUS INFLUENZAE 727 -11537851 166421 hypothetical protein hi0466 (db:pir2.dat) I64007 I64007 Haemophilus influenzae 727 -11537851 7500895344 hi0466 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 44 of 163 of the complete genome.) (nt:similar to pid:887848 gb:u00096 sp:p39179) (le:5903) (re:6745) (di:complement) U32729 U32729 g1573444 Haemophilus influenzae Rd 71421 -11537851 6500733993 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0466 HI0466 Haemophilus influenzae 727 -11537851

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889528	15571	37727	369	122

Description

5000695420 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0476 HI0476 Haemophilus influenzae 727 -11537852 109191 hi0476 (de:hypothetical protein hi0476) (db:swissprot) Y476_HAEIN P44002 HAEMOPHILUS INFLUENZAE 727 -11537852 166423 hypothetical protein hi0476 (db:pir2.dat) B64008 B64008 Haemophilus influenzae 727 -11537852 7500895349 hi0476 h. influenzae predicted coding region hi0476 (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5323) (re:5475) (di:direct) U32730 U32730 g1573464 Haemophilus influenzae Rd 71421 -11537852 6500733994 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0476 HI0476 Haemophilus influenzae 727 -11537852

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889544	15572	37728	951	316

Description

5000695421 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0487 HI0487 Haemophilus influenzae 727 -11537853 112791 hi0487 (de:hypothetical protein hi0487) (db:swissprot) YHFY_HAEIN P44003 HAEMOPHILUS INFLUENZAE 727 -11537853 166424 hypothetical protein hi0487 (db:pir2.dat) C64008 C64008 Haemophilus influenzae 727 -11537853 7500936911 hi0487 h. influenzae predicted coding region hi0487 (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:865) (re:1242) (di:complement) U32731 U32731 g1573467 Haemophilus influenzae Rd 71421 -11537853 6500733995 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0487 HI0487 Haemophilus influenzae 727 -11537853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889556	15573	37729	876	291

Description

5000695422 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0488 HI0488 Haemophilus influenzae 727 -11537854 109193 hi0488 (de:hypothetical protein hi0488) (db:swissprot) YQAB_HAEIN P44004 HAEMOPHILUS INFLUENZAE 727 -11537854 166425 hypothetical protein hi0488 (cl:hypothetical protein b2690) (db:pir2.dat) D64008 D64008 Haemophilus influenzae 727 -11537854 7500895354 hi0488 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1789046 percent ident:) (le:1358) (re:1960) (di:direct) U32731 U32731 g1573468 Haemophilus influenzae Rd 71421 -11537854 6500733996 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0488 HI0488 Haemophilus influenzae 727 -11537854

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889565	15574	37730	450	149

Description

5000695423 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0490 HI0490 Haemophilus influenzae 727 -11537855 109196 hi0490 (de:hypothetical protein hi0490) (db:swissprot) Y490_HAEIN P44006 HAEMOPHILUS INFLUENZAE 727 -11537855 166427 hypothetical protein hi0490 (db:pir2.dat) F64008 F64008 Haemophilus influenzae 727 -11537855 6500733997 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0490 HI0490 Haemophilus influenzae 727 -11537855

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889566	15575	37731	609	202

Description

5000695424 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0489 HI0489 Haemophilus influenzae 727 -11537856 109194 hi0489 (de:hypothetical protein hi0489) (db:swissprot) YQAA_HAEIN P44005 HAEMOPHILUS INFLUENZAE 727 -11537856 166426 hypothetical protein hi0489 (cl:hypothetical protein hi0489) (db:pir2.dat) E64008 E64008 Haemophilus influenzae 727 -11537856 7500895355 hi0489 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1789045 percent ident:) (le:1960) (re:2433) (di:direct) U32731 U32731 g1573469 Haemophilus influenzae Rd 71421 -11537856 6500733998 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0489 HI0489 Haemophilus influenzae 727 -11537856

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889572	15576	37732	414	137

Description

5000695425 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0491 HI0491 Haemophilus influenzae 727 -11537857 166428 hypothetical protein hi0491 (cl:conserved hypothetical protein hi0491) (db:pir2.dat) G64008 G64008 Haemophilus influenzae 727 -11537857 7500960668 hi0491 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to sp:p45578 gb:u00096 pid:1773215) (le:2763) (re:3266) (di:direct) U32731 U32731 g1573470 Haemophilus influenzae Rd 71421 -11537857 6500733999 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0491 HI0491 Haemophilus influenzae 727 -11537857

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889573	15577	37733	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889577	15578	37734	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889603	15579	37735	825	274

Description

5000695426 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0492 HI0492 Haemophilus influenzae 727 -11537858 109197 hi0492 (de:hypothetical protein hi0492) (db:swissprot) Y492_HAEIN P44008 HAEMOPHILUS INFLUENZAE 727 -11537858 166429 hypothetical protein hi0492 (db:pir2.dat) H64008 H64008 Haemophilus influenzae 727 -11537858 6500734000 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0492 HI0492 Haemophilus influenzae 727 -11537858

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889608	15580	37736	429	142

Description

5000695427 acid phosphatase (gtcfc:13.10) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0494 HI0494 Haemophilus influenzae 727 -11537859 166431 acid phosphatase homolog hi0494 (db:pir2.dat) E64153 E64153 Haemophilus influenzae 727 -11537859 7500960646 hi0494 acid phosphatase (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to sp:p32697 gb:x86971 pid:396390) (le:4212) (re:4706) (di:complement) U32731 U32731 g1573472 Haemophilus influenzae Rd 71421 -11537859 6500734001 acid phosphatase (gtcfc:13.10) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0494 HI0494 Haemophilus influenzae 727 -11537859

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889613	15581	37737	1851	616

Description

5000695428 acid phosphatase:gp:x86971_1 (gtcfc:13.10) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0495 HI0495 Haemophilus influenzae 727 -11537860 166432 acid phosphatase homolog hi0495 (db:pir2.dat) I64008 I64008 Haemophilus influenzae 727 -11537860 7500960647 hi0495 acid phosphatase gp:x86971_1 (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to sp:p32697 gb:x86971 pid:396390) (le:4720) (re:4920) (di:complement) U32731 U32731 g1573479 Haemophilus influenzae Rd 71421 -11537860 6500734002 acid phosphatase:gp:x86971_1 (gtcfc:13.10) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0495 HI0495 Haemophilus influenzae 727 -11537860

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889619	15582	37738	606	202

Description

5000695429 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0507 HI0507 Haemophilus influenzae 727 -11537861 115926 hi0507 (de:hypothetical protein hi0507) (db:swissprot) YQHA_HAEIN P44010 HAEMOPHILUS INFLUENZAE 727 -11537861 166434 hypothetical protein hi0507 (cl:conserved hypothetical protein hi0507) (db:pir2.dat) A64009 A64009 Haemophilus influenzae 727 -11537861 7500952467 hi0507 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to pid:882531 sp:p52082 gb:u00096) (le:7468) (re:8019) (di:direct) U32732 U32732 g1573488 Haemophilus influenzae Rd 71421 -11537861 6500734003 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0507 HI0507 Haemophilus influenzae 727 -11537861

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889621	15583	37739	621	207

Description

5000695430 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0523 HI0523 Haemophilus influenzae 727 -11537862 109203 hi0523 (de:hypothetical protein hi0523 precursor) (db:swissprot) Y523_HAEIN P44011 HAEMOPHILUS INFLUENZAE 727 -11537862 166442 hypothetical protein hi0523 (db:pir2.dat) B64009 B64009 Haemophilus influenzae 727 -11537862 7500895377 hi0523 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to gb:ae000511 pid:2314449 percent) (le:6835) (re:7905) (di:complement) U32734 U32734 g1573506 Haemophilus influenzae Rd 71421 -11537862 6500734004 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0523 HI0523 Haemophilus influenzae 727 -11537862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889628	15584	37740	597	199

Description

5000695431 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0526 HI0526 Haemophilus influenzae 727 -11537863 109204 hi0526 (de:probable ribonuclease hi0526 precursor) (db:swissprot) RN26_HAEIN P44012 HAEMOPHILUS INFLUENZAE 727 -11537863 139921 ribonuclease homolog hi0526 (cl:enterobacter ribonuclease) (db:pir2.dat) C64009 C64009 Haemophilus influenzae 727 -11537863 7500890431 hi0526 h. influenzae predicted coding region hi0526 (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:81) (re:899) (di:complement) U32735 U32735 g1573510 Haemophilus influenzae Rd 71421 -11537863 6500734005 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0526 HI0526 Haemophilus influenzae 727 -11537863

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889629	15585	37741	222	73

Description

6500734006 prib:hi0546 primosomal replication protein n (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0546 HI0546 Haemophilus influenzae 727 -11537864 91025 prib:hi0546 (de:primosomal replication protein n) (db:swissprot) PRIB_HAEIN P44748 HAEMOPHILUS INFLUENZAE 727 -11537864 7500888459 hi0546 primosomal replication protein n prib (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p07013 gb:x04022 pid:42846) (le:8551) (re:8835) (di:complement) U32736 U32736 g1573531 Haemophilus influenzae Rd 71421 -11537864 5000695432 (de:(hi0546) (pn:primosomal replication protein n) (gn:prib) (gtcfc:13.7) (ec:) (prib_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0546 HI0546 Haemophilus influenzae 727 10126688

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889639	15586	37742	741	246

Description

5000695433 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0552 HI0552 Haemophilus influenzae 727 -11537865 109209 hi0552 (de:hypothetical protein hi0552) (db:swissprot) Y552_HAEIN P44013 HAEMOPHILUS INFLUENZAE 727 -11537865 166443 hypothetical protein hi0552 (db:pir2.dat) D64009 D64009 Haemophilus influenzae 727 -11537865 7500895398 hi0552 h. influenzae predicted coding region hi0552 (db:genpept-bct1) (de:haemophilus influenzae rd section 52 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:927) (re:1550) (di:direct) U32737 U32737 g1573538 Haemophilus influenzae Rd 71421 -11537865 6500734007 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0552 HI0552 Haemophilus influenzae 727 -11537865

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889647	15587	37743	447	148

Description

5000695434 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0554 HI0554 Haemophilus influenzae 727 -11537866 109210 hi0554 (de:hypothetical protein hi0554) (db:swissprot) Y554_HAEIN P44014 HAEMOPHILUS INFLUENZAE 727 -11537866 166444 hypothetical protein hi0554 (db:pir2.dat) E64009 E64009 Haemophilus influenzae 727 -11537866 7500895401 hi0554 h. influenzae predicted coding region hi0554 (db:genpept-bct1) (de:haemophilus influenzae rd section 52 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3576) (re:4118) (di:complement) U32737 U32737 g1573540 Haemophilus influenzae Rd 71421 -11537866 6500734008 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0554 HI0554 Haemophilus influenzae 727 -11537866

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889652	15588	37744	624	207

Description

5000695435 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0557 HI0557 Haemophilus influenzae 727 -11537867 109212 hi0557 (de:hypothetical protein hi0557) (db:swissprot) Y557_HAEIN P44015 HAEMOPHILUS INFLUENZAE 727 -11537867 166446 hypothetical protein hi0557 (db:pir2.dat) F64009 F64009 Haemophilus influenzae 727 -11537867 7500895404 hi0557 h. influenzae predicted coding region hi0557 (db:genpept-bct1) (de:haemophilus influenzae rd section 52 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5059) (re:5181) (di:complement) U32737 U32737 g1573547 Haemophilus influenzae Rd 71421 -11537867 6500734009 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0557 HI0557 Haemophilus influenzae 727 -11537867

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889660	15589	37745	261	86

Description

5000695436 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0561 HI0561 Haemophilus influenzae 727 -11537868 109213 hi0561/560 (de:hypothetical protein hi0561/560) (db:swissprot) Y561_HAEIN P44016 HAEMOPHILUS INFLUENZAE 727 -11537868 7500895405 hi0561 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 52 of 163 of the complete genome.) (nt:similar to gp:1655665 percent ident: 43.93;) (le:8109) (re:10010) (di:complement) U32737 U32737 g1573546 Haemophilus influenzae Rd 71421 -11537868 6500734010 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0561 HI0561 Haemophilus influenzae 727 -11537868

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889663	15590	37746	651	216

Description

6500734011 hi0560:hin_552 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_552 HIN_552 Haemophilus influenzae 727 -11537869 5000695437 (de:(hin55211) (pn:hypothetical) (gn:hi0560) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN55211 HIN55211 Haemophilus influenzae 727 10126691

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889664	15591	37747	615	204

Description

6500734012 hi0568:hin_559 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_559 HIN_559 Haemophilus influenzae 727 -11537870 1500687419 hi0568 (de:hypothetical protein hi0568) (db:swissprot) YHGF_HAEIN P71353 HAEMOPHILUS INFLUENZAE 727 -11537870 7500936936 hi0568 transcription accessory protein tex (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to sp:q45388 pid:1477402 percent ident:) (le:6383) (re:8671) (di:complement) U32738 U32738 g1573555 Haemophilus influenzae Rd 71421 -11537870 5000695438 (de:(hin55911) (pn:hypothetical protein) (gn:hi0568) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN55911 HIN55911 Haemophilus influenzae 727 10064987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889667	15592	37748	732	243

Description

6500734013 hi0576:hin_568 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_568 HIN_568 Haemophilus influenzae 727 -11537871 5500686603 hi0576.1 (de:hypothetical protein hi0576.1) (db:swissprot) YHEM_HAEIN Q57194 HAEMOPHILUS INFLUENZAE 727 -11537871 7500936877 hi0576.1 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to sp:p45531 pid:606278 gb:u00096) (le:3080) (re:3439) (di:direct) U32739 U32739 g1573566 Haemophilus influenzae Rd 71421 -11537871 5000695439 (de:(hin56811) (pn:hypothetical protein) (gn:hi0576) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN56811 HIN56811 Haemophilus influenzae 727 10126692

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889676	15593	37749	921	306

Description

5000695440 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0577 HI0577 Haemophilus influenzae 727 -11537872 109216 hi0577 (de:hypothetical protein hi0577) (db:swissprot) Y577_HAEIN P44017 HAEMOPHILUS INFLUENZAE 727 -11537872 166455 hypothetical protein hi0577 (db:pir2.dat) H64009 H64009 Haemophilus influenzae 727 -11537872 7500895410 hi0577 h. influenzae predicted coding region hi0577 (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3448) (re:3735) (di:direct) U32739 U32739 g1573571 Haemophilus influenzae Rd 71421 -11537872 6500734014 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0577 HI0577 Haemophilus influenzae 727 -11537872

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889685	15594	37750	807	268

Description

5000695441 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0585 HI0585 Haemophilus influenzae 727 -11537873 109220 hi0585 (de:hypothetical protein hi0585) (db:swissprot) Y585_HAEIN P44018 HAEMOPHILUS INFLUENZAE 727 -11537873 166456 hypothetical protein hi0585 (db:pir2.dat) I64009 I64009 Haemophilus influenzae 727 -11537873 7500895414 hi0585 h. influenzae predicted coding region hi0585 (db:genpept-bct1) (de:haemophilus influenzae rd section 55 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3783) (re:4622) (di:complement) U32740 U32740 g1573575 Haemophilus influenzae Rd 71421 -11537873 6500734015 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0585 HI0585 Haemophilus influenzae 727 -11537873

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889694	15595	37751	765	255

Description

5000695442 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0586 HI0586 Haemophilus influenzae 727 -11537874 109221 hi0586 (de:hypothetical protein hi0586) (db:swissprot) Y586_HAEIN P44019 HAEMOPHILUS INFLUENZAE 727 -11537874 166457 hypothetical protein hi0586 (db:pir2.dat) A64010 A64010 Haemophilus influenzae 727 -11537874 7500895415 hi0586 h. influenzae predicted coding region hi0586 (db:genpept-bct1) (de:haemophilus influenzae rd section 55 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4640) (re:5077) (di:complement) U32740 U32740 g1573576 Haemophilus influenzae Rd 71421 -11537874 6500734016 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0586 HI0586 Haemophilus influenzae 727 -11537874

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889696	15596	37752	210	69

Description

5000695443 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0592 HI0592 Haemophilus influenzae 727 -11537875 109223 hi0592 (de:hypothetical protein hi0592) (db:swissprot) Y592_HAEIN P44021 HAEMOPHILUS INFLUENZAE 727 -11537875 166459 hypothetical protein hi0592 (db:pir2.dat) C64010 C64010 Haemophilus influenzae 727 -11537875 7500895421 hi0592 h. influenzae predicted coding region hi0592 (db:genpept-bct1) (de:haemophilus influenzae rd section 56 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:156) (re:350) (di:complement) U32741 U32741 g1573589 Haemophilus influenzae Rd 71421 -11537875 6500734017 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0592 HI0592 Haemophilus influenzae 727 -11537875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889700	15597	37753	207	68

Description

5000695444 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0594 HI0594 Haemophilus influenzae 727 -11537876 109225 hi0594 (de:hypothetical protein hi0594) (db:swissprot) YFCC_HAEIN P44023 HAEMOPHILUS INFLUENZAE 727 -11537876 166461 hypothetical protein hi0594 (cl:haemophilus influenzae conserved hypothetical protein hi0594) (db:pir2.dat) E64010 E64010 Haemophilus influenzae 727 -11537876 7500923367 hi0594 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 56 of 163 of the complete genome.) (nt:similar to gb:ae000783 percent ident: 35.02;) (le:891) (re:2420) (di:complement) U32741 U32741 g1573583 Haemophilus influenzae Rd 71421 -11537876 6500734018 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0594 HI0594 Haemophilus influenzae 727 -11537876

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889704	15598	37754	684	227

Description

5000695445 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0593 HI0593 Haemophilus influenzae 727 -11537877 109224 hi0593 (de:hypothetical protein hi0593) (db:swissprot) Y593_HAEIN P44022 HAEMOPHILUS INFLUENZAE 727 -11537877 166460 hypothetical protein hi0593 (db:pir2.dat) D64010 D64010 Haemophilus influenzae 727 -11537877 6500734019 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0593 HI0593 Haemophilus influenzae 727 -11537877

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889721	15599	37755	384	127

Description

GTC ORF with score 394 to: (gtcfc:12.16:12.5:12.6) (keggfc:14.2) (sgdfc:7.2.2:7.8.0:9.10.0) (db:gtc-saccharomyces cerevisiae) (gtcfc:cell processes-cellular organization-cytoskeleton/er/golgi/peroxisomal/endosomal/vacuolar-lysosomal: cell ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889736	15600	37756	330	109

Description

5000695446 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0598 HI0598 Haemophilus influenzae 727 -11537878 109226 hi0598 (de:hypothetical protein hi0598) (db:swissprot) Y598_HAEIN P44024 HAEMOPHILUS INFLUENZAE 727 -11537878 166463 hypothetical protein hi0598 (db:pir2.dat) F64010 F64010 Haemophilus influenzae 727 -11537878 6500734020 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0598 HI0598 Haemophilus influenzae 727 -11537878

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889740	15601	37757	1182	393

Description

5000695447 membrane-bound protein with four pro-ser-alarepeats (gtcfc:11.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0608 HI0608 Haemophilus influenzae 727 -11537879 4000709407 hi0608 (de:hypothetical protein hi0608) (db:swissprot) Y608_HAEIN Q57486 HAEMOPHILUS INFLUENZAE 727 -11537879 166984 probable membrane protein hi0608 (db:pir2.dat) I64080 I64080 Haemophilus influenzae 727 -11537879 7500895423 hi0608 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to gb:l77117 sp:q58086 pid:1591386 percent) (le:2853) (re:4238) (di:direct) U32743 U32743 g1573601 Haemophilus influenzae Rd 71421 -11537879 6500734021 membrane-bound protein with four pro-ser-alarepeats (gtcfc:11.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0608 HI0608 Haemophilus influenzae 727 -11537879

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889760	15602	37758	240	79

Description

5000695112 hypothetical proteinb (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0621B HI0621B Haemophilus influenzae 727 -11537880 109683 hi0621.1 (de:hypothetical protein hi0621.1) (db:swissprot) YAED_HAEIN P46452 HAEMOPHILUS INFLUENZAE 727 -11537880 7500896090 hi0621.1 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 59 of 163 of the complete genome.) (nt:similar to sp:p31546 pid:1208967 pid:303564) (le:8958) (re:9512) (di:direct) U32744 U32744 g1573616 Haemophilus influenzae Rd 71421 -11537880 6500734022 hypothetical proteinb (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0621B HI0621B Haemophilus influenzae 727 -11537880

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889761	15603	37759	318	105

Description

6500734023 fmu:hi0624 fmu protein (gtcfc:14.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0624 HI0624 Haemophilus influenzae 727 -11537881 72204 sun:fmu:hi0624 (de:sun protein (fmu protein)) (db:swissprot) SUN_HAEIN P44788 HAEMOPHILUS INFLUENZAE 727 -11537881 166465 hypothetical protein hi0624 (cl:hypothetical protein hi0624) (db:pir2.dat) F64155 F64155 Haemophilus influenzae 727 -11537881 7500892260 hi0624 sun protein sun (db:genpept-bct1) (de:haemophilus influenzae rd section 60 of 163 of the complete genome.) (nt:similar to sp:p36929 sp:p23866 gb:x52114 pid:43136) (le:5485) (re:6840) (di:direct) U32745 U32745 g1573620 Haemophilus influenzae Rd 71421 -11537881 5000695448 (de:(hi0624) (pn:protein) (gn:fmu) (gtcfc:13.7) (ec:) (fmu_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0624 HI0624 Haemophilus influenzae 727 10014755

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889765	15604	37760	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889767	15605	37761	519	172

Description

6500734024 hi0625:hin_618 trk system potassium uptake protein:trka (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_618 HIN_618 Haemophilus influenzae 727 -11537882 7500976253 hi0625 trk system potassium uptake protein trka (db:genpept-bct1) (de:haemophilus influenzae rd section 60 of 163 of the complete genome.) (nt:similar to sp:p23868 gb:x52114 pid:43137 pid:443993) (le:6853) (re:8229) (di:direct) U32745 U32745 g1573621 Haemophilus influenzae Rd 71421 -11537882 5000695449 (de:(hin61811) (pn:trk system potassium uptake protein:trka) (gn:hi0625) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN61811 HIN61811 Haemophilus influenzae 727 10126693

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889772	15606	37762	600	199

Description

6500734025 mscl:hi0626 large conductance mechanosensitive channel (gtcfc:11.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0626 HI0626 Haemophilus influenzae 727 -11537883 84293 mscl:hi0626 (de:large conductance mechanosensitive channel) (db:swissprot) MSCL_HAEIN P44789 HAEMOPHILUS INFLUENZAE 727 -11537883 166466 yhdc yhdc protein (cl:yhdc protein) (db:pir2.dat) G64155 G64155 Haemophilus influenzae 727 -11537883 7500885921 hi0626 large conductance mechanosensitive channel (db:genpept-bct1) (de:haemophilus influenzae rd section 60 of 163 of the complete genome.) (nt:similar to gb:l29458 sp:p23867 gb:u08371 gb:x52114) (le:8302) (re:8688) (di:direct) U32745 U32745 g1573622 Haemophilus influenzae Rd 71421 -11537883 5000695450 (de:(hi0626) (pn:large conductance mechanosensitive channel) (gn:mscl) (gtcfc:13.7) (ec:) (mscl_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0626 HI0626 Haemophilus influenzae 727 10026494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889775	15607	37763	228	75

Description

5000695451 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0627 HI0627 Haemophilus influenzae 727 -11537884 109236 hi0627 (de:hypothetical protein hi0627) (db:swissprot) YGFY_HAEIN P44025 HAEMOPHILUS INFLUENZAE 727 -11537884 166467 hypothetical protein hi0627 (db:pir2.dat) G64010 G64010 Haemophilus influenzae 727 -11537884 7500924173 hi0627 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 60 of 163 of the complete genome.) (nt:similar to pid:887847 gb:u00096 sp:q46825) (le:8778) (re:9035) (di:direct) U32745 U32745 g1573623 Haemophilus influenzae Rd 71421 -11537884 6500734026 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0627 HI0627 Haemophilus influenzae 727 -11537884

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889781	15608	37764	1029	342

Description

5000695452 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0633 HI0633 Haemophilus influenzae 727 -11537885 109237 hi0633 (de:hypothetical protein hi0633) (db:swissprot) Y633_HAEIN P44026 HAEMOPHILUS INFLUENZAE 727 -11537885 166468 hypothetical protein hi0633 (db:pir2.dat) H64010 H64010 Haemophilus influenzae 727 -11537885 7500895431 hi0633 h. influenzae predicted coding region hi0633 (db:genpept-bct1) (de:haemophilus influenzae rd section 61 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4181) (re:4477) (di:direct) U32746 U32746 g1573629 Haemophilus influenzae Rd 71421 -11537885 6500734027 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0633 HI0633 Haemophilus influenzae 727 -11537885

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889783	15609	37765	1479	492

Description

5000695453 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0636 HI0636 Haemophilus influenzae 727 -11537886 109239 hi0636 (de:hypothetical protein hi0636) (db:swissprot) Y636_HAEIN P44027 HAEMOPHILUS INFLUENZAE 727 -11537886 166470 c4-dicarboxylate transport protein homolog hi0636 (cl:c4-dicarboxylate carrier protein) (db:pir2.dat) I64010 I64010 Haemophilus influenzae 727 -11537886 7500895433 hi0636 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 61 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788685 percent ident:) (le:9223) (re:9513) (di:complement) U32746 U32746 g1573632 Haemophilus influenzae Rd 71421 -11537886 6500734028 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0636 HI0636 Haemophilus influenzae 727 -11537886

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889785	15610	37766	573	190

Description

5000695454 mg2+ transport atpase protein c:mgtc (gtcfc:12.6) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0647 HI0647 Haemophilus influenzae 727 -11537887 5500686333 hi0647 (de:hypothetical protein hi0647) (db:swissprot) Y647_HAEIN Q57424 HAEMOPHILUS INFLUENZAE 727 -11537887 166472 mg2+-transporting atpase mgtc homolog hi0647 (cl:mg2+-transporting atpase) (db:pir2.dat) A64156 A64156 Haemophilus influenzae 727 -11537887 7500895437 hi0647 transport protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to gb:m57715 sp:p22037 pid:154179 percent) (le:110) (re:826) (di:complement) U32748 U32748 g1573646 Haemophilus influenzae Rd 71421 -11537887 6500734029 mg2+ transport atpase protein c:mgtc (gtcfc:12.6) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0647 HI0647 Haemophilus influenzae 727 -11537887

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889797	15611	37767	474	157

Description

5000695455 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0650 HI0650 Haemophilus influenzae 727 -11537888 109243 hi0650 (de:hypothetical protein hi0650) (db:swissprot) Y650_HAEIN P44028 HAEMOPHILUS INFLUENZAE 727 -11537888 166473 hypothetical protein hi0650 (cl:hypothetical protein hi0650) (db:pir2.dat) A64011 A64011 Haemophilus influenzae 727 -11537888 7500895438 hi0650 h. influenzae predicted coding region hi0650 (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3990) (re:4202) (di:complement) U32748 U32748 g1573649 Haemophilus influenzae Rd 71421 -11537888 6500734030 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0650 HI0650 Haemophilus influenzae 727 -11537888

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889798	15612	37768	1230	409

Description

5000695456 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0657 HI0657 Haemophilus influenzae 727 -11537889 116130 hi0657 (de:hypothetical protein hi0657) (db:swissprot) YRDD_HAEIN P46494 HAEMOPHILUS INFLUENZAE 727 -11537889 7500952637 hi0656.1 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to sp:p45771 pid:606217 gb:u00096) (le:8716) (re:9252) (di:complement) U32748 U32748 g1573656 Haemophilus influenzae Rd 71421 -11537889 6500734031 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0657 HI0657 Haemophilus influenzae 727 -11537889

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889800	15613	37769	600	199

Description

GTC ORF with score 532 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0235 gene, partial cds.) (nt:similar to d.melanogaster pumilio protein (s22026):) (le:<2) (re:2554) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889804	15614	37770	315	104

Description

5000695457 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0659 HI0659 Haemophilus influenzae 727 -11537890 109245 hi0659 (de:hypothetical protein hi0659) (db:swissprot) Y659_HAEIN P44030 HAEMOPHILUS INFLUENZAE 727 -11537890 166477 hypothetical protein hi0659 (db:pir2.dat) C64011 C64011 Haemophilus influenzae 727 -11537890 7500895443 hi0659 h. influenzae predicted coding region hi0659 (db:genpept-bct1) (de:haemophilus influenzae rd section 64 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:111) (re:407) (di:complement) U32749 U32749 g1573659 Haemophilus influenzae Rd 71421 -11537890 6500734032 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0659 HI0659 Haemophilus influenzae 727 -11537890

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889816	15615	37771	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889823	15616	37772	201	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889835	15617	37773	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889836	15618	37774	720	239

Description

5000695458 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0660 HI0660 Haemophilus influenzae 727 -11537891 109248 hi0660 (de:hypothetical protein hi0660) (db:swissprot) Y660_HAEIN P44031 HAEMOPHILUS INFLUENZAE 727 -11537891 166478 hypothetical protein hi0660 (db:pir2.dat) D64011 D64011 Haemophilus influenzae 727 -11537891 7500895444 hi0660 h. influenzae predicted coding region hi0660 (db:genpept-bct1) (de:haemophilus influenzae rd section 64 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:400) (re:759) (di:complement) U32749 U32749 g1573660 Haemophilus influenzae Rd 71421 -11537891 6500734033 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0660 HI0660 Haemophilus influenzae 727 -11537891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889840	15619	37775	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889842	15620	37776	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889844	15621	37777	585	194

Description

5000695459 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0662 HI0662 Haemophilus influenzae 727 -11537892 109250 hi0662 (de:hypothetical protein hi0662 precursor) (db:swissprot) Y662_HAEIN P44032 HAEMOPHILUS INFLUENZAE 727 -11537892 166479 hypothetical protein hi0662 (db:pir2.dat) E64011 E64011 Haemophilus influenzae 727 -11537892 6500734034 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0662 HI0662 Haemophilus influenzae 727 -11537892

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889845	15622	37778	411	136

Description

6500734035 hi0663:hin_656 transport atp-binding protein:cydd (gtcfc:12.6) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_656 HIN_656 Haemophilus influenzae 727 -11537893 7500976255 hi0663 atp-binding transport protein cydd (db:genpept-bct1) (de:haemophilus influenzae rd section 64 of 163 of the complete genome.) (nt:similar to sp:p27299 gb:z11796 pid:42023 gb:u00096) (le:4609) (re:6291) (di:direct) U32749 U32749 g1573662 Haemophilus influenzae Rd 71421 -11537893 5000695460 (de:(hin65611) (pn:transport atp-binding protein:cydd) (gn:hi0663) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN65611 HIN65611 Haemophilus influenzae 727 10126694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889850	15623	37779	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889858	15624	37780	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889860	15625	37781	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889861	15626	37782	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889863	15627	37783	747	249

Description

5000695461 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0665 HI0665 Haemophilus influenzae 727 -11537894 109251 hi0665 (de:hypothetical protein hi0665) (db:swissprot) Y665_HAEIN P44033 HAEMOPHILUS INFLUENZAE 727 -11537894 166480 hypothetical protein hi0665 (db:pir2.dat) F64011 F64011 Haemophilus influenzae 727 -11537894 7500895455 hi0665 h. influenzae predicted coding region hi0665 (db:genpept-bct1) (de:haemophilus influenzae rd section 64 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8026) (re:9057) (di:complement) U32749 U32749 g1573664 Haemophilus influenzae Rd 71421 -11537894 6500734036 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0665 HI0665 Haemophilus influenzae 727 -11537894

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889866	15628	37784	417	138

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889871	15629	37785	435	144

Description

5000695462 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0666 HI0666 Haemophilus influenzae 727 -11537895 109252 hi0666 (de:hypothetical protein hi0666) (db:swissprot) Y666_HAEIN P44034 HAEMOPHILUS INFLUENZAE 727 -11537895 166481 hypothetical protein hi0666 (db:pir2.dat) G64011 G64011 Haemophilus influenzae 727 -11537895 7500895456 hi0666 h. influenzae predicted coding region hi0666 (db:genpept-bct1) (de:haemophilus influenzae rd section 64 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9054) (re:9374) (di:complement) U32749 U32749 g1573667 Haemophilus influenzae Rd 71421 -11537895 6500734037 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0666 HI0666 Haemophilus influenzae 727 -11537895

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889877	15630	37786	786	261

Description

5000695463 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0673 HI0673 Haemophilus influenzae 727 -11537896 109253 hi0673 (de:hypothetical protein hi0673) (db:swissprot) YGBQ_HAEIN P44035 HAEMOPHILUS INFLUENZAE 727 -11537896 166486 hypothetical protein hi0673 (cl:hypothetical protein hi0673) (db:pir2.dat) H64011 H64011 Haemophilus influenzae 727 -11537896 7500924046 hi0673 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to pid:882641 gb:u00096 pid:1789105 percent) (le:2749) (re:3027) (di:complement) U32750 U32750 g1573674 Haemophilus influenzae Rd 71421 -11537896 6500734038 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0673 HI0673 Haemophilus influenzae 727 -11537896

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889882	15631	37787	507	168

Description

5000695464 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0677 HI0677 Haemophilus influenzae 727 -11537897 109254 hi0677 (de:hypothetical protein hi0677) (db:swissprot) Y677_HAEIN P44036 HAEMOPHILUS INFLUENZAE 727 -11537897 166487 hypothetical protein hi0677 (db:pir2.dat) I64011 I64011 Haemophilus influenzae 727 -11537897 7500895460 hi0677 h. influenzae predicted coding region hi0677 (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6116) (re:6556) (di:complement) U32750 U32750 g1573677 Haemophilus influenzae Rd 71421 -11537897 6500734039 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0677 HI0677 Haemophilus influenzae 727 -11537897

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889886	15632	37788	1359	452

Description

5000695465 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0688 HI0688 Haemophilus influenzae 727 -11537898 109257 hi0688 (de:hypothetical protein hi0688) (db:swissprot) Y688_HAEIN P44037 HAEMOPHILUS INFLUENZAE 727 -11537898 166489 hypothetical protein hi0688 (db:pir2.dat) A64012 A64012 Haemophilus influenzae 727 -11537898 7500895462 hi0688 h. influenzae predicted coding region hi0688 (db:genpept-bct1) (de:haemophilus influenzae rd section 66 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9073) (re:9384) (di:direct) U32751 U32751 g1573691 Haemophilus influenzae Rd 71421 -11537898 6500734040 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0688 HI0688 Haemophilus influenzae 727 -11537898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889888	15633	37789	612	203

Description

5000695466 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0701 HI0701 Haemophilus influenzae 727 -11537899 109263 hi0701 (de:hypothetical protein hi0701) (db:swissprot) YGBO_HAEIN P44039 HAEMOPHILUS INFLUENZAE 727 -11537899 166494 hypothetical protein hi0701 (cl:hypothetical protein hi0701) (db:pir2.dat) C64012 C64012 Haemophilus influenzae 727 -11537899 7500924039 hi0701 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 68 of 163 of the complete genome.) (nt:similar to gb:107942 sp:p36664 pid:1036739) (le:1328) (re:2347) (di:direct) U32753 U32753 g1573704 Haemophilus influenzae Rd 71421 -11537899 6500734041 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0701 HI0701 Haemophilus influenzae 727 -11537899

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889890	15634	37790	459	152

Description

5000695467 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0704 HI0704 Haemophilus influenzae 727 -11537900 109266 hi0704 (de:hypothetical protein hi0704) (db:swissprot) Y704_HAEIN P44040 HAEMOPHILUS INFLUENZAE 727 -11537900 166495 hypothetical protein hi0704 (db:pir2.dat) D64012 D64012 Haemophilus influenzae 727 -11537900 7500895465 hi0704 h. influenzae predicted coding region hi0704 (db:genpept-bct1) (de:haemophilus influenzae rd section 68 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3702) (re:3887) (di:direct) U32753 U32753 g1573706 Haemophilus influenzae Rd 71421 -11537900 6500734042 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0704 HI0704 Haemophilus influenzae 727 -11537900

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889898	15635	37791	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889919	15636	37792	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889936	15637	37793	1215	404

Description

5000695468 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0711 HI0711 Haemophilus influenzae 727 -11537901 109268 hi0711 (de:hypothetical protein hi0711) (db:swissprot) YAFQ_HAEIN P44041 HAEMOPHILUS INFLUENZAE 727 -11537901 166496 hypothetical protein hi0711 (cl:conserved hypothetical protein hi0711) (db:pir2.dat) E64012 E64012 Haemophilus influenzae 727 -11537901 7500896136 hi0711 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to pid:984581 gb:u00096 sp:q47149) (le:440) (re:748) (di:direct) U32754 U32754 g1573713 Haemophilus influenzae Rd 71421 -11537901 6500734043 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0711 HI0711 Haemophilus influenzae 727 -11537901

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889937	15638	37794	2130	709

Description

6500734044 vacj:hi0718 lipoprotein homolog precursor (gtcfc:11.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0718 HI0718 Haemophilus influenzae 727 -11537902 104387 vacj:hi0718 (de:vacj lipoprotein homolog precursor) (db:swissprot) VACJ_HAEIN P44042 HAEMOPHILUS INFLUENZAE 727 -11537902 166497 vacj lipoprotein homolog hi0718 (cl:vacj lipoprotein) (db:pir2.dat) F64012 F64012 Haemophilus influenzae 727 -11537902 7500893954 hi0718 lipoprotein vacj (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to sp:p43262 pid:904221 percent ident:) (le:8875) (re:9627) (di:direct) U32754 U32754 g1573720 Haemophilus influenzae Rd 71421 -11537902 5000695469 (de:(hi0718) (pn:lipoprotein homolog precursor) (gn:vacj) (gtcfc:13.7) (ec:) (vacj_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0718 HI0718 Haemophilus influenzae 727 10046154

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889941	15639	37795	291	96

Description

5000695470 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0725 HI0725 Haemophilus influenzae 727 -11537903 109270 hi0725 (de:hypothetical protein hi0725) (db:swissprot) Y725_HAEIN P44043 HAEMOPHILUS INFLUENZAE 727 -11537903 166502 hypothetical protein hi0725 (db:pir2.dat) G64012 G64012 Haemophilus influenzae 727 -11537903 7500895482 hi0725 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 70 of 163 of the complete genome.) (nt:similar to pid:1685094 percent ident: 47.62;) (le:10069) (re:10509) (di:direct) U32755 U32755 g1573728 Haemophilus influenzae Rd 71421 -11537903 6500734045 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0725 HI0725 Haemophilus influenzae 727 -11537903

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889945	15640	37796	954	317

Description

GTC ORF with score 596 to: (db:genpept-bct2) (de:acinetobacter calcoaceticus benzaldehyde dehydrogenase ii (xylc)and benzyl alcohol dehydrogenase (xylb) genes, complete cds.) (nt:ec_number=1.1.1.90) (le:1816) (re:2931) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889952	15641	37797	489	162

Description

6500734046 hi0727:hin_718 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_718 HIN_718 Haemophilus influenzae 727 -11537904 7500976260 hi0727.1 cyay protein cyay (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:similar to sp:p27838 pid:148206 pid:41188 gb:u00096) (le:2401) (re:2706) (di:direct) U32756 U32756 g1573739 Haemophilus influenzae Rd 71421 -11537904 5000695471 (de:(hin71811) (pn:hypothetical) (gn:hi0727) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN71811 HIN71811 Haemophilus influenzae 727 10126695

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889966	15642	37798	921	306

Description

6500734047 hi0728:hin_719 dna-dependent atpase:dna helicase:recq (gtcfc:10.8) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_719 HIN_719 Haemophilus influenzae 727 -11537905 1500687225 recq:hi0728 (ec:3.6.1.-) (de:atp-dependent dna helicase recq,) (db:swissprot) RECQ_HAEIN P71359 HAEMOPHILUS INFLUENZAE 727 -11537905 7500889585 hi0728 atp-dependent dna helicase recq (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p15043 gb:m30198 pid:147559) (le:2708) (re:4567) (di:direct) U32756 U32756 g1573732 Haemophilus influenzae Rd 71421 -11537905 5000695472 (de:(hin71911) (pn:dna-dependent atpase, dna helicase:recq) (gn:hi0728) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN71911 HIN71911 Haemophilus influenzae 727 10064283

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889985	15643	37799	324	107

Description

GTC ORF with score 173 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid zc328.) (nt:contains strong similarity to a c2h2-type zinc) (le:19:205:736:984) (re:151:449:934:1240) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501889997	15644	37800	1590	529

Description

5000695473 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0731 HI0731 Haemophilus influenzae 727 -11537906 109271 hi0731 (de:hypothetical protein hi0731) (db:swissprot) Y731_HAEIN P44044 HAEMOPHILUS INFLUENZAE 727 -11537906 166504 sufi protein homolog hi0731 (db:pir2.dat) H64012 H64012 Haemophilus influenzae 727 -11537906 7500895483 hi0731 h. influenzae predicted coding region hi0731 (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8926) (re:9309) (di:complement) U32756 U32756 g1573735 Haemophilus influenzae Rd 71421 -11537906 6500734048 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0731 HI0731 Haemophilus influenzae 727 -11537906

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890015	15645	37801	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890017	15646	37802	1557	518

Description

5000695474 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0732 HI0732 Haemophilus influenzae 727 -11537907 109272 hi0732 (de:hypothetical protein hi0732) (db:swissprot) Y732_HAEIN P44045 HAEMOPHILUS INFLUENZAE 727 -11537907 166505 hypothetical protein hi0732 (db:pir2.dat) I64012 I64012 Haemophilus influenzae 727 -11537907 7500895484 hi0732 h. influenzae predicted coding region hi0732 (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9263) (re:9415) (di:complement) U32756 U32756 g1573738 Haemophilus influenzae Rd 71421 -11537907 6500734049 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0732 HI0732 Haemophilus influenzae 727 -11537907

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890052	15647	37803	1080	359

Description

GTC ORF with score 174 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f59a6.) (nt:similar to glycoproteins) (le:13300:13899:15490:15579) (re:13615:15440:15533:15701) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890054	15648	37804	1227	408

Description

GTC ORF with score 490 to: (sr:candida albicans (strain:atcc10231) dna) (db:genpept) (de:candida albicans gene for alpha subunit of geranylgeranyltransferaes type 2, complete cds, strain atcc10231.) (le:43:130) (re:45:1242) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890057	15649	37805	555	184

Description

6500734050 sufi:hi0733 protein homolog precursor (gtcfc:14.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0733 HI0733 Haemophilus influenzae 727 -11537908 99812 sufi:hi0733 (de:sufi protein homolog precursor) (db:swissprot) SUFI_HAEIN P44847 HAEMOPHILUS INFLUENZAE 727 -11537908 166506 sufi protein homolog hi0733 (db:pir2.dat) H64157 H64157 Haemophilus influenzae 727 -11537908 7500892237 hi0733 sufi protein sufi (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:similar to gb:m63491 sp:p26648 pid:147299) (le:9396) (re:10331) (di:complement) U32756 U32756 g1573736 Haemophilus influenzae Rd 71421 -11537908 5000695475 (de:(hi0733) (pn:protein homolog precursor) (gn:sufi) (gtcfc:13.7) (ec:) (sufi_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0733 HI0733 Haemophilus influenzae 727 10041667

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890058	15650	37806	282	93

Description

5000695476 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0735 HI0735 Haemophilus influenzae 727 -11537909 110207 hi0735 (de:hypothetical protein hi0735) (db:swissprot) YBBF_HAEIN P44046 HAEMOPHILUS INFLUENZAE 727 -11537909 166507 hypothetical protein hi0735 (cl:hypothetical protein hi0735) (db:pir2.dat) A64013 A64013 Haemophilus influenzae 727 -11537909 7500896569 hi0735 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 72 of 163 of the complete genome.) (nt:similar to sp:p43341 gb:u00096 pid:1773205) (le:73) (re:786) (di:direct) U32757 U32757 g1573741 Haemophilus influenzae Rd 71421 -11537909 6500734051 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0735 HI0735 Haemophilus influenzae 727 -11537909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890059	15651	37807	588	196

Description

5000695477 phosphomannomutase:gb:l13289_5 (gtcfc:1.5) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0740 HI0740 Haemophilus influenzae 727 -11537910 5500686367 hi0740 (ec:5.4.2.8) (de:probable phosphomannomutase, (pmm)) (db:swissprot) Y740_HAEIN Q57290 HAEMOPHILUS INFLUENZAE 727 -11537910 166508 hypothetical protein hi0740 (db:pir2.dat) I64157 I64157 Haemophilus influenzae 727 -11537910 7500895489 hi0740 phosphomannomutase yhxb (db:genpept-bct1) (de:haemophilus influenzae rd section 73 of 163 of the complete genome.) (nt:similar to gb:m34393 sp:p18159 pid:142994) (le:247) (re:1704) (di:direct) U32758 U32758 g1573748 Haemophilus influenzae Rd 71421 -11537910 6500734052 phosphomannomutase:gb:l13289_5 (gtcfc:1.5) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0740 HI0740 Haemophilus influenzae 727 -11537910

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890063	15652	37808	408	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890067	15653	37809	1131	377

Description

5000695478 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0742 HI0742 Haemophilus influenzae 727 -11537911 109274 hi0742 (de:hypothetical protein hi0742) (db:swissprot) Y742_HAEIN P44047 HAEMOPHILUS INFLUENZAE 727 -11537911 166509 hypothetical protein hi0742 (db:pir2.dat) B64013 B64013 Haemophilus influenzae 727 -11537911 7500895490 hi0742 h. influenzae predicted coding region hi0742 (db:genpept-bct1) (de:haemophilus influenzae rd section 73 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1853) (re:2182) (di:direct) U32758 U32758 g1573749 Haemophilus influenzae Rd 71421 -11537911 6500734053 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0742 HI0742 Haemophilus influenzae 727 -11537911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890081	15654	37810	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890086	15655	37811	1656	551

Description

5000695479 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0760 HI0760 Haemophilus influenzae 727 -11537912 112363 hi0760 (de:hypothetical protein hi0760) (db:swissprot) YGGX_HAEIN P44048 HAEMOPHILUS INFLUENZAE 727 -11537912 166514 hypothetical protein hi0760 (db:pir2.dat) C64013 C64013 Haemophilus influenzae 727 -11537912 7500924209 hi0760 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to pid:882491 sp:p52065 gb:u00096) (le:3776) (re:4048) (di:direct) U32760 U32760 g1573769 Haemophilus influenzae Rd 71421 -11537912 6500734054 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0760 HI0760 Haemophilus influenzae 727 -11537912

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890093	15656	37812	1683	560

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890094	15657	37813	1446	481

Description

5000695480 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0761 HI0761 Haemophilus influenzae 727 -11537913 112365 mltc:hi0761 (ec:3.2.1.-) (de:(murein hydrolase c)) (db:swissprot) MLTC_HAEIN P44049 HAEMOPHILUS INFLUENZAE 727 -11537913 166515 hypothetical protein hi0761 (db:pir2.dat) D64013 D64013 Haemophilus influenzae 727 -11537913 7500885687 hi0761 membrane-bound lytic murein transglycosylase c (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to pid:882493 sp:p52066 gb:u00096) (le:4063) (re:5136) (di:direct) U32760 U32760 g1573770 Haemophilus influenzae Rd 71421 -11537913 6500734055 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0761 HI0761 Haemophilus influenzae 727 -11537913

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890104	15658	37814	531	176

Description

5000695481 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0762 HI0762 Haemophilus influenzae 727 -11537914 109277 hi0762 (de:hypothetical protein hi0762) (db:swissprot) Y762_HAEIN P44050 HAEMOPHILUS INFLUENZAE 727 -11537914 166516 probable phosphoesterase:hi0762 (cl:unassigned probable phosphoesterases:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) E64013 E64013 Haemophilus influenzae 727 -11537914 7500895498 hi0762 h. influenzae predicted coding region hi0762 (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5747) (re:6427) (di:complement) U32760 U32760 g1573779 Haemophilus influenzae Rd 71421 -11537914 6500734056 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0762 HI0762 Haemophilus influenzae 727 -11537914

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890105	15659	37815	201	66

Description

5000695482 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0772 HI0772 Haemophilus influenzae 727 -11537915 109278 atoe:hi0772 (de:short-chain fatty acids transporter) (db:swissprot) ATOE_HAEIN P44051 HAEMOPHILUS INFLUENZAE 727 -11537915 166518 hypothetical protein hi0772 (cl:conserved hypothetical integral membrane protein hp0693) (db:pir2.dat) F64013 F64013 Haemophilus influenzae 727 -11537915 7500877344 hi0772 short-chain fatty acids transporter atoe (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p76460 pid:1788553 percent) (le:1274) (re:2617) (di:complement) U32761 U32761 g1573782 Haemophilus influenzae Rd 71421 -11537915 6500734057 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0772 HI0772 Haemophilus influenzae 727 -11537915

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890139	15660	37816	2247	748

Description

5000695483 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0787 HI0787 Haemophilus influenzae 727 -11537916 109281 hi0787 (de:hypothetical protein hi0787) (db:swissprot) Y787_HAEIN P44052 HAEMOPHILUS INFLUENZAE 727 -11537916 166519 hypothetical protein hi0787 (db:pir2.dat) G64013 G64013 Haemophilus influenzae 727 -11537916 7500895508 hi0787 h. influenzae predicted coding region hi0787 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:226) (re:831) (di:direct) U32762 U32762 g1573816 Haemophilus influenzae Rd 71421 -11537916 6500734058 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0787 HI0787 Haemophilus influenzae 727 -11537916

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890179	15661	37817	279	92

Description

5000694540 rpmj:rpl36:hi0798b 50s ribosomal protein l36 (gtcfc:10.4) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0798B HI0798B Haemophilus influenzae 727 -11537917 95237 rpmj:rpl36:hi0798.1 (de:50s ribosomal protein l36) (db:swissprot) RL36_HAEIN P46361 HAEMOPHILUS INFLUENZAE 727 -11537917 7500890243 hi0798.1 ribosomal protein l36 rpl36 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to sp:p21194 gb:m12432 pid:42990 pid:606233) (le:6525) (re:6638) (di:direct) U32762 U32762 g1573809 Haemophilus influenzae Rd 71421 -11537917 6500734059 rpmj:rpl36 50s ribosomal protein l36 (gtcfc:10.4) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0798B HI0798B Haemophilus influenzae 727 -11537917

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890189	15662	37818	1386	462

Description

5000695484 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0804 HI0804 Haemophilus influenzae 727 -11537918 109291 hi0804 (de:hypothetical protein hi0804) (db:swissprot) Y804_HAEIN P44053 HAEMOPHILUS INFLUENZAE 727 -11537918 166520 hypothetical protein hi0804 (db:pir2.dat) H64013 H64013 Haemophilus influenzae 727 -11537918 7500895528 hi0804 h. influenzae predicted coding region hi0804 (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9963) (re:10352) (di:complement) U32762 U32762 g1573815 Haemophilus influenzae Rd 71421 -11537918 6500734060 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0804 HI0804 Haemophilus influenzae 727 -11537918

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890190	15663	37819	630	209

Description

5000695485 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0806 HI0806 Haemophilus influenzae 727 -11537919 109292 hi0806 (de:hypothetical protein hi0806) (db:swissprot) Y806_HAEIN P44054 HAEMOPHILUS INFLUENZAE 727 -11537919 166521 hypothetical protein hi0806 (db:pir2.dat) I64013 I64013 Haemophilus influenzae 727 -11537919 7500895532 hi0806 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 78 of 163 of the complete genome.) (nt:similar to gb:l77117 sp:q57883 pid:1591145 percent) (le:924) (re:1730) (di:direct) U32763 U32763 g1573818 Haemophilus influenzae Rd 71421 -11537919 6500734061 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0806 HI0806 Haemophilus influenzae 727 -11537919

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890191	15664	37820	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890192	15665	37821	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890209	15666	37822	1257	418

Description

GTC ORF with score 227 to: (db:genpept-bct2) (de:bacillus subtilis plsx (plsx), malonyl-coa:acyl carrier proteintransacylase (fabd) and 3-ketoacyl-acyl carrier protein reductase(fabg) genes, complete cds, and acyl carrier protein (acpp) gene,partial ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890214	15667	37823	2229	743

Description

5000695486 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0807 HI0807 Haemophilus influenzae 727 -11537920 109698 dxr:hi0807 (ec:1.1.1.-) (de:reductoisomerase)) (db:swissprot) DXR_HAEIN P44055 HAEMOPHILUS INFLUENZAE 727 -11537920 166522 conserved hypothetical protein hi0807 (cl:conserved hypothetical protein hi0807) (db:pir2.dat) A64014 A64014 Haemophilus influenzae 727 -11537920 7500896097 hi0807 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 78 of 163 of the complete genome.) (nt:similar to sp:p45568 gb:u00096 pid:1552750) (le:1762) (re:2955) (di:complement) U32763 U32763 g1573819 Haemophilus influenzae Rd 71421 -11537920 6500734062 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0807 HI0807 Haemophilus influenzae 727 -11537920

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890229	15668	37824	1485	494

Description

5000695487 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0825 HI0825 Haemophilus influenzae 727 -11537921 109293 hi0825 (de:hypothetical protein hi0825) (db:swissprot) Y825_HAEIN P44056 HAEMOPHILUS INFLUENZAE 727 -11537921 166525 hypothetical protein hi0825 (db:pir2.dat) B64014 B64014 Haemophilus influenzae 727 -11537921 7500895546 hi0825 h. influenzae predicted coding region hi0825 (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:103) (re:837) (di:direct) U32765 U32765 g1573839 Haemophilus influenzae Rd 71421 -11537921 6500734063 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0825 HI0825 Haemophilus influenzae 727 -11537921

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890230	15669	37825	654	217

Description

6500734064 cpxr:hi0837 transcriptional regulatory protein homolog (gtcfc:10.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0837 HI0837 Haemophilus influenzae 727 -11537922 66238 cpxr:hi0837 (de:transcriptional regulatory protein cpxr homolog) (db:swissprot) CPXR_HAEIN P44895 HAEMOPHILUS INFLUENZAE 727 -11537922 166528 transcription factor hi0837 (cl:ompr protein:response regulator homology) (db:pir2.dat) C64159 C64159 Haemophilus influenzae 727 -11537922 7500879352 hi0837 response regulator cpxr (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p16244 gb:l14579 gb:x13307) (le:9939) (re:10622) (di:complement) U32765 U32765 g1573851 Haemophilus influenzae Rd 71421 -11537922 5000695488 (de:(hi0837) (pn:transcriptional regulatory protein homolog) (gn:cpxr) (gtcfc:13.7) (ec:) (cpxr_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0837 HI0837 Haemophilus influenzae 727 10008869

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890232	15670	37826	342	113

Description

5000695489 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0838 HI0838 Haemophilus influenzae 727 -11537923 109294 hi0838 (de:hypothetical protein hi0838) (db:swissprot) Y838_HAEIN P44057 HAEMOPHILUS INFLUENZAE 727 -11537923 166529 hypothetical protein hi0838 (db:pir2.dat) C64014 C64014 Haemophilus influenzae 727 -11537923 7500895550 hi0838 small protein a:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to sp:p23089 percent ident: 49.51;) (le:10676) (re:11245) (di:complement) U32765 U32765 g1573852 Haemophilus influenzae Rd 71421 -11537923 6500734065 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0838 HI0838 Haemophilus influenzae 727 -11537923

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890241	15671	37827	819	272

Description

5000695490 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0842 HI0842 Haemophilus influenzae 727 -11537924 109295 hi0842 (de:hypothetical protein hi0842 precursor) (db:swissprot) Y842_HAEIN P44058 HAEMOPHILUS INFLUENZAE 727 -11537924 166533 hypothetical protein hi0842 (db:pir2.dat) D64014 D64014 Haemophilus influenzae 727 -11537924 7500895557 hi0842 h. influenzae predicted coding region hi0842 (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2264) (re:3094) (di:direct) U32766 U32766 g1573857 Haemophilus influenzae Rd 71421 -11537924 6500734066 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0842 HI0842 Haemophilus influenzae 727 -11537924

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890284	15672	37828	906	301

Description

5000695491 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0843 HI0843 Haemophilus influenzae 727 -11537925 109296 hi0843 (de:hypothetical protein hi0843) (db:swissprot) Y843_HAEIN P44059 HAEMOPHILUS INFLUENZAE 727 -11537925 166534 hypothetical protein hi0843 (db:pir2.dat) E64014 E64014 Haemophilus influenzae 727 -11537925 7500895558 hi0843 h. influenzae predicted coding region hi0843 (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3118) (re:3255) (di:direct) U32766 U32766 g1573867 Haemophilus influenzae Rd 71421 -11537925 6500734067 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0843 HI0843 Haemophilus influenzae 727 -11537925

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890303	15673	37829	708	236

Description

5000695492 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0854 HI0854 Haemophilus influenzae 727 -11537926 109298 hi0854 (de:hypothetical protein hi0854) (db:swissprot) Y854_HAEIN P44061 HAEMOPHILUS INFLUENZAE 727 -11537926 166540 hypothetical protein hi0854 (cl:conserved hypothetical protein hp0318) (db:pir2.dat) G64014 G64014 Haemophilus influenzae 727 -11537926 7500895560 hi0854 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to gb:ae000511 pid:2313418 percent) (le:1926) (re:2687) (di:direct) U32767 U32767 g1573877 Haemophilus influenzae Rd 71421 -11537926 6500734068 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0854 HI0854 Haemophilus influenzae 727 -11537926

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890308	15674	37830	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890331	15675	37831	750	249

Description

5000695493 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0857 HI0857 Haemophilus influenzae 727 -11537927 112322 hi0857 (de:hypothetical protein hi0857) (db:swissprot) YGFE_HAEIN P44062 HAEMOPHILUS INFLUENZAE 727 -11537927 166542 hypothetical protein hi0857 (cl:hypothetical protein hi0857) (db:pir2.dat) H64014 H64014 Haemophilus influenzae 727 -11537927 7500924152 hi0857 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to sp:p45580 pid:882440 gb:u00096) (le:6127) (re:6429) (di:direct) U32767 U32767 g1573872 Haemophilus influenzae Rd 71421 -11537927 6500734069 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0857 HI0857 Haemophilus influenzae 727 -11537927

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890332	15676	37832	411	136

Description

5000695494 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0866 HI0866 Haemophilus influenzae 727 -11537928 109300 hi0866 (de:hypothetical protein hi0866) (db:swissprot) Y866_HAEIN P44063 HAEMOPHILUS INFLUENZAE 727 -11537928 166546 hypothetical protein hi0866 (db:pir2.dat) I64014 I64014 Haemophilus influenzae 727 -11537928 6500734070 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0866 HI0866 Haemophilus influenzae 727 -11537928

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890337	15677	37833	585	194

Description

5000695495 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0869 HI0869 Haemophilus influenzae 727 -11537929 109301 hi0869 (de:hypothetical protein hi0869) (db:swissprot) Y869_HAEIN P44064 HAEMOPHILUS INFLUENZAE 727 -11537929 166547 hypothetical protein hi0869 (db:pir2.dat) A64015 A64015 Haemophilus influenzae 727 -11537929 7500895575 hi0869 h. influenzae predicted coding region hi0869 (db:genpept-bct1) (de:haemophilus influenzae rd section 83 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8496) (re:9053) (di:direct) U32768 U32768 g1573886 Haemophilus influenzae Rd 71421 -11537929 6500734071 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0869 HI0869 Haemophilus influenzae 727 -11537929

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890338	15678	37834	780	259

Description

5000695496 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0870 HI0870 Haemophilus influenzae 727 -11537930 109302 hi0870 (de:hypothetical protein hi0870) (db:swissprot) Y870_HAEIN P44065 HAEMOPHILUS INFLUENZAE 727 -11537930 166548 hypothetical protein hi0870 (db:pir2.dat) B64015 B64015 Haemophilus influenzae 727 -11537930 7500895576 hi0870 h. influenzae predicted coding region hi0870 (db:genpept-bct1) (de:haemophilus influenzae rd section 83 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9142) (re:9246) (di:direct) U32768 U32768 g1573887 Haemophilus influenzae Rd 71421 -11537930 6500734072 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0870 HI0870 Haemophilus influenzae 727 -11537930

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890339	15679	37835	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890343	15680	37836	420	139

Description

5000695497 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0871 HI0871 Haemophilus influenzae 727 -11537931 109303 hi0871 (de:hypothetical protein hi0871) (db:swissprot) Y871_HAEIN P44066 HAEMOPHILUS INFLUENZAE 727 -11537931 166549 hypothetical protein hi0871 (db:pir2.dat) C64015 C64015 Haemophilus influenzae 727 -11537931 7500895577 hi0871 h. influenzae predicted coding region hi0871 (db:genpept-bct1) (de:haemophilus influenzae rd section 84 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:657) (re:1577) (di:direct) U32769 U32769 g1573889 Haemophilus influenzae Rd 71421 -11537931 6500734073 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0871 HI0871 Haemophilus influenzae 727 -11537931

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890344	15681	37837	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890346	15682	37838	477	158

Description

5000695498 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0874 HI0874 Haemophilus influenzae 727 -11537932 109304 hi0874 (de:hypothetical protein hi0874) (db:swissprot) Y874_HAEIN P44067 HAEMOPHILUS INFLUENZAE 727 -11537932 166550 hypothetical protein hi0874 (db:pir2.dat) D64015 D64015 Haemophilus influenzae 727 -11537932 7500895584 hi0874 h. influenzae predicted coding region hi0874 (db:genpept-bct1) (de:haemophilus influenzae rd section 84 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4113) (re:5312) (di:complement) U32769 U32769 g1573892 Haemophilus influenzae Rd 71421 -11537932 6500734074 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0874 HI0874 Haemophilus influenzae 727 -11537932

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890347	15683	37839	330	109

Description

6500734075 hi0878:hin_868 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_868 HIN_868 Haemophilus influenzae 727 -11537933 7500976266 hi0878 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 84 of 163 of the complete genome.) (nt:similar to sp:p28636 pid:216638 pid:606122) (le:8468) (re:9388) (di:complement) U32769 U32769 g1573895 Haemophilus influenzae Rd 71421 -11537933 5000695499 (de:(hin86811) (pn:hypothetical) (gn:hi0878) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN86811 HIN86811 Haemophilus influenzae 727 10126699

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890348	15684	37840	234	77

Description

5000695500 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0882 HI0882 Haemophilus influenzae 727 -11537934 109305 hi0882 (de:hypothetical protein hi0882) (db:swissprot) Y882_HAEIN P44068 HAEMOPHILUS INFLUENZAE 727 -11537934 166552 hypothetical protein hi0882 (db:pir2.dat) E64015 E64015 Haemophilus influenzae 727 -11537934 7500895603 hi0882 h. influenzae predicted coding region hi0882 (db:genpept-bct1) (de:haemophilus influenzae rd section 85 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1177) (re:1914) (di:direct) U32770 U32770 g1573906 Haemophilus influenzae Rd 71421 -11537934 6500734076 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0882 HI0882 Haemophilus influenzae 727 -11537934

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890359	15685	37841	489	163

Description

5000695501 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0886 HI0886 Haemophilus influenzae 727 -11537935 109307 hi0886 (de:hypothetical protein hi0886) (db:swissprot) Y886_HAEIN P44069 HAEMOPHILUS INFLUENZAE 727 -11537935 166553 hypothetical protein hi0886 (db:pir2.dat) F64015 F64015 Haemophilus influenzae 727 -11537935 7500895608 hi0886 h. influenzae predicted coding region hi0886 (db:genpept-bct1) (de:haemophilus influenzae rd section 85 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6494) (re:6898) (di:direct) U32770 U32770 g1573903 Haemophilus influenzae Rd 71421 -11537935 6500734077 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0886 HI0886 Haemophilus influenzae 727 -11537935

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890360	15686	37842	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890362	15687	37843	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890376	15688	37844	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890385	15689	37845	453	150

Description

5000695502 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0903 HI0903 Haemophilus influenzae 727 -11537936 109317 hi0903 (de:hypothetical protein hi0903) (db:swissprot) Y903_HAEIN P44071 HAEMOPHILUS INFLUENZAE 727 -11537936 166557 hypothetical protein hi0903 (db:pir2.dat) H64015 H64015 Haemophilus influenzae 727 -11537936 6500734078 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0903 HI0903 Haemophilus influenzae 727 -11537936

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890387	15690	37846	432	143

Description

5000695503 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0902 HI0902 Haemophilus influenzae 727 -11537937 109316 hi0902 (de:hypothetical protein hi0902) (db:swissprot) Y902_HAEIN P44070 HAEMOPHILUS INFLUENZAE 727 -11537937 166556 hypothetical protein hi0902 (db:pir2.dat) G64015 G64015 Haemophilus influenzae 727 -11537937 7500895636 hi0902 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to gb:177117 sp:q57883 pid:1591145 percent) (le:2482) (re:3276) (di:direct) U32772 U32772 g1573922 Haemophilus influenzae Rd 71421 -11537937 6500734079 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0902 HI0902 Haemophilus influenzae 727 -11537937

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890388	15691	37847	1227	408

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890390	15692	37848	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890393	15693	37849	351	117

Description

5000695504 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0907 HI0907 Haemophilus influenzae 727 -11537938 109318 hi0907 (de:hypothetical protein hi0907) (db:swissprot) Y907_HAEIN P44072 HAEMOPHILUS INFLUENZAE 727 -11537938 166559 hypothetical protein hi0907 (db:pir2.dat) I64015 I64015 Haemophilus influenzae 727 -11537938 7500895653 hi0907 h. influenzae predicted coding region hi0907 (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5501) (re:5815) (di:complement) U32772 U32772 g1573930 Haemophilus influenzae Rd 71421 -11537938 6500734080 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0907 HI0907 Haemophilus influenzae 727 -11537938

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890415	15694	37850	480	159

Description

5000695505 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0908 HI0908 Haemophilus influenzae 727 -11537939 109319 hi0908 (de:hypothetical protein hi0908) (db:swissprot) Y908_HAEIN P44073 HAEMOPHILUS INFLUENZAE 727 -11537939 166560 hypothetical protein hi0908 (db:pir2.dat) A64016 A64016 Haemophilus influenzae 727 -11537939 7500895657 hi0908 h. influenzae predicted coding region hi0908 (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5895) (re:6197) (di:direct) U32772 U32772 g1573931 Haemophilus influenzae Rd 71421 -11537939 6500734081 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0908 HI0908 Haemophilus influenzae 727 -11537939

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890422	15695	37851	1605	534

Description

5000695506 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0925 HI0925 Haemophilus influenzae 727 -11537940 109322 hi0925 (de:hypothetical protein hi0925) (db:swissprot) Y925_HAEIN P44075 HAEMOPHILUS INFLUENZAE 727 -11537940 166564 hypothetical protein hi0925 (cl:hypothetical protein hi0925) (db:pir2.dat) C64016 C64016 Haemophilus influenzae 727 -11537940 7500895684 hi0925 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 89 of 163 of the complete genome.) (nt:similar to sp:p45736 gb:u00096 pid:1279405) (le:7010) (re:7375) (di:complement) U32774 U32774 g1573947 Haemophilus influenzae Rd 71421 -11537940 6500734082 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0925 HI0925 Haemophilus influenzae 727 -11537940

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890423	15696	37852	1677	558

Description

5000695507 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0926 HI0926 Haemophilus influenzae 727 -11537941 109323 hi0926 (de:hypothetical protein hi0926) (db:swissprot) Y926_HAEIN P44076 HAEMOPHILUS INFLUENZAE 727 -11537941 166565 hypothetical protein hi0926 (db:pir2.dat) D64016 D64016 Haemophilus influenzae 727 -11537941 7500895689 hi0926 h. influenzae predicted coding region hi0926 (db:genpept-bct1) (de:haemophilus influenzae rd section 89 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7405) (re:7665) (di:complement) U32774 U32774 g1573950 Haemophilus influenzae Rd 71421 -11537941 6500734083 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0926 HI0926 Haemophilus influenzae 727 -11537941

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890444	15697	37853	918	305

Description

5000695508 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0930 HI0930 Haemophilus influenzae 727 -11537942 109324 hi0930 (de:hypothetical protein hi0930) (db:swissprot) Y930_HAEIN P44077 HAEMOPHILUS INFLUENZAE 727 -11537942 166567 hypothetical protein hi0930 (db:pir2.dat) E64016 E64016 Haemophilus influenzae 727 -11537942 7500895701 hi0930 h. influenzae predicted coding region hi0930 (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1328) (re:1948) (di:complement) U32775 U32775 g1573966 Haemophilus influenzae Rd 71421 -11537942 6500734084 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0930 HI0930 Haemophilus influenzae 727 -11537942

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890455	15698	37854	1656	552

Description

5000695509 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0931 HI0931 Haemophilus influenzae 727 -11537943 109325 hi0931 (de:hypothetical protein hi0931) (db:swissprot) Y931_HAEIN P44078 HAEMOPHILUS INFLUENZAE 727 -11537943 166568 hypothetical protein hi0931 (db:pir2.dat) F64016 F64016 Haemophilus influenzae 727 -11537943 7500895702 hi0931 h. influenzae predicted coding region hi0931 (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1921) (re:2406) (di:complement) U32775 U32775 g1573967 Haemophilus influenzae Rd 71421 -11537943 6500734085 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0931 HI0931 Haemophilus influenzae 727 -11537943

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890459	15699	37855	699	232

Description

6500734086 dsbe-2:hi0935 thiol disulfide interchange protein dsbe homolog 2 precursor (gtcfc:2.7) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0935 HI0935 Haemophilus influenzae 727 -11537944 69322 dsbe-2:hi0935 (de:thiol:disulfide interchange protein dsbe homolog 2 precursor) (db:swissprot) DSE2_HAEIN P44943 HAEMOPHILUS INFLUENZAE 727 -11537944 166571 hypothetical protein hi0935 (cl:cytochrome c biogenesis protein cycx) (db:pir2.dat) I64161 I64161 Haemophilus influenzae 727 -11537944 7500880677 hi0935 th:disulfide interchange protein dsbe (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to sp:p33926 pid:405920 gb:u00096) (le:6208) (re:6738) (di:complement) U32775 U32775 g1573956 Haemophilus influenzae Rd 71421 -11537944 5000695510 (de:(hi0935) (pn:thiol:disulfide interchange protein dsbe homolog 2 precursor) (gn:dsbe-2) (gtcfc:13.7) (ec:) (dse2_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0935 HI0935 Haemophilus influenzae 727 10011905

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890476	15700	37856	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890486	15701	37857	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890494	15702	37858	846	281

Description

6500734087 nrfe:hi0936 cytochrome c-type biogenesis protein (gtcfc:2.8) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0936 HI0936 Haemophilus influenzae 727 -11537945 86508 nrfe:hi0936 (de:cytochrome c-type biogenesis protein nrfe) (db:swissprot) NRFE_HAEIN P44944 HAEMOPHILUS INFLUENZAE 727 -11537945 136990 cyck protein homolog hi0936 (cl:nrfe protein) (db:pir2.dat) A64162 A64162 Haemophilus influenzae 727 -11537945 7500886590 hi0936 cytochrome c-type biogenesis (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to sp:p32710 gb:x72298 pid:581146 gb:u00096) (le:6738) (re:8645) (di:complement) U32775 U32775 g1573957 Haemophilus influenzae Rd 71421 -11537945 5000695511 (de:(hi0936) (pn:cytochrome c-type biogenesis protein) (gn:nrfe) (gtcfc:13.7) (ec:) (nrfe_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0936 HI0936 Haemophilus influenzae 727 10028673

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890496	15703	37859	786	261

Description

5000695512 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0938 HI0938 Haemophilus influenzae 727 -11537946 109326 hi0938 (de:hypothetical protein hi0938) (db:swissprot) Y938_HAEIN P44079 HAEMOPHILUS INFLUENZAE 727 -11537946 166572 hypothetical protein hi0938 (db:pir2.dat) G64016 G64016 Haemophilus influenzae 727 -11537946 7500895709 hi0938 h. influenzae predicted coding region hi0938 (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9758) (re:10270) (di:direct) U32775 U32775 g1573959 Haemophilus influenzae Rd 71421 -11537946 6500734088 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0938 HI0938 Haemophilus influenzae 727 -11537946

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890521	15704	37860	975	324

Description

GTC ORF with score 177 to: (sr:humicola grisea var. thermoidea (strain:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea gene for actin, complete cds.) (le:371:515:723:880:987) (re:377:545:778:910:1758) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890531	15705	37861	273	90

Description

5000695513 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0939 HI0939 Haemophilus influenzae 727 -11537947 109327 hi0939 (de:hypothetical protein hi0939) (db:swissprot) Y939_HAEIN P44080 HAEMOPHILUS INFLUENZAE 727 -11537947 166573 hypothetical protein hi0939 (db:pir2.dat) H64016 H64016 Haemophilus influenzae 727 -11537947 7500895710 hi0939 h. influenzae predicted coding region hi0939 (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10270) (re:10986) (di:direct) U32775 U32775 g1573960 Haemophilus influenzae Rd 71421 -11537947 6500734089 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0939 HI0939 Haemophilus influenzae 727 -11537947

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890532	15706	37862	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890542	15707	37863	717	238

Description

5000695514 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0940 HI0940 Haemophilus influenzae 727 -11537948 109328 hi0940 (de:hypothetical protein hi0940) (db:swissprot) Y940_HAEIN P44081 HAEMOPHILUS INFLUENZAE 727 -11537948 166574 hypothetical protein hi0940 (db:pir2.dat) I64016 I64016 Haemophilus influenzae 727 -11537948 7500895711 hi0940 h. influenzae predicted coding region hi0940 (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10986) (re:11669) (di:direct) U32775 U32775 g1573968 Haemophilus influenzae Rd 71421 -11537948 6500734090 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0940 HI0940 Haemophilus influenzae 727 -11537948

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890545	15708	37864	657	218

Description

5000695515 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0941 HI0941 Haemophilus influenzae 727 -11537949 109329 hi0941 (de:hypothetical protein hi0941 precursor) (db:swissprot) Y941_HAEIN P44082 HAEMOPHILUS INFLUENZAE 727 -11537949 166575 hypothetical protein hi0941 (db:pir2.dat) A64017 A64017 Haemophilus influenzae 727 -11537949 7500895712 hi0941 h. influenzae predicted coding region hi0941 (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11644) (re:11949) (di:direct) U32775 U32775 g1573961 Haemophilus influenzae Rd 71421 -11537949 6500734091 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0941 HI0941 Haemophilus influenzae 727 -11537949

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890546	15709	37865	435	144

Description

GTC ORF with score 131 to: (db:genpept-pln2) (de:emericella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj),(stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890563	15710	37866	681	226

Description

6500734092 hi0946:hin_937 l-2:4-diaminobutyrate decarboxylase (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_937 HIN_937 Haemophilus influenzae 727 -11537950 7500960705 l-2:4-diaminobutyrate decarboxylase (ec:4.1.1.-) (db:pir2.dat) JC5880 JC5880 Haemophilus influenzae 727 -11537950 7500960706 hi0946.1 l-2:4-diaminobutyrate decarboxylase (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to pid:893355 percent ident: 75.54;) (le:1115) (re:2650) (di:complement) U32776 U32776 g1573971 Haemophilus influenzae Rd 71421 -11537950 5000695516 (de:(hin93711) (pn:l-2,4-diaminobutyrate decarboxylase) (gn:hi0946) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN93711 HIN93711 Haemophilus influenzae 727 10126702

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890566	15711	37867	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890567	15712	37868	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890579	15713	37869	1563	520

Description

6500734093 ttk:hi0955 protein homolog (gtcfc:14.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0955 HI0955 Haemophilus influenzae 727 -11537951 102706 ttk:hi0955 (de:ttk protein homolog) (db:swissprot) TTK_HAEIN P29280 HAEMOPHILUS INFLUENZAE 727 -11537951 166216 hypothetical protein hi0955 (cl:hypothetical protein hi0955) (db:pir2.dat) D64162 D64162 Haemophilus influenzae 727 -11537951 7500893571 hi0955 transcriptional regulator ttk (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p06969 gb:v01578 gb:x01714) (le:8330) (re:8986) (di:direct) U32776 U32776 g1573980 Haemophilus influenzae Rd 71421 -11537951 5000695517 (de:(hi0955) (pn:protein homolog) (gn:ttk) (gtcfc:13.7) (ec:) (ttk_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0955 HI0955 Haemophilus influenzae 727 10044524

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890581	15714	37870	600	200

Description

5000695518 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0959 HI0959 Haemophilus influenzae 727 -11537952 109332 hi0959 (de:hypothetical protein hi0959) (db:swissprot) YCFO_HAEIN P44955 HAEMOPHILUS INFLUENZAE 727 -11537952 166580 probable glucosidase:hi0959 (ec:3.2.1.-) (db:pir2.dat) F64162 F64162 Haemophilus influenzae 727 -11537952 7500921746 hi0959 beta-hexosaminidase exoii (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:similar to pid:1750216 percent ident: 49.69;) (le:1384) (re:2439) (di:complement) U32777 U32777 g1573985 Haemophilus influenzae Rd 71421 -11537952 6500734094 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0959 HI0959 Haemophilus influenzae 727 -11537952

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890586	15715	37871	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890619	15716	37872	1062	353

Description

5000695519 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0960 HI0960 Haemophilus influenzae 727 -11537953 109334 hi0960 (de:hypothetical protein hi0960 precursor) (db:swissprot) Y960_HAEIN P44084 HAEMOPHILUS INFLUENZAE 727 -11537953 166581 hypothetical protein hi0960 (db:pir2.dat) C64017 C64017 Haemophilus influenzae 727 -11537953 7500895745 hi0960 h. influenzae predicted coding region hi0960 (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2443) (re:2793) (di:complement) U32777 U32777 g1573994 Haemophilus influenzae Rd 71421 -11537953 6500734095 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0960 HI0960 Haemophilus influenzae 727 -11537953

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890630	15717	37873	1548	515

Description

5000695520 hypothetical hit-like protein hi0961 (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0961 HI0961 Haemophilus influenzae 727 -11537954 166582 histidine triad protein homolog hi0961 (cl:protein kinase c inhibitor:histidine triad homology) (db:pir2.dat) G64162 G64162 Haemophilus influenzae 727 -11537954 7500954136 hi0961 hit-related protein (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:similar to sp:p44956 percent ident: 100.00;) (le:2793) (re:3185) (di:complement) U32777 U32777 g1573986 Haemophilus influenzae Rd 71421 -11537954 6500734096 hypothetical hit-like protein hi0961 (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0961 HI0961 Haemophilus influenzae 727 -11537954

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890631	15718	37874	399	132

Description

6500734097 mvin:hi0964 virulence factor homolog (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0964 HI0964 Haemophilus influenzae 727 -11537955 84763 mvin:hi0964 (de:virulence factor mvin homolog) (db:swissprot) MVIN_HAEIN P44958 HAEMOPHILUS INFLUENZAE 727 -11537955 166584 mvin protein homolog hi0964 (cl:mvin protein) (db:pir2.dat) I64162 I64162 Haemophilus influenzae 727 -11537955 7500886176 hi0964 virulence factor mvin (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:similar to gb:d25292 sp:p37169 gb:z26133 pid:438252) (le:7087) (re:8619) (di:complement) U32777 U32777 g1573989 Haemophilus influenzae Rd 71421 -11537955 5000695521 (de:(hi0964) (pn:virulence factor homolog) (gn:mvin) (gtcfc:13.7) (ec:) (mvin_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0964 HI0964 Haemophilus influenzae 727 10026954

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890634	15719	37875	1182	394

Description

6500734098 rpst:hi0965 30s ribosomal protein s20 (gtcfc:10.4) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0965 HI0965 Haemophilus influenzae 727 -11537956 148637 ribosomal protein s20 (cl:escherichia coli ribosomal protein s20) (db:pir2.dat) A64163 A64163 Haemophilus influenzae 727 -11537956 5000695522 (de:(hi0965) (pn:30s ribosomal protein s20) (gn:rpst) (gtcfc:13.7) (ec:) (rs20_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI0965 HI0965 Haemophilus influenzae 727 10077766

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890640	15720	37876	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890647	15721	37877	1119	372

Description

5000695523 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0966 HI0966 Haemophilus influenzae 727 -11537957 109335 hi0966 (de:hypothetical protein hi0966) (db:swissprot) Y966_HAEIN P44085 HAEMOPHILUS INFLUENZAE 727 -11537957 166585 hypothetical protein hi0966 (db:pir2.dat) D64017 D64017 Haemophilus influenzae 727 -11537957 7500895749 hi0966 h. influenzae predicted coding region hi0966 (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9264) (re:9830) (di:complement) U32777 U32777 g1573995 Haemophilus influenzae Rd 71421 -11537957 6500734099 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0966 HI0966 Haemophilus influenzae 727 -11537957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890661	15722	37878	993	330

Description

GTC ORF with score 344 to: (fn:has both arabinofuranosidase and exoxylanase) (db:genpept-bct1) (de:caldicellulosiruptor saccharolyticus putative transport protein(xyng), putative transport protein (xynh), xylanase (xynf),xylanase (xyne), xylanase ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890662	15723	37879	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890671	15724	37880	444	147

Description

5000695524 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0967 HI0967 Haemophilus influenzae 727 -11537958 109336 hi0967 (de:hypothetical protein hi0967) (db:swissprot) Y967_HAEIN P44086 HAEMOPHILUS INFLUENZAE 727 -11537958 166586 hypothetical protein hi0967 (db:pir2.dat) E64017 E64017 Haemophilus influenzae 727 -11537958 7500895750 hi0967 h. influenzae predicted coding region hi0967 (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9856) (re:9960) (di:direct) U32777 U32777 g1573996 Haemophilus influenzae Rd 71421 -11537958 6500734100 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0967 HI0967 Haemophilus influenzae 727 -11537958

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890674	15725	37881	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890680	15726	37882	777	258

Description

5000695525 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0974 HI0974 Haemophilus influenzae 727 -11537959 109337 hi0974 (de:hypothetical protein hi0974) (db:swissprot) Y974_HAEIN P44087 HAEMOPHILUS INFLUENZAE 727 -11537959 166587 hypothetical protein hi0974 (db:pir2.dat) F64017 F64017 Haemophilus influenzae 727 -11537959 7500895773 hi0974 h. influenzae predicted coding region hi0974 (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3178) (re:4284) (di:direct) U32778 U32778 g1574001 Haemophilus influenzae Rd 71421 -11537959 6500734101 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0974 HI0974 Haemophilus influenzae 727 -11537959

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890700	15727	37883	720	239

Description

5000695168 hypothetical proteinb (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0974B HI0974B Haemophilus influenzae 727 -11537960 112733 hi0974.1 (de:hypothetical protein hi0974.1) (db:swissprot) YHDT_HAEIN P46455 HAEMOPHILUS INFLUENZAE 727 -11537960 7500936858 hi0974.1 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:similar to sp:p45566 pid:606197 gb:u00096) (le:4735) (re:4992) (di:direct) U32778 U32778 g1574002 Haemophilus influenzae Rd 71421 -11537960 6500734102 hypothetical proteinb (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0974B HI0974B Haemophilus influenzae 727 -11537960

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890702	15728	37884	465	154

Description

5000695526 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0979 HI0979 Haemophilus influenzae 727 -11537961 112720 hi0979 (de:hypothetical protein hi0979) (db:swissprot) YHDG_HAEIN P44965 HAEMOPHILUS INFLUENZAE 727 -11537961 166590 hypothetical protein hi0979 (db:pir2.dat) C64163 C64163 Haemophilus influenzae 727 -11537961 7500936838 hi0979 nitrogen fixation protein nifr3 (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:similar to sp:p45672 pid:599600 percent ident:) (le:9091) (re:10083) (di:direct) U32778 U32778 g1574007 Haemophilus influenzae Rd 71421 -11537961 6500734103 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0979 HI0979 Haemophilus influenzae 727 -11537961

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890710	15729	37885	429	142

Description

5000695527 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0996 HI0996 Haemophilus influenzae 727 -11537962 109341 hi0996 (de:hypothetical protein hi0996) (db:swissprot) Y996_HAEIN P44089 HAEMOPHILUS INFLUENZAE 727 -11537962 166594 hypothetical protein hi0996 (db:pir2.dat) H64017 H64017 Haemophilus influenzae 727 -11537962 7500895805 hi0996 h. influenzae predicted coding region hi0996 (db:genpept-bct1) (de:haemophilus influenzae rd section 95 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8642) (re:9082) (di:direct) U32780 U32780 g1574027 Haemophilus influenzae Rd 71421 -11537962 6500734104 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0996 HI0996 Haemophilus influenzae 727 -11537962

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890712	15730	37886	1371	456

Description

5000695528 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0997 HI0997 Haemophilus influenzae 727 -11537963 109342 hi0997 (de:hypothetical protein hi0997) (db:swissprot) Y997_HAEIN P44090 HAEMOPHILUS INFLUENZAE 727 -11537963 166595 hypothetical protein hi0997 (db:pir2.dat) I64017 I64017 Haemophilus influenzae 727 -11537963 7500895812 hi0997 h. influenzae predicted coding region hi0997 (db:genpept-bct1) (de:haemophilus influenzae rd section 95 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9398) (re:10087) (di:direct) U32780 U32780 g1574026 Haemophilus influenzae Rd 71421 -11537963 6500734105 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI0997 HI0997 Haemophilus influenzae 727 -11537963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890716	15731	37887	216	71

Description

5000695529 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1003 HI1003 Haemophilus influenzae 727 -11537964 109356 hi1003 (de:hypothetical protein hi1003) (db:swissprot) YA03_HAEIN P44091 HAEMOPHILUS INFLUENZAE 727 -11537964 166598 hypothetical protein hi1003 (db:pir2.dat) A64018 A64018 Haemophilus influenzae 727 -11537964 6500734106 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1003 HI1003 Haemophilus influenzae 727 -11537964

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890719	15732	37888	486	161

Description

5000695530 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1004 HI1004 Haemophilus influenzae 727 -11537965 166599 hypothetical protein hi1004 (cl:hypothetical protein hi1004) (db:pir2.dat) B64018 B64018 Haemophilus influenzae 727 -11537965 7500960677 hi1004 peptidyl-prolyl cis-trans isomerse:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77241 pid:1580712) (le:4272) (re:6056) (di:direct) U32781 U32781 g1574034 Haemophilus influenzae Rd 71421 -11537965 6500734107 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1004 HI1004 Haemophilus influenzae 727 -11537965 109358 ya04_haein (de:hypothetical protein hi1004.) P44092 P44092 Haemophilus influenzae 727 -11537965

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890723	15733	37889	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890725	15734	37890	1269	422

Description

5000695531 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1011 HI1011 Haemophilus influenzae 727 -11537966 109365 hi1011 (de:hypothetical protein hi1011) (db:swissprot) YGBK_HAEIN P44093 HAEMOPHILUS INFLUENZAE 727 -11537966 166603 hypothetical protein hi1011 (db:pir2.dat) C64018 C64018 Haemophilus influenzae 727 -11537966 7500924033 hi1011 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to pid:882630 gb:u00096 pid:1789093 percent) (le:1018) (re:2259) (di:direct) U32782 U32782 g1574043 Haemophilus influenzae Rd 71421 -11537966 6500734108 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1011 HI1011 Haemophilus influenzae 727 -11537966

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890726	15735	37891	222	73

Description

5000695532 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1014 HI1014 Haemophilus influenzae 727 -11537967 109368 hi1014 (de:hypothetical protein hi1014) (db:swissprot) YA14_HAEIN P44094 HAEMOPHILUS INFLUENZAE 727 -11537967 166604 hypothetical protein hi1014 (db:pir2.dat) D64018 D64018 Haemophilus influenzae 727 -11537967 7500895826 hi1014 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to pid:695275 percent ident: 47.92;) (le:3723) (re:4670) (di:direct) U32782 U32782 g1574046 Haemophilus influenzae Rd 71421 -11537967 6500734109 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1014 HI1014 Haemophilus influenzae 727 -11537967

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890733	15736	37892	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890746	15737	37893	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890754	15738	37894	816	272

Description

5000695533 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1016 HI1016 Haemophilus influenzae 727 -11537968 109370 hi1016 (de:hypothetical protein hi1016) (db:swissprot) YA16_HAEIN P44095 HAEMOPHILUS INFLUENZAE 727 -11537968 166605 hypothetical protein hi1016 (db:pir2.dat) E64018 E64018 Haemophilus influenzae 727 -11537968 7500895827 hi1016 h. influenzae predicted coding region hi1016 (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6165) (re:6593) (di:direct) U32782 U32782 g1574051 Haemophilus influenzae Rd 71421 -11537968 6500734110 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1016 HI1016 Haemophilus influenzae 727 -11537968

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890756	15739	37895	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890761	15740	37896	981	326

Description

5000695535 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1034 HI1034 Haemophilus influenzae 727 -11537969 109392 hi1034 (de:hypothetical protein hi1034) (db:swissprot) YAJQ_HAEIN P44096 HAEMOPHILUS INFLUENZAE 727 -11537969 166617 conserved hypothetical protein hi1034 (cl:hypothetical protein b0426) (db:pir2.dat) F64018 F64018 Haemophilus influenzae 727 -11537969 7500896238 hi1034 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77482 pid:1773110) (le:2036) (re:2527) (di:direct) U32784 U32784 g1574067 Haemophilus influenzae Rd 71421 -11537969 6500734111 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1034 HI1034 Haemophilus influenzae 727 -11537969

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890770	15741	37897	300	99

Description

5000695536 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1038 HI1038 Haemophilus influenzae 727 -11537970 109396 hi1038 (de:hypothetical protein hi1038) (db:swissprot) YA38_HAEIN P44099 HAEMOPHILUS INFLUENZAE 727 -11537970 166620 hypothetical protein hi1038 (db:pir2.dat) I64018 I64018 Haemophilus influenzae 727 -11537970 7500895860 hi1038 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to gb:l77117 pid:1592175 percent ident:) (le:5758) (re:6960) (di:direct) U32784 U32784 g1574071 Haemophilus influenzae Rd 71421 -11537970 6500734112 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1038 HI1038 Haemophilus influenzae 727 -11537970

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890771	15742	37898	897	298

Description

GTC ORF with score 330 to: (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.).) (nt:orf_id:o332#10; similar to (swissprot accession) (le:10741) (re:11985) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890778	15743	37899	489	162

Description

5000695537 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1039 HI1039 Haemophilus influenzae 727 -11537971 109398 hi1039 (de:hypothetical protein hi1039) (db:swissprot) YA39_HAEIN P44100 HAEMOPHILUS INFLUENZAE 727 -11537971 166621 hypothetical protein hi1039 (db:pir2.dat) A64019 A64019 Haemophilus influenzae 727 -11537971 6500734113 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1039 HI1039 Haemophilus influenzae 727 -11537971

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890783	15744	37900	1092	364

Description

5000695538 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1044 HI1044 Haemophilus influenzae 727 -11537972 109406 hi1044 (de:hypothetical protein hi1044) (db:swissprot) YNFI_HAEIN P44102 HAEMOPHILUS INFLUENZAE 727 -11537972 166623 ycdy protein homolog hi1044 (cl:escherichia coli ycdy protein) (db:pir2.dat) C64019 C64019 Haemophilus influenzae 727 -11537972 7500951815 hi1044 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787874 percent ident:) (le:582) (re:1193) (di:complement) U32785 U32785 g1574078 Haemophilus influenzae Rd 71421 -11537972 6500734114 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1044 HI1044 Haemophilus influenzae 727 -11537972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890787	15745	37901	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890793	15746	37902	1047	348

Description

5000695539 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1048 HI1048 Haemophilus influenzae 727 -11537973 109410 hi1048 (de:hypothetical protein hi1048 precursor) (db:swissprot) YA48_HAEIN P44103 HAEMOPHILUS INFLUENZAE 727 -11537973 166624 hypothetical protein hi1048 (db:pir2.dat) D64019 D64019 Haemophilus influenzae 727 -11537973 7500895863 hi1048 h. influenzae predicted coding region hi1048 (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5448) (re:6557) (di:direct) U32785 U32785 g1574085 Haemophilus influenzae Rd 71421 -11537973 6500734115 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1048 HI1048 Haemophilus influenzae 727 -11537973

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890796	15747	37903	201	66

Description

5000695540 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1054 HI1054 Haemophilus influenzae 727 -11537974 109421 hi1054 (de:hypothetical protein hi1054) (db:swissprot) YA54_HAEIN P44104 HAEMOPHILUS INFLUENZAE 727 -11537974 166626 hypothetical protein hi1054 (db:pir2.dat) E64019 E64019 Haemophilus influenzae 727 -11537974 7500895883 hi1054 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to pid:1381738 percent ident: 92.49;) (le:1518) (re:2900) (di:complement) U32786 U32786 g1574617 Haemophilus influenzae Rd 71421 -11537974 6500734116 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1054 HI1054 Haemophilus influenzae 727 -11537974

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890799	15748	37904	282	93

Description

5000695541 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1055 HI1055 Haemophilus influenzae 727 -11537975 109422 hi1055 (de:hypothetical protein hi1055) (db:swissprot) YA55_HAEIN P44105 HAEMOPHILUS INFLUENZAE 727 -11537975 166627 hypothetical protein hi1055 (db:pir2.dat) F64019 F64019 Haemophilus influenzae 727 -11537975 7500895887 hi1055 h. influenzae predicted coding region hi1055 (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2788) (re:4332) (di:complement) U32786 U32786 g1574608 Haemophilus influenzae Rd 71421 -11537975 6500734117 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1055 HI1055 Haemophilus influenzae 727 -11537975

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890802	15749	37905	672	223

Description

GTC ORF with score 683 to: (sr:homo sapiens male myeloblast cell_line kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0098 gene, partial cds.) (nt:kiaa0098 is a human counterpart of mouse chaperonin) (le:<1) (re:1643) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890811	15750	37906	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890817	15751	37907	426	141

Description

5000695542 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1058 HI1058 Haemophilus influenzae 727 -11537976 109424 hi1058 (de:hypothetical protein hi1058 precursor) (db:swissprot) YA58_HAEIN P44106 HAEMOPHILUS INFLUENZAE 727 -11537976 166628 hypothetical protein hi1058 (db:pir2.dat) G64019 G64019 Haemophilus influenzae 727 -11537976 7500895890 hi1058 h. influenzae predicted coding region hi1058 (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5958) (re:6542) (di:complement) U32786 U32786 g1574618 Haemophilus influenzae Rd 71421 -11537976 6500734118 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1058 HI1058 Haemophilus influenzae 727 -11537976

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890823	15752	37908	2658	885

Description

5000695543 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1063 HI1063 Haemophilus influenzae 727 -11537977 109427 hi1063 (de:hypothetical protein hi1063) (db:swissprot) YA63_HAEIN P44107 HAEMOPHILUS INFLUENZAE 727 -11537977 166629 hypothetical protein hi1063 (db:pir2.dat) H64019 H64019 Haemophilus influenzae 727 -11537977 7500895894 hi1063 h. influenzae predicted coding region hi1063 (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9917) (re:10129) (di:complement) U32786 U32786 g1574614 Haemophilus influenzae Rd 71421 -11537977 6500734119 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1063 HI1063 Haemophilus influenzae 727 -11537977

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890829	15753	37909	408	135

Description

5000695544 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1074 HI1074 Haemophilus influenzae 727 -11537978 109442 hi1074 (de:hypothetical protein hi1074) (db:swissprot) YEAL_HAEIN P44110 HAEMOPHILUS INFLUENZAE 727 -11537978 166635 hypothetical protein hi1074 (cl:hypothetical protein ytwi) (db:pir2.dat) B64020 B64020 Haemophilus influenzae 727 -11537978 7500922865 hi1074 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788090 percent ident:) (le:8574) (re:9026) (di:complement) U32787 U32787 g1574625 Haemophilus influenzae Rd 71421 -11537978 6500734120 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1074 HI1074 Haemophilus influenzae 727 -11537978

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890849	15754	37910	1203	400

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890862	15755	37911	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890863	15756	37912	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890882	15757	37913	498	165

Description

6500734121 pnuc:hi1077:hin_1066 nicotinamide mononucleotide transporter:pnuc (gtcfc:12.3:9.4) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_1066 HIN_1066 Haemophilus influenzae 727 -11537979 4000708221 hi1077.1 (de:hypothetical protein hi1077.1) (db:swissprot) YA7B_HAEIN Q57425 HAEMOPHILUS INFLUENZAE 727 -11537979 7500895919 hi1077.1 h. influenzae predicted coding region hi1077.1 (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2286) (re:2690) (di:complement) U32788 U32788 g1574631 Haemophilus influenzae Rd 71421 -11537979 5000695545 (de:(hin106611) (pn:nicotinamide mononucleotide transporter:pnuc) (gn:hi1077) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN106611 HIN106611 Haemophilus influenzae 727 10126709

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890889	15758	37914	504	167

Description

5000695547 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1098 HI1098 Haemophilus influenzae 727 -11537980 109464 hi1098 (de:hypothetical protein hi1098) (db:swissprot) YA98_HAEIN P44111 HAEMOPHILUS INFLUENZAE 727 -11537980 166647 hypothetical protein hi1098 (db:pir2.dat) C64020 C64020 Haemophilus influenzae 727 -11537980 7500895944 hi1098 h. influenzae predicted coding region hi1098 (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8501) (re:8635) (di:direct) U32789 U32789 g1574652 Haemophilus influenzae Rd 71421 -11537980 6500734122 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1098 HI1098 Haemophilus influenzae 727 -11537980

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890894	15759	37915	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890895	15760	37916	753	250

Description

5000695548 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1099 HI1099 Haemophilus influenzae 727 -11537981 109466 hi1099 (de:hypothetical protein hi1099) (db:swissprot) YA99_HAEIN P44112 HAEMOPHILUS INFLUENZAE 727 -11537981 166648 hypothetical protein hi1099 (db:pir2.dat) D64020 D64020 Haemophilus influenzae 727 -11537981 7500895945 hi1099 h. influenzae predicted coding region hi1099 (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8637) (re:8945) (di:direct) U32789 U32789 g1574653 Haemophilus influenzae Rd 71421 -11537981 6500734123 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1099 HI1099 Haemophilus influenzae 727 -11537981

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890904	15761	37917	480	159

Description

5000695549 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1101 HI1101 Haemophilus influenzae 727 -11537982 110038 zipa:hi1101 (de:cell division protein zipa homolog) (db:swissprot) ZIPA_HAEIN P44113 HAEMOPHILUS INFLUENZAE 727 -11537982 166649 hypothetical protein hi1101 (db:pir2.dat) E64020 E64020 Haemophilus influenzae 727 -11537982 7500953131 hi1101 cell division protein zipa:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 105 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77173 pid:1788752) (le:73) (re:1059) (di:complement) U32790 U32790 g1574655 Haemophilus influenzae Rd 71421 -11537982 6500734124 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1101 HI1101 Haemophilus influenzae 727 -11537982

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890914	15762	37918	216	71

Description

5000695550 sialic acid transporter:nant (gtcfc:12.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1104 HI1104 Haemophilus influenzae 727 -11537983 166650 hypothetical protein hi1104 (cl:hypothetical protein hi1104) (db:pir2.dat) C64167 C64167 Haemophilus influenzae 727 -11537983 7500960680 hi1104 transporter protein (db:genpept-bct1) (de:haemophilus influenzae rd section 105 of 163 of the completegenome.) (nt:similar to pid:1842056 percent ident: 29.56;) (le:3803) (re:5026) (di:direct) U32790 U32790 g1574658 Haemophilus influenzae Rd 71421 -11537983 6500734125 sialic acid transporter:nant (gtcfc:12.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1104 HI1104 Haemophilus influenzae 727 -11537983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890928	15763	37919	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890930	15764	37920	402	133

Description

5000695552 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1126 HI1126 Haemophilus influenzae 727 -11537984 110069 hi1126 (de:hypothetical protein hi1126) (db:swissprot) YB26_HAEIN P44114 HAEMOPHILUS INFLUENZAE 727 -11537984 166652 hypothetical protein hi1126 (db:pir2.dat) F64020 F64020 Haemophilus influenzae 727 -11537984 7500896350 hi1126 h. influenzae predicted coding region hi1126 (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9163) (re:9393) (di:complement) U32792 U32792 g1574681 Haemophilus influenzae Rd 71421 -11537984 6500734126 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1126 HI1126 Haemophilus influenzae 727 -11537984

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890931	15765	37921	291	96

Description

5000695553 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1128 HI1128 Haemophilus influenzae 727 -11537985 110071 hi1128 (de:hypothetical protein hi1128) (db:swissprot) YB28_HAEIN P44115 HAEMOPHILUS INFLUENZAE 727 -11537985 166653 hypothetical protein hi1128 (db:pir2.dat) G64020 G64020 Haemophilus influenzae 727 -11537985 7500896353 hi1128 h. influenzae predicted coding region hi1128 (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:11001) (re:11177) (di:direct) U32792 U32792 g1574682 Haemophilus influenzae Rd 71421 -11537985 6500734127 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1128 HI1128 Haemophilus influenzae 727 -11537985

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890935	15766	37922	210	70

Description

5000695554 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1162 HI1162 Haemophilus influenzae 727 -11537986 110830 hi1162 (de:hypothetical protein hi1162) (db:swissprot) YCJD_HAEIN P44116 HAEMOPHILUS INFLUENZAE 727 -11537986 166662 hypothetical protein hi1162 (cl:hypothetical protein hi0925) (db:pir2.dat) H64020 H64020 Haemophilus influenzae 727 -11537986 7500921846 hi1162 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 111 of 163 of the completegenome.) (nt:similar to sp:p45736 gb:u00096 pid:1279405) (le:2006) (re:2479) (di:complement) U32796 U32796 g1574089 Haemophilus influenzae Rd 71421 -11537986 6500734128 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1162 HI1162 Haemophilus influenzae 727 -11537986

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890945	15767	37923	2064	688

Description

GTC ORF with score 622 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890946	15768	37924	1143	380

Description

GTC ORF with score 668 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890980	15769	37925	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890981	15770	37926	456	151

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890983	15771	37927	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890984	15772	37928	723	241

Description

5000695555 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1168 HI1168 Haemophilus influenzae 727 -11537987 110101 hi1168 (de:hypothetical protein hi1168) (db:swissprot) YEEX_HAEIN P44117 HAEMOPHILUS INFLUENZAE 727 -11537987 166664 hypothetical protein hi1168 (db:pir2.dat) I64020 I64020 Haemophilus influenzae 727 -11537987 7500922985 hi1168 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788317 percent ident:) (le:126) (re:470) (di:direct) U32797 U32797 g1574108 Haemophilus influenzae Rd 71421 -11537987 6500734129 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1168 HI1168 Haemophilus influenzae 727 -11537987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501890991	15773	37929	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891013	15774	37930	630	209

Description

5000695556 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1169 HI1169 Haemophilus influenzae 727 -11537988 110102 hi1169 (de:hypothetical protein hi1169) (db:swissprot) YB69_HAEIN P44118 HAEMOPHILUS INFLUENZAE 727 -11537988 166665 hypothetical protein hi1169 (db:pir2.dat) A64021 A64021 Haemophilus influenzae 727 -11537988 7500896436 hi1169 h. influenzae predicted coding region hi1169 (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:511) (re:1077) (di:complement) U32797 U32797 g1574096 Haemophilus influenzae Rd 71421 -11537988 6500734130 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1169 HI1169 Haemophilus influenzae 727 -11537988

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891018	15775	37931	2193	730

Description

5000695557 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1176 HI1176 Haemophilus influenzae 727 -11537989 110108 hi1176 (de:hypothetical protein hi1176) (db:swissprot) YB76_HAEIN P44120 HAEMOPHILUS INFLUENZAE 727 -11537989 166667 hypothetical protein hi1176 (db:pir2.dat) C64021 C64021 Haemophilus influenzae 727 -11537989 7500896446 hi1176 h. influenzae predicted coding region hi1176 (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5487) (re:5708) (di:complement) U32797 U32797 g1574109 Haemophilus influenzae Rd 71421 -11537989 6500734131 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1176 HI1176 Haemophilus influenzae 727 -11537989

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891019	15776	37932	864	287

Description

5000695558 h (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1182 HI1182 Haemophilus influenzae 727 -11537990 166669 hypothetical protein hi1182 (db:pir2.dat) D64021 D64021 Haemophilus influenzae 727 -11537990 7500960682 hi1182 h. influenzae predicted coding region hi1182 (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9653) (re:10210) (di:direct) U32797 U32797 g1574107 Haemophilus influenzae Rd 71421 -11537990 6500734132 h (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1182 HI1182 Haemophilus influenzae 727 -11537990

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891020	15777	37933	189	62

Description

5000695559 h (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1183 HI1183 Haemophilus influenzae 727 -11537991 166670 hypothetical protein hi1183 (db:pir2.dat) E64021 E64021 Haemophilus influenzae 727 -11537991 7500960683 hi1183 h. influenzae predicted coding region hi1183 (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:66) (re:242) (di:direct) U32798 U32798 g1574121 Haemophilus influenzae Rd 71421 -11537991 6500734133 h (gtcfc:14.3) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1183 HI1183 Haemophilus influenzae 727 -11537991

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891027	15778	37934	1554	517

Description

5000695560 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1190 HI1190 Haemophilus influenzae 727 -11537992 110131 hi1190 (de:hypothetical protein hi1190) (db:swissprot) YB90_HAEIN P44123 HAEMOPHILUS INFLUENZAE 727 -11537992 166671 hypothetical protein hi1190 (db:pir2.dat) F64021 F64021 Haemophilus influenzae 727 -11537992 7500896480 hi1190 6-pyruvoyl tetrahydrobiopterin synthase (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to pid:882658 gb:u00096 sp:q46903) (le:7682) (re:8107) (di:complement) U32798 U32798 g1574117 Haemophilus influenzae Rd 71421 -11537992 6500734134 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1190 HI1190 Haemophilus influenzae 727 -11537992

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891031	15779	37935	405	134

Description

5000695561 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1191 HI1191 Haemophilus influenzae 727 -11537993 110133 hi1191 (de:hypothetical protein hi1191) (db:swissprot) YBAX_HAEIN P44124 HAEMOPHILUS INFLUENZAE 727 -11537993 166672 hypothetical protein hi1191 (cl:conserved hypothetical protein hi1191) (db:pir2.dat) G64021 G64021 Haemophilus influenzae 727 -11537993 7500896550 hi1191 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to gb:al009126 percent ident: 56.42;) (le:8197) (re:8787) (di:complement) U32798 U32798 g1574118 Haemophilus influenzae Rd 71421 -11537993 6500734135 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1191 HI1191 Haemophilus influenzae 727 -11537993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891033	15780	37936	474	157

Description

5000695562 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1192 HI1192 Haemophilus influenzae 727 -11537994 110135 hi1192 (de:hypothetical protein hi1192 precursor) (db:swissprot) YB92_HAEIN P44125 HAEMOPHILUS INFLUENZAE 727 -11537994 166673 hypothetical protein hi1192 (db:pir2.dat) H64021 H64021 Haemophilus influenzae 727 -11537994 7500896482 hi1192 h. influenzae predicted coding region hi1192 (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8943) (re:9086) (di:direct) U32798 U32798 g1574119 Haemophilus influenzae Rd 71421 -11537994 6500734136 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1192 HI1192 Haemophilus influenzae 727 -11537994

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891036	15781	37937	570	189

Description

GTC ORF with score 187 to: (fn:morphogenesis in fission yeast) (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe putative alpha-glucan synthase (ags1)mrna, partial cds.) (nt:ags1p) (le:<1) (re:1008) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891040	15782	37938	594	197

Description

5000695563 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1202 HI1202 Haemophilus influenzae 727 -11537995 110430 hi1202 (de:hypothetical protein hi1202) (db:swissprot) YC02_HAEIN P44126 HAEMOPHILUS INFLUENZAE 727 -11537995 166677 hypothetical protein hi1202 (db:pir2.dat) I64021 I64021 Haemophilus influenzae 727 -11537995 7500921417 hi1202 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788671 percent ident:) (le:8318) (re:8821) (di:direct) U32799 U32799 g1574132 Haemophilus influenzae Rd 71421 -11537995 6500734137 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1202 HI1202 Haemophilus influenzae 727 -11537995

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891047	15783	37939	480	159

Description

GTC ORF with score 165 to: (fn:morphogenesis in fission yeast) (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe putative alpha-glucan synthase (ags1)mrna, partial cds.) (nt:ags1p) (le:<1) (re:1008) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891049	15784	37940	588	195

Description

GTC ORF with score 442 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1110.) (nt:unnamed protein product) (le:<1) (re:1106) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891051	15785	37941	1401	466

Description

5000695564 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1205 HI1205 Haemophilus influenzae 727 -11537996 110431 hi1205 (de:hypothetical protein hi1205) (db:swissprot) YC05_HAEIN P44127 HAEMOPHILUS INFLUENZAE 727 -11537996 166679 hypothetical protein hi1205 (cl:hypothetical protein hi1205) (db:pir2.dat) A64022 A64022 Haemophilus influenzae 727 -11537996 7500921418 hi1205 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 115 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788632 gb:u00096) (le:1484) (re:1927) (di:direct) U32800 U32800 g1574135 Haemophilus influenzae Rd 71421 -11537996 6500734138 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1205 HI1205 Haemophilus influenzae 727 -11537996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891063	15786	37942	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891069	15787	37943	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891085	15788	37944	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891090	15789	37945	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891093	15790	37946	699	232

Description

5000695565 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1215 HI1215 Haemophilus influenzae 727 -11537997 110443 hi1215 (de:hypothetical protein hi1215 precursor) (db:swissprot) YC15_HAEIN P44128 HAEMOPHILUS INFLUENZAE 727 -11537997 166680 hypothetical protein hi1215 (db:pir2.dat) B64022 B64022 Haemophilus influenzae 727 -11537997 7500921436 hi1215 th:disulfide interchange protein dsba (db:genpept-bct1) (de:haemophilus influenzae rd section 116 of 163 of the completegenome.) (nt:similar to pid:840949 sp:p50024 percent ident:) (le:1895) (re:2602) (di:direct) U32801 U32801 g1574145 Haemophilus influenzae Rd 71421 -11537997 6500734139 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1215 HI1215 Haemophilus influenzae 727 -11537997

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891104	15791	37947	825	274

Description

6500734140 pfs:hi1216 protein homolog (gtcfc:14.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1216 HI1216 Haemophilus influenzae 727 -11537998 89208 pfs:hi1216 (ec:3.2.2.16:3.2.2.9) (de:nucleosidase, (mta/sah nucleosidase)) (db:swissprot) PFS_HAEIN P45113 HAEMOPHILUS INFLUENZAE 727 -11537998 166681 pfs pfs protein (cl:escherichia coli pfs protein) (db:pir2.dat) C64169 C64169 Haemophilus influenzae 727 -11537998 7500887918 hi1216 pfs protein pfs (db:genpept-bct1) (de:haemophilus influenzae rd section 116 of 163 of the completegenome.) (nt:similar to gb:d26562 sp:p24247 gb:m83735 pid:473817) (le:2599) (re:3288) (di:direct) U32801 U32801 g1574146 Haemophilus influenzae Rd 71421 -11537998 5000695566 (de:(hi1216) (pn:protein homolog) (gn:pfs) (gtcfc:13.7) (ec:) (pfs_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI1216 HI1216 Haemophilus influenzae 727 10031331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891105	15792	37948	246	81

Description

6500734141 hi1220:hin_1203 ribosomal protein s1:rps1 (gtcfc:10.4) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_1203 HIN_1203 Haemophilus influenzae 727 -11537999 121180 rpsa:hi1220 (de:30s ribosomal protein s1) (db:swissprot) RS1_HAEIN Q48082 HAEMOPHILUS INFLUENZAE 727 -11537999 7500890984 hi1220 ribosomal protein s1 rps1 (db:genpept-bct1) (de:haemophilus influenzae rd section 116 of 163 of the completegenome.) (nt:similar to sp:p02349 gb:v00342 gb:v00352 gb:x04864) (le:9010) (re:10659) (di:direct) U32801 U32801 g1574150 Haemophilus influenzae Rd 71421 -11537999 5000695567 (de:(hin120311) (pn:ribosomal protein s1:rps1) (gn:hi1220) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN120311 HIN120311 Haemophilus influenzae 727 10064457

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891112	15793	37949	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891124	15794	37950	342	113

Description

5000695568 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1222 HI1222 Haemophilus influenzae 727 -11538000 110465 hi1222 (de:hypothetical protein hi1222) (db:swissprot) YCIS_HAEIN P44129 HAEMOPHILUS INFLUENZAE 727 -11538000 166682 hypothetical protein hi1222 (cl:hypothetical protein hi1222) (db:pir2.dat) C64022 C64022 Haemophilus influenzae 727 -11538000 7500921836 hi1222 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 117 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787535 percent ident:) (le:451) (re:744) (di:direct) U32802 U32802 g1574153 Haemophilus influenzae Rd 71421 -11538000 6500734142 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1222 HI1222 Haemophilus influenzae 727 -11538000

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891125	15795	37951	960	320

Description

5000695569 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1223 HI1223 Haemophilus influenzae 727 -11538001 110822 hi1223 (de:hypothetical protein hi1223 precursor) (db:swissprot) YCIM_HAEIN P44130 HAEMOPHILUS INFLUENZAE 727 -11538001 166683 hypothetical protein hi1223 (cl:hypothetical protein hi1223:tetratricopeptide repeat homology) (db:pir2.dat) D64022 D64022 Haemophilus influenzae 727 -11538001 7500921830 hi1223 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 117 of 163 of the completegenome.) (nt:similar to sp:p45576 gb:u00096 pid:2367116 percent) (le:744) (re:1934) (di:direct) U32802 U32802 g1574154 Haemophilus influenzae Rd 71421 -11538001 6500734143 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1223 HI1223 Haemophilus influenzae 727 -11538001

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891134	15796	37952	960	319

Description

5000695570 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1235 HI1235 Haemophilus influenzae 727 -11538002 110499 hi1235 (de:hypothetical protein hi1235 precursor) (db:swissprot) YC35_HAEIN P44131 HAEMOPHILUS INFLUENZAE 727 -11538002 166685 hypothetical protein hi1235 (db:pir2.dat) E64022 E64022 Haemophilus influenzae 727 -11538002 7500921461 hi1235 h. influenzae predicted coding region hi1235 (db:genpept-bct1) (de:haemophilus influenzae rd section 118 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5427) (re:5894) (di:complement) U32803 U32803 g1574169 Haemophilus influenzae Rd 71421 -11538002 6500734144 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1235 HI1235 Haemophilus influenzae 727 -11538002

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891144	15797	37953	207	68

Description

5000695571 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1241 HI1241 Haemophilus influenzae 727 -11538003 110514 hi1241 (de:hypothetical protein hi1241) (db:swissprot) YC41_HAEIN P44133 HAEMOPHILUS INFLUENZAE 727 -11538003 166688 hypothetical protein hi1241 (db:pir2.dat) G64022 G64022 Haemophilus influenzae 727 -11538003 7500921469 hi1241 h. influenzae predicted coding region hi1241 (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2104) (re:2904) (di:direct) U32804 U32804 g1574173 Haemophilus influenzae Rd 71421 -11538003 6500734145 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1241 HI1241 Haemophilus influenzae 727 -11538003

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891145	15798	37954	570	189

Description

5000695572 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1244 HI1244 Haemophilus influenzae 727 -11538004 110520 hi1244 (de:hypothetical protein hi1244) (db:swissprot) YC44_HAEIN P44134 HAEMOPHILUS INFLUENZAE 727 -11538004 166690 hypothetical protein hi1244 (db:pir2.dat) H64022 H64022 Haemophilus influenzae 727 -11538004 7500921476 hi1244 h. influenzae predicted coding region hi1244 (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4923) (re:5543) (di:complement) U32804 U32804 g1574179 Haemophilus influenzae Rd 71421 -11538004 6500734146 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1244 HI1244 Haemophilus influenzae 727 -11538004

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891156	15799	37955	1419	472

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891158	15800	37956	492	164

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891167	15801	37957	711	236

Description

5000695573 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1246 HI1246 Haemophilus influenzae 727 -11538005 110525 hi1246 (de:hypothetical protein hi1246) (db:swissprot) YC46_HAEIN P44135 HAEMOPHILUS INFLUENZAE 727 -11538005 166691 hypothetical protein hi1246 (db:pir2.dat) I64022 I64022 Haemophilus influenzae 727 -11538005 7500921481 hi1246 h. influenzae predicted coding region hi1246 (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8221) (re:10164) (di:direct) U32804 U32804 g1574177 Haemophilus influenzae Rd 71421 -11538005 6500734147 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1246 HI1246 Haemophilus influenzae 727 -11538005

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891168	15802	37958	741	246

Description

5000695574 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1248 HI1248 Haemophilus influenzae 727 -11538006 110530 hi1248 (de:hypothetical protein hi1248) (db:swissprot) YC48_HAEIN P44136 HAEMOPHILUS INFLUENZAE 727 -11538006 166692 hypothetical protein hi1248 (db:pir2.dat) A64023 A64023 Haemophilus influenzae 727 -11538006 7500921487 hi1248 h. influenzae predicted coding region hi1248 (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:425) (re:1393) (di:complement) U32805 U32805 g1574190 Haemophilus influenzae Rd 71421 -11538006 6500734148 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1248 HI1248 Haemophilus influenzae 727 -11538006

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891172	15803	37959	291	96

Description

5000695575 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1249 HI1249 Haemophilus influenzae 727 -11538007 110531 hi1249 (de:hypothetical protein hi1249 precursor) (db:swissprot) YC49_HAEIN P44137 HAEMOPHILUS INFLUENZAE 727 -11538007 166693 hypothetical protein hi1249 (db:pir2.dat) B64023 B64023 Haemophilus influenzae 727 -11538007 7500921488 hi1249 h. influenzae predicted coding region hi1249 (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1396) (re:2016) (di:complement) U32805 U32805 g1574181 Haemophilus influenzae Rd 71421 -11538007 6500734149 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1249 HI1249 Haemophilus influenzae 727 -11538007

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891182	15804	37960	585	194

Description

5000695576 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1250 HI1250 Haemophilus influenzae 727 -11538008 110536 hi1250 (de:hypothetical protein hi1250) (db:swissprot) YC50_HAEIN P44138 HAEMOPHILUS INFLUENZAE 727 -11538008 166694 hypothetical protein hi1250 (db:pir2.dat) C64023 C64023 Haemophilus influenzae 727 -11538008 7500921490 hi1250 h. influenzae predicted coding region hi1250 (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2341) (re:2646) (di:direct) U32805 U32805 g1574182 Haemophilus influenzae Rd 71421 -11538008 6500734150 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1250 HI1250 Haemophilus influenzae 727 -11538008

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891184	15805	37961	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891186	15806	37962	639	212

Description

5000695577 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1253 HI1253 Haemophilus influenzae 727 -11538009 110537 hi1253 (de:hypothetical protein hi1253) (db:swissprot) YC53_HAEIN P44139 HAEMOPHILUS INFLUENZAE 727 -11538009 166696 hypothetical protein hi1253 (cl:hypothetical protein hi1253) (db:pir2.dat) D64023 D64023 Haemophilus influenzae 727 -11538009 7500921491 hi1253 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:similar to pid:968932 gb:u00096 pid:1787464 percent) (le:4833) (re:5216) (di:direct) U32805 U32805 g1574185 Haemophilus influenzae Rd 71421 -11538009 6500734151 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1253 HI1253 Haemophilus influenzae 727 -11538009

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891190	15807	37963	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891199	15808	37964	234	77

Description

5000695578 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1254 HI1254 Haemophilus influenzae 727 -11538010 110538 hi1254 (de:hypothetical protein hi1254 precursor) (db:swissprot) YC54_HAEIN P44140 HAEMOPHILUS INFLUENZAE 727 -11538010 166697 hypothetical protein hi1254 (db:pir2.dat) E64023 E64023 Haemophilus influenzae 727 -11538010 7500921492 hi1254 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p76562 pid:1788818 percent) (le:5221) (re:6282) (di:direct) U32805 U32805 g1574186 Haemophilus influenzae Rd 71421 -11538010 6500734152 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1254 HI1254 Haemophilus influenzae 727 -11538010

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891200	15809	37965	483	160

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891222	15810	37966	357	118

Description

5000695579 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1255 HI1255 Haemophilus influenzae 727 -11538011 110540 hi1255 (de:hypothetical protein hi1255) (db:swissprot) YC55_HAEIN P44141 HAEMOPHILUS INFLUENZAE 727 -11538011 166698 hypothetical protein hi1255 (db:pir2.dat) F64023 F64023 Haemophilus influenzae 727 -11538011 7500921497 hi1255 h. influenzae predicted coding region hi1255 (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6505) (re:6729) (di:direct) U32805 U32805 g1574187 Haemophilus influenzae Rd 71421 -11538011 6500734153 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1255 HI1255 Haemophilus influenzae 727 -11538011

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891234	15811	37967	504	167

Description

5000695580 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1256 HI1256 Haemophilus influenzae 727 -11538012 110541 hi1256 (de:hypothetical protein hi1256) (db:swissprot) YC56_HAEIN P44142 HAEMOPHILUS INFLUENZAE 727 -11538012 166699 hypothetical protein hi1256 (db:pir2.dat) G64023 G64023 Haemophilus influenzae 727 -11538012 7500921498 hi1256 h. influenzae predicted coding region hi1256 (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6726) (re:7190) (di:direct) U32805 U32805 g1574191 Haemophilus influenzae Rd 71421 -11538012 6500734154 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1256 HI1256 Haemophilus influenzae 727 -11538012

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891240	15812	37968	1557	518

Description

5000695581 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1257 HI1257 Haemophilus influenzae 727 -11538013 110542 hi1257 (de:hypothetical protein hi1257) (db:swissprot) YC57_HAEIN P44143 HAEMOPHILUS INFLUENZAE 727 -11538013 166700 hypothetical protein hi1257 (db:pir2.dat) H64023 H64023 Haemophilus influenzae 727 -11538013 7500921502 hi1257 h. influenzae predicted coding region hi1257 (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7187) (re:7360) (di:direct) U32805 U32805 g1574192 Haemophilus influenzae Rd 71421 -11538013 6500734155 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1257 HI1257 Haemophilus influenzae 727 -11538013

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891254	15813	37969	480	159

Description

5000695582 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1265 HI1265 Haemophilus influenzae 727 -11538014 110543 hi1265 (de:hypothetical protein hi1265) (db:swissprot) YCAO_HAEIN P44144 HAEMOPHILUS INFLUENZAE 727 -11538014 7500921552 hi1265 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 121 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75838 pid:1787133 percent) (le:7804) (re:9567) (di:complement) U32806 U32806 g1574723 Haemophilus influenzae Rd 71421 -11538014 6500734156 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1265 HI1265 Haemophilus influenzae 727 -11538014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891257	15814	37970	2178	725

Description

5000695583 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1266 HI1266 Haemophilus influenzae 727 -11538015 110544 hi1266 (de:hypothetical protein hi1266) (db:swissprot) YC66_HAEIN P44145 HAEMOPHILUS INFLUENZAE 727 -11538015 166703 hypothetical protein hi1266 (db:pir2.dat) A64024 A64024 Haemophilus influenzae 727 -11538015 7500921505 hi1266 h. influenzae predicted coding region hi1266 (db:genpept-bct1) (de:haemophilus influenzae rd section 121 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9704) (re:10090) (di:complement) U32806 U32806 g1574724 Haemophilus influenzae Rd 71421 -11538015 6500734157 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1266 HI1266 Haemophilus influenzae 727 -11538015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891294	15815	37971	531	176

Description

5000695584 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1267 HI1267 Haemophilus influenzae 727 -11538016 110545 hi1267 (de:hypothetical protein hi1267) (db:swissprot) YC67_HAEIN P44146 HAEMOPHILUS INFLUENZAE 727 -11538016 166704 hypothetical protein hi1267 (db:pir2.dat) B64024 B64024 Haemophilus influenzae 727 -11538016 6500734158 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1267 HI1267 Haemophilus influenzae 727 -11538016

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891295	15816	37972	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891296	15817	37973	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891297	15818	37974	1131	376

Description

GTC ORF with score 437 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone c1241.) (nt:similar to h.sapience basic transcription factor) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891303	15819	37975	1125	374

Description

5000695585 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1268 HI1268 Haemophilus influenzae 727 -11538017 110546 hi1268 (de:hypothetical protein hi1268) (db:swissprot) YC68_HAEIN P44147 HAEMOPHILUS INFLUENZAE 727 -11538017 166705 hypothetical protein hi1268 (db:pir2.dat) C64024 C64024 Haemophilus influenzae 727 -11538017 7500921506 hi1268 h. influenzae predicted coding region hi1268 (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:189) (re:368) (di:direct) U32807 U32807 g1574737 Haemophilus influenzae Rd 71421 -11538017 6500734159 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1268 HI1268 Haemophilus influenzae 727 -11538017

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891333	15820	37976	780	260

Description

5000695586 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1269 HI1269 Haemophilus influenzae 727 -11538018 110547 hi1269 (de:hypothetical protein hi1269) (db:swissprot) YC69_HAEIN P44148 HAEMOPHILUS INFLUENZAE 727 -11538018 166706 hypothetical protein hi1269 (db:pir2.dat) D64024 D64024 Haemophilus influenzae 727 -11538018 7500921507 hi1269 h. influenzae predicted coding region hi1269 (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:362) (re:478) (di:direct) U32807 U32807 g1574738 Haemophilus influenzae Rd 71421 -11538018 6500734160 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1269 HI1269 Haemophilus influenzae 727 -11538018

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891348	15821	37977	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891349	15822	37978	393	130

Description

5000695587 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1270 HI1270 Haemophilus influenzae 727 -11538019 110548 hi1270 (de:hypothetical protein hi1270) (db:swissprot) YC70_HAEIN P44149 HAEMOPHILUS INFLUENZAE 727 -11538019 166707 hypothetical protein hi1270 (db:pir2.dat) E64024 E64024 Haemophilus influenzae 727 -11538019 6500734161 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1270 HI1270 Haemophilus influenzae 727 -11538019

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891356	15823	37979	192	63

Description

5000695588 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1273 HI1273 Haemophilus influenzae 727 -11538020 110549 hi1273 (de:hypothetical protein hi1273) (db:swissprot) YC73_HAEIN P44150 HAEMOPHILUS INFLUENZAE 727 -11538020 166708 hypothetical protein hi1273 (db:pir2.dat) F64024 F64024 Haemophilus influenzae 727 -11538020 7500921509 hi1273 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:similar to pid:1816658 percent ident: 37.25;) (le:1990) (re:2796) (di:direct) U32807 U32807 g1574728 Haemophilus influenzae Rd 71421 -11538020 6500734162 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1273 HI1273 Haemophilus influenzae 727 -11538020

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891358	15824	37980	555	184

Description

5000695589 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1286 HI1286 Haemophilus influenzae 727 -11538021 110551 hi1286 (de:hypothetical protein hi1286) (db:swissprot) YC86_HAEIN P44152 HAEMOPHILUS INFLUENZAE 727 -11538021 166710 hypothetical protein hi1286 (db:pir2.dat) H64024 H64024 Haemophilus influenzae 727 -11538021 7500921514 hi1286 type i restriction/modification specificity (db:genpept-bct1) (de:haemophilus influenzae rd section 123 of 163 of the completegenome.) (nt:similar to pid:1685099 percent ident: 37.25;) (le:8961) (re:10340) (di:complement) U32808 U32808 g1574744 Haemophilus influenzae Rd 71421 -11538021 6500734163 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1286 HI1286 Haemophilus influenzae 727 -11538021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891359	15825	37981	1305	434

Description

5000695590 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1291 HI1291 Haemophilus influenzae 727 -11538022 110552 hi1291 (de:hypothetical protein hi1291) (db:swissprot) YQCD_HAEIN P44153 HAEMOPHILUS INFLUENZAE 727 -11538022 166711 hypothetical protein hi1291 (cl:hypothetical protein ykvm) (db:pir2.dat) I64024 I64024 Haemophilus influenzae 727 -11538022 7500952379 hi1291 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to pid:882689 gb:u00096 sp:q46920) (le:2838) (re:3677) (di:complement) U32809 U32809 g1574750 Haemophilus influenzae Rd 71421 -11538022 6500734164 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1291 HI1291 Haemophilus influenzae 727 -11538022

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891360	15826	37982	1059	352

Description

5000695591 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1292 HI1292 Haemophilus influenzae 727 -11538023 110554 hi1292 (de:hypothetical protein hi1292) (db:swissprot) YC92_HAEIN P44154 HAEMOPHILUS INFLUENZAE 727 -11538023 166712 hypothetical protein hi1292 (db:pir2.dat) A64025 A64025 Haemophilus influenzae 727 -11538023 7500921528 hi1292 h. influenzae predicted coding region hi1292 (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3804) (re:4589) (di:complement) U32809 U32809 g1574751 Haemophilus influenzae Rd 71421 -11538023 6500734165 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1292 HI1292 Haemophilus influenzae 727 -11538023

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891365	15827	37983	780	259

Description

5000695592 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1293 HI1293 Haemophilus influenzae 727 -11538024 166713 hypothetical protein hi1293 (db:pir2.dat) B64025 B64025 Haemophilus influenzae 727 -11538024 6500734166 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1293 HI1293 Haemophilus influenzae 727 -11538024 110555 yc93_haein (de:hypothetical protein hi1293.) P44155 P44155 Haemophilus influenzae 727 -11538024

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891368	15828	37984	1203	400

Description

5000695593 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1294 HI1294 Haemophilus influenzae 727 -11538025 166714 hypothetical protein hi1294 (db:pir2.dat) C64025 C64025 Haemophilus influenzae 727 -11538025 6500734167 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1294 HI1294 Haemophilus influenzae 727 -11538025

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891370	15829	37985	828	275

Description

5000695594 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1306 HI1306 Haemophilus influenzae 727 -11538026 111078 pgpa:hi1306 (ec:3.1.3.27) (de:phosphatidylglycerophosphatase a,) (db:swissprot) PGPA_HAEIN P44157 HAEMOPHILUS INFLUENZAE 727 -11538026 166719 hypothetical protein hi1306 (cl:conserved hypothetical protein hi1306) (db:pir2.dat) D64025 D64025 Haemophilus influenzae 727 -11538026 7500887981 hi1306 phosphatidylglycerophosphatase a pgpa (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1773102 pid:1786620) (le:3659) (re:4150) (di:direct) U32810 U32810 g1574765 Haemophilus influenzae Rd 71421 -11538026 6500734168 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1306 HI1306 Haemophilus influenzae 727 -11538026

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891377	15830	37986	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891400	15831	37987	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891414	15832	37988	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891418	15833	37989	456	151

Description

5000695595 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1309 HI1309 Haemophilus influenzae 727 -11538027 111800 hi1309 (de:hypothetical protein hi1309) (db:swissprot) YFAE_HAEIN P45154 HAEMOPHILUS INFLUENZAE 727 -11538027 166720 conserved hypothetical protein hi1309 (db:pir2.dat) G64170 G64170 Haemophilus influenzae 727 -11538027 7500923317 hi1309 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to sp:p37910 gb:u00096 pid:1788568 percent) (le:5603) (re:5851) (di:complement) U32810 U32810 g1574768 Haemophilus influenzae Rd 71421 -11538027 6500734169 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1309 HI1309 Haemophilus influenzae 727 -11538027

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891419	15834	37990	306	101

Description

5000695596 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1310 HI1310 Haemophilus influenzae 727 -11538028 111081 hi1310 (de:hypothetical protein hi1310) (db:swissprot) YD10_HAEIN P44158 HAEMOPHILUS INFLUENZAE 727 -11538028 166721 hypothetical protein hi1310 (db:pir2.dat) E64025 E64025 Haemophilus influenzae 727 -11538028 7500922058 hi1310 h. influenzae predicted coding region hi1310 (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5876) (re:6637) (di:direct) U32810 U32810 g1574773 Haemophilus influenzae Rd 71421 -11538028 6500734170 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1310 HI1310 Haemophilus influenzae 727 -11538028

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891424	15835	37991	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891425	15836	37992	432	143

Description

GTC ORF with score 216 to: (or:Caenorhabditis elegans) (db:genpept) (de:caenorhabditis elegans cosmid y54g11a, complete sequence.) (nt:predicted using genefinder; cdna est yk433c6.3) (le:823:993:2148:2322:3615) (re:912:1100:2270:2431:3816) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891426	15837	37993	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891460	15838	37994	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891463	15839	37995	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891473	15840	37996	384	127

Description

5000695597 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1316 HI1316 Haemophilus influenzae 727 -11538029 111087 hi1316 (de:hypothetical protein hi1316) (db:swissprot) YD16_HAEIN P44159 HAEMOPHILUS INFLUENZAE 727 -11538029 166724 hypothetical protein hi1316 (db:pir2.dat) F64025 F64025 Haemophilus influenzae 727 -11538029 7500922061 hi1316 h. influenzae predicted coding region hi1316 (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:819) (re:1403) (di:direct) U32811 U32811 g1574776 Haemophilus influenzae Rd 71421 -11538029 6500734171 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1316 HI1316 Haemophilus influenzae 727 -11538029

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891474	15841	37997	1314	437

Description

5000695598 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1323 HI1323 Haemophilus influenzae 727 -11538030 110595 hi1323 (de:hypothetical protein hi1323) (db:swissprot) YCBG_HAEIN P44161 HAEMOPHILUS INFLUENZAE 727 -11538030 166726 hypothetical protein hi1323 (db:pir2.dat) H64025 H64025 Haemophilus influenzae 727 -11538030 7500921573 hi1323 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:similar to sp:p45569 gb:u00096 pid:1787190 percent) (le:9542) (re:9988) (di:complement) U32811 U32811 g1574783 Haemophilus influenzae Rd 71421 -11538030 6500734172 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1323 HI1323 Haemophilus influenzae 727 -11538030

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891476	15842	37998	360	119

Description

5000695599 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1326 HI1326 Haemophilus influenzae 727 -11538031 111101 hi1326 (de:hypothetical protein hi1326) (db:swissprot) YD26_HAEIN P44162 HAEMOPHILUS INFLUENZAE 727 -11538031 166727 hypothetical protein hi1326 (db:pir2.dat) I64025 I64025 Haemophilus influenzae 727 -11538031 7500922074 hi1326 h. influenzae predicted coding region hi1326 (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2820) (re:3548) (di:direct) U32812 U32812 g1574787 Haemophilus influenzae Rd 71421 -11538031 6500734173 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1326 HI1326 Haemophilus influenzae 727 -11538031

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891483	15843	37999	396	131

Description

5000695600 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1327 HI1327 Haemophilus influenzae 727 -11538032 111103 hi1327 (de:hypothetical protein hi1327) (db:swissprot) YD27_HAEIN P44163 HAEMOPHILUS INFLUENZAE 727 -11538032 166728 hypothetical protein hi1327 (db:pir2.dat) A64026 A64026 Haemophilus influenzae 727 -11538032 7500922075 hi1327 h. influenzae predicted coding region hi1327 (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3545) (re:3682) (di:direct) U32812 U32812 g1574794 Haemophilus influenzae Rd 71421 -11538032 6500734174 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1327 HI1327 Haemophilus influenzae 727 -11538032

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891484	15844	38000	588	195

Description

6500734175 hi1333:hin_1311 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_1311 HIN_1311 Haemophilus influenzae 727 -11538033 7500936786 hi1333 (de:hypothetical protein hi1333) (db:swissprot) YHBY_HAEIN P71376 HAEMOPHILUS INFLUENZAE 727 -11538033 7500936787 hi1333 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 127 of 163 of the completegenome.) (nt:similar to sp:p42550 pid:606118 gb:u00096) (le:6977) (re:7276) (di:complement) U32812 U32812 g1574791 Haemophilus influenzae Rd 71421 -11538033 5000695601 (de:(hin131111) (pn:hypothetical) (gn:hi1333) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN131111 HIN131111 Haemophilus influenzae 727 10126714

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891499	15845	38001	420	139

Description

5000695602 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1338 HI1338 Haemophilus influenzae 727 -11538034 111119 sixa:hi1338 (ec:3.1.3.-) (de:phosphohistidine phosphatase sixa homolog,) (db:swissprot) SIXA_HAEIN P44164 HAEMOPHILUS INFLUENZAE 727 -11538034 166729 hypothetical protein hi1338 (cl:hypothetical protein hi1338) (db:pir2.dat) B64026 B64026 Haemophilus influenzae 727 -11538034 7500891667 hi1338 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788681 percent ident:) (le:2347) (re:2841) (di:direct) U32813 U32813 g1574807 Haemophilus influenzae Rd 71421 -11538034 7500891668 hi1462.2 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 139 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788681 percent ident:) (le:4581) (re:5075) (di:complement) U32824 U32824 g3212224 Haemophilus influenzae Rd 71421 -11538034 6500734176 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1338 HI1338 Haemophilus influenzae 727 -11538034

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891511	15846	38002	621	206

Description

5000695603 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1340 HI1340 Haemophilus influenzae 727 -11538035 111126 hi1340 (de:hypothetical protein hi1340) (db:swissprot) YD40_HAEIN P44165 HAEMOPHILUS INFLUENZAE 727 -11538035 166730 hypothetical protein hi1340 (db:pir2.dat) C64026 C64026 Haemophilus influenzae 727 -11538035 7500922092 hi1340 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to pid:882689 gb:u00096 sp:q46920) (le:3510) (re:4835) (di:complement) U32813 U32813 g1574800 Haemophilus influenzae Rd 71421 -11538035 6500734177 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1340 HI1340 Haemophilus influenzae 727 -11538035

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891520	15847	38003	462	153

Description

5000695604 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1341 HI1341 Haemophilus influenzae 727 -11538036 111127 hi1341 (de:hypothetical protein hi1341) (db:swissprot) YD41_HAEIN P44166 HAEMOPHILUS INFLUENZAE 727 -11538036 166731 hypothetical protein hi1341 (db:pir2.dat) D64026 D64026 Haemophilus influenzae 727 -11538036 7500922095 hi1341 h. influenzae predicted coding region hi1341 (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4962) (re:5573) (di:complement) U32813 U32813 g1574808 Haemophilus influenzae Rd 71421 -11538036 6500734178 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1341 HI1341 Haemophilus influenzae 727 -11538036

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891528	15848	38004	429	142

Description

5000695605 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1349 HI1349 Haemophilus influenzae 727 -11538037 111138 hi1349 (de:hypothetical protein hi1349) (db:swissprot) YD49_HAEIN P45173 HAEMOPHILUS INFLUENZAE 727 -11538037 166733 hypothetical protein hi1349 (cl:hypothetical protein hi1349) (db:pir2.dat) C64171 C64171 Haemophilus influenzae 727 -11538037 7500922096 hi1349 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 129 of 163 of the completegenome.) (nt:similar to pid:1652428 percent ident: 31.37;) (le:1967) (re:2449) (di:complement) U32814 U32814 g1574811 Haemophilus influenzae Rd 71421 -11538037 6500734179 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1349 HI1349 Haemophilus influenzae 727 -11538037

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891529	15849	38005	798	265

Description

5000695606 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1351 HI1351 Haemophilus influenzae 727 -11538038 111144 hi1351 (de:hypothetical protein hi1351) (db:swissprot) YECP_HAEIN P44167 HAEMOPHILUS INFLUENZAE 727 -11538038 166734 hypothetical protein hi1351 (cl:conserved hypothetical protein hp0419:bioc homology) (db:pir2.dat) E64026 E64026 Haemophilus influenzae 727 -11538038 7500922953 hi1351 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 129 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788178 percent ident:) (le:3644) (re:4609) (di:complement) U32814 U32814 g1574813 Haemophilus influenzae Rd 71421 -11538038 6500734180 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1351 HI1351 Haemophilus influenzae 727 -11538038

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891530	15850	38006	513	170

Description

5000695607 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1355 HI1355 Haemophilus influenzae 727 -11538039 111147 hi1355 (de:hypothetical protein hi1355) (db:swissprot) YCGN_HAEIN P44168 HAEMOPHILUS INFLUENZAE 727 -11538039 166735 hypothetical protein hi1355 (cl:hypothetical protein hi1355) (db:pir2.dat) F64026 F64026 Haemophilus influenzae 727 -11538039 7500921794 hi1355 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 129 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787429 percent ident:) (le:9870) (re:10334) (di:direct) U32814 U32814 g1574817 Haemophilus influenzae Rd 71421 -11538039 6500734181 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1355 HI1355 Haemophilus influenzae 727 -11538039

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891533	15851	38007	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891538	15852	38008	618	205

Description

6500734182 hi1371:hin_1350 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_1350 HIN_1350 Haemophilus influenzae 727 -11538040 5500686519 hi1371.1 (de:hypothetical protein hi1371.1) (db:swissprot) YDAO_HAEIN Q57184 HAEMOPHILUS INFLUENZAE 727 -11538040 7500922155 hi1371.1 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 132 of 163 of the completegenome.) (nt:similar to gb:d21139 pid:415267 gb:u00096 sp:p76055) (le:3293) (re:4234) (di:complement) U32817 U32817 g1574205 Haemophilus influenzae Rd 71421 -11538040 5000695608 (de:(hin135011) (pn:hypothetical) (gn:hi1371) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN135011 HIN135011 Haemophilus influenzae 727 10126715

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891542	15853	38009	435	144

Description

5000695609 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1375 HI1375 Haemophilus influenzae 727 -11538041 111173 hi1375 (de:hypothetical protein hi1375) (db:swissprot) YD75_HAEIN P44169 HAEMOPHILUS INFLUENZAE 727 -11538041 166740 hypothetical protein hi1375 (db:pir2.dat) H64026 H64026 Haemophilus influenzae 727 -11538041 7500922107 hi1375 h. influenzae predicted coding region hi1375 (db:genpept-bct1) (de:haemophilus influenzae rd section 133 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:66) (re:974) (di:direct) U32818 U32818 g1574217 Haemophilus influenzae Rd 71421 -11538041 6500734183 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1375 HI1375 Haemophilus influenzae 727 -11538041

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891550	15854	38010	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891564	15855	38011	2943	980

Description

5000695610 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1376 HI1376 Haemophilus influenzae 727 -11538042 111174 hi1376 (de:hypothetical protein hi1376) (db:swissprot) YD76_HAEIN P44170 HAEMOPHILUS INFLUENZAE 727 -11538042 166741 hypothetical protein hi1376 (db:pir2.dat) I64026 I64026 Haemophilus influenzae 727 -11538042 7500922108 hi1376 h. influenzae predicted coding region hi1376 (db:genpept-bct1) (de:haemophilus influenzae rd section 133 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:977) (re:1852) (di:direct) U32818 U32818 g1574210 Haemophilus influenzae Rd 71421 -11538042 6500734184 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1376 HI1376 Haemophilus influenzae 727 -11538042

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891568	15856	38012	573	190

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891596	15857	38013	723	240

Description

GTC ORF with score 105 to: (db:genpept) (de:sphingomonas sp. a8an3 catechol 2,3-dioxygenase gene, complete cdsand 2-hydroxymuconic semialdehyde hydrolase and 2-hydroxymuconicsemialdehyde dehydrogenase genes, partial cds.) (le:<1) (re:688) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891601	15858	38014	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891614	15859	38015	462	153

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891617	15860	38016	1008	335

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891628	15861	38017	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891643	15862	38018	318	105

Description

6500734185 hi1378:hin_1357 phosphate regulon sensor protein:phor (gtcfc:12.13) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_1357 HIN_1357 Haemophilus influenzae 727 -11538043 7500976281 hi1378 phosphate regulon sensor protein phor (db:genpept-bct1) (de:haemophilus influenzae rd section 133 of 163 of the completegenome.) (nt:similar to sp:p08400 gb:x04704 pid:581188 gb:u00096) (le:3977) (re:5254) (di:complement) U32818 U32818 g1574212 Haemophilus influenzae Rd 71421 -11538043 5000695611 (de:(hin135711) (pn:phosphate regulon sensor protein:phor) (gn:hi1378) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN135711 HIN135711 Haemophilus influenzae 727 10126716

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891649	15863	38019	828	276

Description

5000695612 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1386 HI1386 Haemophilus influenzae 727 -11538044 111180 hi1386 (de:hypothetical protein hi1386) (db:swissprot) YD86_HAEIN P44171 HAEMOPHILUS INFLUENZAE 727 -11538044 166742 hypothetical protein hi1386 (db:pir2.dat) A64027 A64027 Haemophilus influenzae 727 -11538044 7500922126 hi1386 h. influenzae predicted coding region hi1386 (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1807) (re:2253) (di:direct) U32819 U32819 g1574228 Haemophilus influenzae Rd 71421 -11538044 6500734186 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1386 HI1386 Haemophilus influenzae 727 -11538044

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891650	15864	38020	831	276

Description

GTC ORF with score 262 to: (fn:hydrolyses c3-acetyl ester and c6-acetyl ester) (sr:rhodococcus sp) (db:genpept-bct2) (de:rhodococcus sp. heroin esterase (her) gene, complete cds.) (nt:acetylmorphine carboxyesterase; ser-160 is the) (le:572) (re:1540) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891664	15865	38021	2385	794

Description

5000695613 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1394 HI1394 Haemophilus influenzae 727 -11538045 111189 hi1394 (de:hypothetical protein hi1394) (db:swissprot) YQFB_HAEIN P44172 HAEMOPHILUS INFLUENZAE 727 -11538045 166743 hypothetical protein hi1394 (db:pir2.dat) B64027 B64027 Haemophilus influenzae 727 -11538045 7500952418 hi1394 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to pid:887850 gb:u00096 sp:q46828) (le:12461) (re:12832) (di:complement) U32819 U32819 g1574227 Haemophilus influenzae Rd 71421 -11538045 6500734187 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1394 HI1394 Haemophilus influenzae 727 -11538045

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891679	15866	38022	477	158

Description

5000695614 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1395 HI1395 Haemophilus influenzae 727 -11538046 111190 hi1395 (de:hypothetical protein hi1395) (db:swissprot) YD95_HAEIN P44173 HAEMOPHILUS INFLUENZAE 727 -11538046 166744 hypothetical protein hi1395 (db:pir2.dat) C64027 C64027 Haemophilus influenzae 727 -11538046 7500922135 hi1395 h. influenzae predicted coding region hi1395 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:141) (re:563) (di:complement) U32820 U32820 g1574232 Haemophilus influenzae Rd 71421 -11538046 6500734188 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1395 HI1395 Haemophilus influenzae 727 -11538046

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891693	15867	38023	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891712	15868	38024	2751	916

Description

5000695615 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1396 HI1396 Haemophilus influenzae 727 -11538047 111193 hi1396 (de:hypothetical protein hi1396) (db:swissprot) YD96_HAEIN P44174 HAEMOPHILUS INFLUENZAE 727 -11538047 166745 hypothetical protein hi1396 (db:pir2.dat) D64027 D64027 Haemophilus influenzae 727 -11538047 7500922137 hi1396 h. influenzae predicted coding region hi1396 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:529) (re:699) (di:complement) U32820 U32820 g1574239 Haemophilus influenzae Rd 71421 -11538047 6500734189 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1396 HI1396 Haemophilus influenzae 727 -11538047

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891716	15869	38025	522	173

Description

6500734190 hi1398:hin_1377 fumarate hydratase class ii:fumarase:fumc (gtcfc:1.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_1377 HIN_1377 Haemophilus influenzae 727 -11538048 7500976285 hi1398 fumarate hydratase:class ii fumc (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:similar to sp:p05042 gb:x00522 gb:x04065 pid:41513) (le:1453) (re:2847) (di:direct) U32820 U32820 g1574234 Haemophilus influenzae Rd 71421 -11538048 5000695616 (de:(hin137711) (pn:fumarate hydratase class ii:fumarase:fumc) (gn:hi1398) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN137711 HIN137711 Haemophilus influenzae 727 10126719

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891733	15870	38026	537	178

Description

5000695617 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1399 HI1399 Haemophilus influenzae 727 -11538049 111197 hi1399 (de:hypothetical protein hi1399) (db:swissprot) YD99_HAEIN P44175 HAEMOPHILUS INFLUENZAE 727 -11538049 166746 hypothetical protein hi1399 (db:pir2.dat) E64027 E64027 Haemophilus influenzae 727 -11538049 7500922143 hi1399 h. influenzae predicted coding region hi1399 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2975) (re:3583) (di:direct) U32820 U32820 g1574240 Haemophilus influenzae Rd 71421 -11538049 6500734191 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1399 HI1399 Haemophilus influenzae 727 -11538049

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891734	15871	38027	702	233

Description

GTC ORF with score 158 to: (fn:integrin analogue) (sr:saccharomyces cerevisiae (library: lambda gt11) dna) (db:genpept-pln1) (de:saccharomyces cerevisiae integrin analogue gene, complete cds.) (nt:putative) (le:1) (re:3049) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891735	15872	38028	252	83

Description

5000695618 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1400 HI1400 Haemophilus influenzae 727 -11538050 111387 hi1400 (de:hypothetical protein hi1400) (db:swissprot) YCIV_HAEIN P44176 HAEMOPHILUS INFLUENZAE 727 -11538050 166747 hypothetical protein hi1400 (cl:hypothetical protein hi1400) (db:pir2.dat) F64027 F64027 Haemophilus influenzae 727 -11538050 7500921842 hi1400 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787520 percent ident:) (le:3682) (re:4506) (di:complement) U32820 U32820 g1574235 Haemophilus influenzae Rd 71421 -11538050 6500734192 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1400 HI1400 Haemophilus influenzae 727 -11538050

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891761	15873	38029	1320	439

Description

5000695619 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1402 HI1402 Haemophilus influenzae 727 -11538051 111388 hi1402 (de:hypothetical protein hi1402) (db:swissprot) YE02_HAEIN P44177 HAEMOPHILUS INFLUENZAE 727 -11538051 166748 hypothetical protein hi1402 (db:pir2.dat) G64027 G64027 Haemophilus influenzae 727 -11538051 7500922568 hi1402 h. influenzae predicted coding region hi1402 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5755) (re:5961) (di:complement) U32820 U32820 g1574241 Haemophilus influenzae Rd 71421 -11538051 6500734193 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1402 HI1402 Haemophilus influenzae 727 -11538051

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891768	15874	38030	945	314

Description

5000695620 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1403 HI1403 Haemophilus influenzae 727 -11538052 111389 hi1403 (de:hypothetical protein hi1403) (db:swissprot) YE03_HAEIN P44178 HAEMOPHILUS INFLUENZAE 727 -11538052 166749 hypothetical protein hi1403 (db:pir2.dat) H64027 H64027 Haemophilus influenzae 727 -11538052 7500922571 hi1403 h. influenzae predicted coding region hi1403 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5994) (re:6542) (di:complement) U32820 U32820 g1574237 Haemophilus influenzae Rd 71421 -11538052 6500734194 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1403 HI1403 Haemophilus influenzae 727 -11538052

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891769	15875	38031	420	139

Description

5000695621 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1404 HI1404 Haemophilus influenzae 727 -11538053 111390 hi1404 (de:hypothetical protein hi1404) (db:swissprot) YE04_HAEIN P44179 HAEMOPHILUS INFLUENZAE 727 -11538053 166750 hypothetical protein hi1404 (db:pir2.dat) I64027 I64027 Haemophilus influenzae 727 -11538053 7500922574 hi1404 h. influenzae predicted coding region hi1404 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6575) (re:6694) (di:complement) U32820 U32820 g1574242 Haemophilus influenzae Rd 71421 -11538053 6500734195 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1404 HI1404 Haemophilus influenzae 727 -11538053

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891770	15876	38032	930	309

Description

5000695622 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1405 HI1405 Haemophilus influenzae 727 -11538054 111392 hi1405 (de:hypothetical protein hi1405) (db:swissprot) YE05_HAEIN P44180 HAEMOPHILUS INFLUENZAE 727 -11538054 166751 hypothetical protein hi1405 (db:pir2.dat) A64028 A64028 Haemophilus influenzae 727 -11538054 7500922576 hi1405 h. influenzae predicted coding region hi1405 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7040) (re:8140) (di:complement) U32820 U32820 g1574243 Haemophilus influenzae Rd 71421 -11538054 6500734196 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1405 HI1405 Haemophilus influenzae 727 -11538054

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891772	15877	38033	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891780	15878	38034	249	82

Description

5000695623 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1406 HI1406 Haemophilus influenzae 727 -11538055 111394 hi1406 (de:hypothetical protein hi1406) (db:swissprot) YE06_HAEIN P44181 HAEMOPHILUS INFLUENZAE 727 -11538055 166752 hypothetical protein hi1406 (db:pir2.dat) B64028 B64028 Haemophilus influenzae 727 -11538055 7500922581 hi1406 h. influenzae predicted coding region hi1406 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8201) (re:8557) (di:complement) U32820 U32820 g1574244 Haemophilus influenzae Rd 71421 -11538055 6500734197 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1406 HI1406 Haemophilus influenzae 727 -11538055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891793	15879	38035	810	269

Description

5000695624 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1409 HI1409 Haemophilus influenzae 727 -11538056 111397 hi1409 (de:hypothetical protein hi1409) (db:swissprot) YE09_HAEIN P44183 HAEMOPHILUS INFLUENZAE 727 -11538056 166754 hypothetical protein hi1409 (db:pir2.dat) D64028 D64028 Haemophilus influenzae 727 -11538056 7500922589 hi1409 h. influenzae predicted coding region hi1409 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:10312) (re:11622) (di:complement) U32820 U32820 g1574246 Haemophilus influenzae Rd 71421 -11538056 6500734198 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1409 HI1409 Haemophilus influenzae 727 -11538056

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891795	15880	38036	1125	374

Description

5000695625 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1408 HI1408 Haemophilus influenzae 727 -11538057 111396 hi1408 (de:hypothetical protein hi1408) (db:swissprot) YE08_HAEIN P44182 HAEMOPHILUS INFLUENZAE 727 -11538057 166753 hypothetical protein hi1408 (db:pir2.dat) C64028 C64028 Haemophilus influenzae 727 -11538057 6500734199 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1408 HI1408 Haemophilus influenzae 727 -11538057

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891809	15881	38037	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891821	15882	38038	195	64

Description

5000695626 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1410 HI1410 Haemophilus influenzae 727 -11538058 111398 hi1410 (de:hypothetical protein hi1410) (db:swissprot) YE10_HAEIN P44184 HAEMOPHILUS INFLUENZAE 727 -11538058 166755 hypothetical protein hi1410 (db:pir2.dat) E64028 E64028 Haemophilus influenzae 727 -11538058 7500922602 hi1410 h. influenzae predicted coding region hi1410 (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:11624) (re:12808) (di:complement) U32820 U32820 g1574247 Haemophilus influenzae Rd 71421 -11538058 6500734200 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1410 HI1410 Haemophilus influenzae 727 -11538058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891851	15883	38039	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891856	15884	38040	810	269

Description

5000695627 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1413 HI1413 Haemophilus influenzae 727 -11538059 111402 hi1413 (de:hypothetical protein hi1413) (db:swissprot) YE13_HAEIN P44185 HAEMOPHILUS INFLUENZAE 727 -11538059 166757 hypothetical protein hi1413 (db:pir2.dat) F64028 F64028 Haemophilus influenzae 727 -11538059 7500922615 hi1413 h. influenzae predicted coding region hi1413 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1277) (re:1558) (di:complement) U32821 U32821 g1574251 Haemophilus influenzae Rd 71421 -11538059 6500734201 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1413 HI1413 Haemophilus influenzae 727 -11538059

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891860	15885	38041	1338	445

Description

5000695628 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1414 HI1414 Haemophilus influenzae 727 -11538060 111404 hi1414 (de:hypothetical protein hi1414) (db:swissprot) YE14_HAEIN P44186 HAEMOPHILUS INFLUENZAE 727 -11538060 166758 hypothetical protein hi1414 (db:pir2.dat) G64028 G64028 Haemophilus influenzae 727 -11538060 7500922617 hi1414 h. influenzae predicted coding region hi1414 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1470) (re:1745) (di:complement) U32821 U32821 g1574262 Haemophilus influenzae Rd 71421 -11538060 6500734202 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1414 HI1414 Haemophilus influenzae 727 -11538060

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891862	15886	38042	570	189

Description

5000695629 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1415 HI1415 Haemophilus influenzae 727 -11538061 111406 hi1415 (de:hypothetical protein hi1415) (db:swissprot) YE15_HAEIN P44187 HAEMOPHILUS INFLUENZAE 727 -11538061 166759 hypothetical protein hi1415 (db:pir2.dat) H64028 H64028 Haemophilus influenzae 727 -11538061 7500922623 hi1415 h. influenzae predicted coding region hi1415 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1738) (re:2340) (di:complement) U32821 U32821 g1574252 Haemophilus influenzae Rd 71421 -11538061 6500734203 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1415 HI1415 Haemophilus influenzae 727 -11538061

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891874	15887	38043	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891875	15888	38044	744	247

Description

GTC ORF with score 161 to: (fn:possible cell cycle progression role - by) (sr:fission yeast) (db:genpept) (de:s.pombe chromosome i cosmid c637.) (nt:spac637.14, len:938, similarity:saccharomyces) (le:31510) (re:34326) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891890	15889	38045	588	195

Description

5000695630 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1416 HI1416 Haemophilus influenzae 727 -11538062 111408 hi1416 (de:hypothetical protein hi1416 precursor) (db:swissprot) YE16_HAEIN P44188 HAEMOPHILUS INFLUENZAE 727 -11538062 166760 hypothetical protein hi1416 (db:pir2.dat) I64028 I64028 Haemophilus influenzae 727 -11538062 7500922625 hi1416 h. influenzae predicted coding region hi1416 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2309) (re:2665) (di:complement) U32821 U32821 g1574253 Haemophilus influenzae Rd 71421 -11538062 6500734204 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1416 HI1416 Haemophilus influenzae 727 -11538062

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891893	15890	38046	489	162

Description

5000695631 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1418 HI1418 Haemophilus influenzae 727 -11538063 111411 hi1418 (de:hypothetical protein hi1418) (db:swissprot) YE18_HAEIN P44189 HAEMOPHILUS INFLUENZAE 727 -11538063 166761 hypothetical protein hi1418 (db:pir2.dat) A64029 A64029 Haemophilus influenzae 727 -11538063 7500922630 hi1418 h. influenzae predicted coding region hi1418 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3103) (re:3708) (di:complement) U32821 U32821 g1574254 Haemophilus influenzae Rd 71421 -11538063 6500734205 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1418 HI1418 Haemophilus influenzae 727 -11538063

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891899	15891	38047	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891900	15892	38048	1158	385

Description

5000695632 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1419 HI1419 Haemophilus influenzae 727 -11538064 111413 hi1419 (de:hypothetical protein hi1419) (db:swissprot) YE19_HAEIN P44190 HAEMOPHILUS INFLUENZAE 727 -11538064 166762 hypothetical protein hi1419 (db:pir2.dat) B64029 B64029 Haemophilus influenzae 727 -11538064 7500922635 hi1419 h. influenzae predicted coding region hi1419 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4030) (re:4329) (di:direct) U32821 U32821 g1574255 Haemophilus influenzae Rd 71421 -11538064 6500734206 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1419 HI1419 Haemophilus influenzae 727 -11538064

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891905	15893	38049	519	172

Description

5000695633 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1420 HI1420 Haemophilus influenzae 727 -11538065 111416 hi1420 (de:hypothetical protein hi1420) (db:swissprot) YE20_HAEIN P44191 HAEMOPHILUS INFLUENZAE 727 -11538065 166763 hypothetical protein hi1420 (db:pir2.dat) C64029 C64029 Haemophilus influenzae 727 -11538065 7500922658 hi1420 h. influenzae predicted coding region hi1420 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4326) (re:4619) (di:direct) U32821 U32821 g1574263 Haemophilus influenzae Rd 71421 -11538065 6500734207 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1420 HI1420 Haemophilus influenzae 727 -11538065

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891913	15894	38050	1548	515

Description

5000695634 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1421 HI1421 Haemophilus influenzae 727 -11538066 111418 hi1421 (de:hypothetical protein hi1421) (db:swissprot) YE21_HAEIN P44192 HAEMOPHILUS INFLUENZAE 727 -11538066 166764 hypothetical protein hi1421 (db:pir2.dat) D64029 D64029 Haemophilus influenzae 727 -11538066 7500922661 hi1421 h. influenzae predicted coding region hi1421 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4650) (re:4928) (di:complement) U32821 U32821 g1574264 Haemophilus influenzae Rd 71421 -11538066 6500734208 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1421 HI1421 Haemophilus influenzae 727 -11538066

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891920	15895	38051	429	142

Description

5000695635 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1422 HI1422 Haemophilus influenzae 727 -11538067 111419 hi1422 (de:hypothetical protein hi1422) (db:swissprot) YE22_HAEIN P44193 HAEMOPHILUS INFLUENZAE 727 -11538067 166765 hypothetical protein hi1422 (db:pir2.dat) E64029 E64029 Haemophilus influenzae 727 -11538067 7500922662 hi1422 h. influenzae predicted coding region hi1422 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5081) (re:5656) (di:direct) U32821 U32821 g1574256 Haemophilus influenzae Rd 71421 -11538067 6500734209 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1422 HI1422 Haemophilus influenzae 727 -11538067

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891929	15896	38052	315	104

Description

5000695636 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1423 HI1423 Haemophilus influenzae 727 -11538068 111420 hi1423 (de:hypothetical protein hi1423) (db:swissprot) YE23_HAEIN P44194 HAEMOPHILUS INFLUENZAE 727 -11538068 166766 hypothetical protein hi1423 (db:pir2.dat) F64029 F64029 Haemophilus influenzae 727 -11538068 7500922663 hi1423 h. influenzae predicted coding region hi1423 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5942) (re:6226) (di:direct) U32821 U32821 g1574257 Haemophilus influenzae Rd 71421 -11538068 6500734210 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1423 HI1423 Haemophilus influenzae 727 -11538068

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891936	15897	38053	438	146

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891948	15898	38054	339	112

Description

5000695637 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1427 HI1427 Haemophilus influenzae 727 -11538069 111423 hi1427 (de:hypothetical protein hi1427 precursor) (db:swissprot) YE27_HAEIN P44196 HAEMOPHILUS INFLUENZAE 727 -11538069 166768 hypothetical protein hi1427 (db:pir2.dat) H64029 H64029 Haemophilus influenzae 727 -11538069 7500922673 hi1427 h. influenzae predicted coding region hi1427 (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9676) (re:10512) (di:direct) U32821 U32821 g1574261 Haemophilus influenzae Rd 71421 -11538069 6500734211 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1427 HI1427 Haemophilus influenzae 727 -11538069

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891952	15899	38055	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891960	15900	38056	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891961	15901	38057	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891963	15902	38058	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891964	15903	38059	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501891973	15904	38060	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892007	15905	38061	1458	485

Description

6500734212 cspd:hi1434b cold shock-like protein (gtcfc:12.7) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1434B HI1434B Haemophilus influenzae 727 -11538070 66664 cspd:hi1434.1 (de:cold shock-like protein cspd) (db:swissprot) CSPD_HAEIN P46449 HAEMOPHILUS INFLUENZAE 727 -11538070 7500879495 hi1434.1 cold shock-like protein cspd (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to sp:p24245 gb:u00096 pid:1651400) (le:6537) (re:6755) (di:complement) U32822 U32822 g1574273 Haemophilus influenzae Rd 71421 -11538070 5000695638 (de:(hi1434b) (pn:cold shock-like protein) (gn:cspd) (gtcfc:13.7) (ec:) (cspd_haein) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HI1434B HI1434B Haemophilus influenzae 727 10009282

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892012	15906	38062	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892018	15907	38063	849	282

Description

5000695639 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1439 HI1439 Haemophilus influenzae 727 -11538071 111425 dxs:hi1439 (de:1-deoxyxylulose-5-phosphate synthase (dxp synthase)) (db:swissprot) DXS_HAEIN P45205 HAEMOPHILUS INFLUENZAE 727 -11538071 166773 dxs dxs protein (cl:hypothetical protein c2814) (db:pir2.dat) B64172 B64172 Haemophilus influenzae 727 -11538071 7500880718 hi1439 1-deoxyxylulose-5-phosphate synthase dxs (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77488 pid:1773104) (le:10906) (re:12783) (di:direct) U32822 U32822 g1574278 Haemophilus influenzae Rd 71421 -11538071 6500734213 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1439 HI1439 Haemophilus influenzae 727 -11538071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892023	15908	38064	603	200

Description

5000695640 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1446 HI1446 Haemophilus influenzae 727 -11538072 111426 hi1446 (de:hypothetical protein hi1446) (db:swissprot) YCGL_HAEIN P44198 HAEMOPHILUS INFLUENZAE 727 -11538072 166774 hypothetical protein hi1446 (cl:hypothetical protein b1179) (db:pir2.dat) A64030 A64030 Haemophilus influenzae 727 -11538072 7500921790 hi1446 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787427 percent ident:) (le:3220) (re:3543) (di:complement) U32823 U32823 g1574295 Haemophilus influenzae Rd 71421 -11538072 6500734214 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1446 HI1446 Haemophilus influenzae 727 -11538072

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892033	15909	38065	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892040	15910	38066	618	205

Description

5000695641 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1450 HI1450 Haemophilus influenzae 727 -11538073 111427 hi1450 (de:hypothetical protein hi1450) (db:swissprot) YCIU_HAEIN P44199 HAEMOPHILUS INFLUENZAE 727 -11538073 166775 hypothetical protein hi1450 (cl:hypothetical protein hi1450) (db:pir2.dat) B64030 B64030 Haemophilus influenzae 727 -11538073 7500922700 hi1450 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787501 percent ident:) (le:6357) (re:6680) (di:direct) U32823 U32823 g1574289 Haemophilus influenzae Rd 71421 -11538073 6500734215 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1450 HI1450 Haemophilus influenzae 727 -11538073

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892044	15911	38067	639	212

Description

5000695642 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1452 HI1452 Haemophilus influenzae 727 -11538074 111429 hi1452 (de:hypothetical protein hi1452) (db:swissprot) YBJE_HAEIN P44201 HAEMOPHILUS INFLUENZAE 727 -11538074 166777 hypothetical protein hi1452 (db:pir2.dat) D64030 D64030 Haemophilus influenzae 727 -11538074 7500896856 hi1452 h. influenzae predicted coding region hi1452 (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6748) (re:7335) (di:complement) U32823 U32823 g1574290 Haemophilus influenzae Rd 71421 -11538074 6500734216 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1452 HI1452 Haemophilus influenzae 727 -11538074

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892049	15912	38068	462	153

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892058	15913	38069	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892071	15914	38070	591	196

Description

5000695643 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1451 HI1451 Haemophilus influenzae 727 -11538075 111428 hi1451 (de:hypothetical protein hi1451) (db:swissprot) YE51_HAEIN P44200 HAEMOPHILUS INFLUENZAE 727 -11538075 166776 hypothetical protein hi1451 (db:pir2.dat) C64030 C64030 Haemophilus influenzae 727 -11538075 6500734217 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1451 HI1451 Haemophilus influenzae 727 -11538075

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892078	15915	38071	405	134

Description

5000695644 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1456 HI1456 Haemophilus influenzae 727 -11538076 111432 hi1456 (de:hypothetical protein hi1456) (db:swissprot) YE56_HAEIN P44203 HAEMOPHILUS INFLUENZAE 727 -11538076 166779 hypothetical protein hi1456 (db:pir2.dat) F64030 F64030 Haemophilus influenzae 727 -11538076 7500922710 hi1456 h. influenzae predicted coding region hi1456 (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9994) (re:10500) (di:complement) U32823 U32823 g1574297 Haemophilus influenzae Rd 71421 -11538076 6500734218 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1456 HI1456 Haemophilus influenzae 727 -11538076

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892087	15916	38072	1959	652

Description

5000695645 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1458 HI1458 Haemophilus influenzae 727 -11538077 111433 hi1458 (de:hypothetical protein hi1458) (db:swissprot) YE58_HAEIN P44204 HAEMOPHILUS INFLUENZAE 727 -11538077 166780 hypothetical protein hi1458 (db:pir2.dat) G64030 G64030 Haemophilus influenzae 727 -11538077 7500922714 hi1458 h. influenzae predicted coding region hi1458 (db:genpept-bct1) (de:haemophilus influenzae rd section 139 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:178) (re:420) (di:direct) U32824 U32824 g1574300 Haemophilus influenzae Rd 71421 -11538077 6500734219 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1458 HI1458 Haemophilus influenzae 727 -11538077

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892094	15917	38073	603	200

Description

5000695646 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1469 HI1469 Haemophilus influenzae 727 -11538078 111438 hi1469 (de:hypothetical protein hi1469) (db:swissprot) YE69_HAEIN P44205 HAEMOPHILUS INFLUENZAE 727 -11538078 166782 hypothetical protein hi1469 (db:pir2.dat) H64030 H64030 Haemophilus influenzae 727 -11538078 7500922730 hi1469 h. influenzae predicted coding region hi1469 (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3486) (re:3833) (di:complement) U32825 U32825 g1574310 Haemophilus influenzae Rd 71421 -11538078 6500734220 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1469 HI1469 Haemophilus influenzae 727 -11538078

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892102	15918	38074	429	142

Description

5000695647 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1472 HI1472 Haemophilus influenzae 727 -11538079 111439 hi1472 (de:hypothetical protein hi1472 precursor) (db:swissprot) YE72_HAEIN P44206 HAEMOPHILUS INFLUENZAE 727 -11538079 166783 hypothetical protein hi1472 (db:pir2.dat) I64030 I64030 Haemophilus influenzae 727 -11538079 7500922743 hi1472 iron chelatin abc transporter (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to gb:ae000511 pid:2314746 percent) (le:5597) (re:6652) (di:complement) U32825 U32825 g1574313 Haemophilus influenzae Rd 71421 -11538079 6500734221 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1472 HI1472 Haemophilus influenzae 727 -11538079

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892103	15919	38075	636	211

Description

GTC ORF with score 316 to: (fn:carboxyl transfer from substrate to biotin) (sr:veillonella parvula dna) (db:genpept-bct2) (de:veillonella parvula methylmalonyl-coa decarboxylase alpha, beta,delta, epsilon, gamma subunits gene, complete cds.) (le:403) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892109	15920	38076	360	119

Description

5000695648 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1476 HI1476 Haemophilus influenzae 727 -11538080 111440 hi1476 (de:hypothetical protein hi1476) (db:swissprot) YE76_HAEIN P44207 HAEMOPHILUS INFLUENZAE 727 -11538080 166784 hypothetical protein hi1476 (db:pir2.dat) A64031 A64031 Haemophilus influenzae 727 -11538080 7500922754 hi1476 transcriptional regulatory protein (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:similar to sp:q37906 pid:403436 percent ident:) (le:8763) (re:9482) (di:complement) U32825 U32825 g1574317 Haemophilus influenzae Rd 71421 -11538080 6500734222 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1476 HI1476 Haemophilus influenzae 727 -11538080

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892120	15921	38077	657	218

Description

5000695649 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1479 HI1479 Haemophilus influenzae 727 -11538081 111441 hi1479 (de:hypothetical protein hi1479) (db:swissprot) YE79_HAEIN P44208 HAEMOPHILUS INFLUENZAE 727 -11538081 166785 hypothetical protein hi1479 (db:pir2.dat) B64031 B64031 Haemophilus influenzae 727 -11538081 7500922755 hi1479 h. influenzae predicted coding region hi1479 (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:12133) (re:12405) (di:direct) U32825 U32825 g1574319 Haemophilus influenzae Rd 71421 -11538081 6500734223 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1479 HI1479 Haemophilus influenzae 727 -11538081

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892123	15922	38078	516	171

Description

5000695650 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1480 HI1480 Haemophilus influenzae 727 -11538082 111442 hi1480 (de:hypothetical protein hi1480) (db:swissprot) YE80_HAEIN P44209 HAEMOPHILUS INFLUENZAE 727 -11538082 166786 hypothetical protein hi1480 (db:pir2.dat) C64031 C64031 Haemophilus influenzae 727 -11538082 7500922762 hi1480 h. influenzae predicted coding region hi1480 (db:genpept-bct1) (de:haemophilus influenzae rd section 140 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:12338) (re:12808) (di:complement) U32825 U32825 g1574321 Haemophilus influenzae Rd 71421 -11538082 6500734224 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1480 HI1480 Haemophilus influenzae 727 -11538082

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892124	15923	38079	1086	361

Description

5000695651 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1482 HI1482 Haemophilus influenzae 727 -11538083 111443 hi1482 (de:hypothetical protein hi1482) (db:swissprot) YE82_HAEIN P44210 HAEMOPHILUS INFLUENZAE 727 -11538083 166787 hypothetical protein hi1482 (db:pir2.dat) D64031 D64031 Haemophilus influenzae 727 -11538083 7500922763 hi1482 h. influenzae predicted coding region hi1482 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:61) (re:378) (di:direct) U32826 U32826 g1574328 Haemophilus influenzae Rd 71421 -11538083 6500734225 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1482 HI1482 Haemophilus influenzae 727 -11538083

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892126	15924	38080	660	219

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892135	15925	38081	483	160

Description

5000695652 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1484 HI1484 Haemophilus influenzae 727 -11538084 111444 hi1484 (de:hypothetical protein hi1484) (db:swissprot) YE84_HAEIN P44211 HAEMOPHILUS INFLUENZAE 727 -11538084 166788 hypothetical protein hi1484 (db:pir2.dat) E64031 E64031 Haemophilus influenzae 727 -11538084 7500922764 hi1484 h. influenzae predicted coding region hi1484 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:899) (re:1060) (di:direct) U32826 U32826 g1574329 Haemophilus influenzae Rd 71421 -11538084 6500734226 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1484 HI1484 Haemophilus influenzae 727 -11538084

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892137	15926	38082	957	318

Description

GTC ORF with score 119 to: (sr:saccharomyces cerevisiae (strain:grf88) dna, clone_lib:ycp5) (db:genpept-pln1) (de:saccharomyces cerevisiae dna for thi2 positive regulatory proteinof thiamin synthesis, complete cds.) (le:721) (re:2073) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892168	15927	38083	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892177	15928	38084	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892179	15929	38085	516	171

Description

5000695653 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1485 HI1485 Haemophilus influenzae 727 -11538085 111445 hi1485 (de:hypothetical protein hi1485) (db:swissprot) YE85_HAEIN P44212 HAEMOPHILUS INFLUENZAE 727 -11538085 166789 hypothetical protein hi1485 (db:pir2.dat) F64031 F64031 Haemophilus influenzae 727 -11538085 7500922765 hi1485 h. influenzae predicted coding region hi1485 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1532) (re:1753) (di:direct) U32826 U32826 g1574330 Haemophilus influenzae Rd 71421 -11538085 6500734227 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1485 HI1485 Haemophilus influenzae 727 -11538085

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892182	15930	38086	738	245

Description

5000695654 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1486 HI1486 Haemophilus influenzae 727 -11538086 111446 hi1486 (de:hypothetical protein hi1486) (db:swissprot) YE86_HAEIN P44213 HAEMOPHILUS INFLUENZAE 727 -11538086 166790 hypothetical protein hi1486 (db:pir2.dat) G64031 G64031 Haemophilus influenzae 727 -11538086 7500922768 hi1486 h. influenzae predicted coding region hi1486 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1753) (re:1926) (di:direct) U32826 U32826 g1574331 Haemophilus influenzae Rd 71421 -11538086 6500734228 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1486 HI1486 Haemophilus influenzae 727 -11538086

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892186	15931	38087	378	125

Description

5000695655 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1487 HI1487 Haemophilus influenzae 727 -11538087 111447 hi1487 (de:hypothetical protein hi1487) (db:swissprot) YE87_HAEIN P44214 HAEMOPHILUS INFLUENZAE 727 -11538087 166791 hypothetical protein hi1487 (db:pir2.dat) H64031 H64031 Haemophilus influenzae 727 -11538087 7500922771 hi1487 h. influenzae predicted coding region hi1487 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1929) (re:2489) (di:direct) U32826 U32826 g1574332 Haemophilus influenzae Rd 71421 -11538087 6500734229 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1487 HI1487 Haemophilus influenzae 727 -11538087

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892206	15932	38088	528	175

Description

5000695656 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1489 HI1489 Haemophilus influenzae 727 -11538088 111448 hi1489 (de:hypothetical protein hi1489) (db:swissprot) YE89_HAEIN P44215 HAEMOPHILUS INFLUENZAE 727 -11538088 166792 hypothetical protein hi1489 (db:pir2.dat) I64031 I64031 Haemophilus influenzae 727 -11538088 7500922776 hi1489 h. influenzae predicted coding region hi1489 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3217) (re:3771) (di:direct) U32826 U32826 g1574333 Haemophilus influenzae Rd 71421 -11538088 6500734230 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1489 HI1489 Haemophilus influenzae 727 -11538088

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892208	15933	38089	1491	496

Description

5000695657 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1490 HI1490 Haemophilus influenzae 727 -11538089 111449 hi1490 (de:hypothetical protein hi1490) (db:swissprot) YE90_HAEIN P44216 HAEMOPHILUS INFLUENZAE 727 -11538089 166793 hypothetical protein hi1490 (db:pir2.dat) A64032 A64032 Haemophilus influenzae 727 -11538089 7500922781 hi1490 positive regulator of late transcription (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:similar to sp:p06022 pid:15812 pid:215521) (le:3963) (re:4178) (di:direct) U32826 U32826 g1574334 Haemophilus influenzae Rd 71421 -11538089 6500734231 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1490 HI1490 Haemophilus influenzae 727 -11538089

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892214	15934	38090	474	157

Description

5000695658 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1492 HI1492 Haemophilus influenzae 727 -11538090 111450 hi1492 (de:hypothetical protein hi1492 precursor) (db:swissprot) YE92_HAEIN P44217 HAEMOPHILUS INFLUENZAE 727 -11538090 166794 hypothetical protein hi1492 (db:pir2.dat) B64032 B64032 Haemophilus influenzae 727 -11538090 7500922785 hi1492 h. influenzae predicted coding region hi1492 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4405) (re:4911) (di:direct) U32826 U32826 g1574335 Haemophilus influenzae Rd 71421 -11538090 6500734232 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1492 HI1492 Haemophilus influenzae 727 -11538090

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892239	15935	38091	1281	426

Description

5000695659 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1493 HI1493 Haemophilus influenzae 727 -11538091 111451 hi1493 (de:hypothetical protein hi1493) (db:swissprot) YE93_HAEIN P44218 HAEMOPHILUS INFLUENZAE 727 -11538091 166795 hypothetical protein hi1493 (db:pir2.dat) C64032 C64032 Haemophilus influenzae 727 -11538091 7500922786 hi1493 h. influenzae predicted coding region hi1493 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4993) (re:5277) (di:direct) U32826 U32826 g1574336 Haemophilus influenzae Rd 71421 -11538091 6500734233 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1493 HI1493 Haemophilus influenzae 727 -11538091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892244	15936	38092	207	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892255	15937	38093	837	278

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892263	15938	38094	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892274	15939	38095	486	161

Description

5000695660 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1495 HI1495 Haemophilus influenzae 727 -11538092 111452 hi1495 (de:hypothetical protein hi1495) (db:swissprot) YE95_HAEIN P44219 HAEMOPHILUS INFLUENZAE 727 -11538092 166796 hypothetical protein hi1495 (db:pir2.dat) D64032 D64032 Haemophilus influenzae 727 -11538092 7500922789 hi1495 h. influenzae predicted coding region hi1495 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5544) (re:5804) (di:direct) U32826 U32826 g1574337 Haemophilus influenzae Rd 71421 -11538092 6500734234 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1495 HI1495 Haemophilus influenzae 727 -11538092

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892275	15940	38096	234	77

Description

5000695661 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1496 HI1496 Haemophilus influenzae 727 -11538093 111453 hi1496 (de:hypothetical protein hi1496) (db:swissprot) YE96_HAEIN P44220 HAEMOPHILUS INFLUENZAE 727 -11538093 166797 hypothetical protein hi1496 (db:pir2.dat) E64032 E64032 Haemophilus influenzae 727 -11538093 7500922792 hi1496 h. influenzae predicted coding region hi1496 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5801) (re:6055) (di:direct) U32826 U32826 g1574338 Haemophilus influenzae Rd 71421 -11538093 6500734235 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1496 HI1496 Haemophilus influenzae 727 -11538093

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892293	15941	38097	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892294	15942	38098	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892300	15943	38099	1218	405

Description

5000695662 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1498 HI1498 Haemophilus influenzae 727 -11538094 111455 hi1498 (de:hypothetical protein hi1498) (db:swissprot) YE98_HAEIN P44222 HAEMOPHILUS INFLUENZAE 727 -11538094 166799 hypothetical protein hi1498 (db:pir2.dat) G64032 G64032 Haemophilus influenzae 727 -11538094 7500922794 hi1498 h. influenzae predicted coding region hi1498 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6307) (re:6726) (di:direct) U32826 U32826 g1574339 Haemophilus influenzae Rd 71421 -11538094 6500734236 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1498 HI1498 Haemophilus influenzae 727 -11538094

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892323	15944	38100	468	155

Description

GTC ORF with score 524 to: (sr:coccidioides immitis (individual_isolate c735) mycelial dna) (db:genpept-pln1) (de:coccidioides immitis t-cell reactive protein (trcp) gene exons 1-4,complete cds.) (nt:homology to 4-hydroxyphenylpyruvate dioxygenase and)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892326	15945	38101	732	243

Description

GTC ORF with score 809 to: (sr:coccidioides immitis (individual_isolate c735) mycelial dna) (db:genpept-pln1) (de:coccidioides immitis t-cell reactive protein (trcp) gene exons 1-4,complete cds.) (nt:homology to 4-hydroxyphenylpyruvate dioxygenase and)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892332	15946	38102	447	148

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892354	15947	38103	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892356	15948	38104	1611	536

Description

5000695663 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1499 HI1499 Haemophilus influenzae 727 -11538095 111456 hi1499 (de:hypothetical protein hi1499) (db:swissprot) YE99_HAEIN P44223 HAEMOPHILUS INFLUENZAE 727 -11538095 166800 hypothetical protein hi1499 (db:pir2.dat) H64032 H64032 Haemophilus influenzae 727 -11538095 7500922797 hi1499 h. influenzae predicted coding region hi1499 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7051) (re:7620) (di:direct) U32826 U32826 g1574340 Haemophilus influenzae Rd 71421 -11538095 6500734237 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1499 HI1499 Haemophilus influenzae 727 -11538095

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892362	15949	38105	1116	371

Description

5000695664 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1500 HI1500 Haemophilus influenzae 727 -11538096 111741 hi1500 (de:hypothetical protein hi1500) (db:swissprot) YF00_HAEIN P44224 HAEMOPHILUS INFLUENZAE 727 -11538096 166801 hypothetical protein hi1500 (db:pir2.dat) I64032 I64032 Haemophilus influenzae 727 -11538096 7500923202 hi1500 h. influenzae predicted coding region hi1500 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7620) (re:9146) (di:direct) U32826 U32826 g1574341 Haemophilus influenzae Rd 71421 -11538096 6500734238 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1500 HI1500 Haemophilus influenzae 727 -11538096

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892367	15950	38106	552	183

Description

5000695665 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1501 HI1501 Haemophilus influenzae 727 -11538097 111742 hi1501 (de:hypothetical protein hi1501) (db:swissprot) YF01_HAEIN P44225 HAEMOPHILUS INFLUENZAE 727 -11538097 166802 hypothetical protein hi1501 (db:pir2.dat) A64033 A64033 Haemophilus influenzae 727 -11538097 7500923203 hi1501 h. influenzae predicted coding region hi1501 (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9158) (re:10720) (di:direct) U32826 U32826 g1574342 Haemophilus influenzae Rd 71421 -11538097 6500734239 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1501 HI1501 Haemophilus influenzae 727 -11538097

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892389	15951	38107	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892410	15952	38108	1797	598

Description

5000695666 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1502 HI1502 Haemophilus influenzae 727 -11538098 111743 hi1502 (de:hypothetical protein hi1502) (db:swissprot) YF02_HAEIN P44226 HAEMOPHILUS INFLUENZAE 727 -11538098 166803 hypothetical protein hi1502 (db:pir2.dat) B64033 B64033 Haemophilus influenzae 727 -11538098 7500923205 hi1502 h. influenzae predicted coding region hi1502 (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:76) (re:1320) (di:direct) U32827 U32827 g1574344 Haemophilus influenzae Rd 71421 -11538098 6500734240 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1502 HI1502 Haemophilus influenzae 727 -11538098

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892419	15953	38109	435	144

Description

5000695667 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1505 HI1505 Haemophilus influenzae 727 -11538099 111744 hi1505 (de:hypothetical protein hi1505) (db:swissprot) YF05_HAEIN P44227 HAEMOPHILUS INFLUENZAE 727 -11538099 166804 hypothetical protein hi1505 (db:pir2.dat) C64033 C64033 Haemophilus influenzae 727 -11538099 7500923211 hi1505 h. influenzae predicted coding region hi1505 (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3196) (re:4122) (di:direct) U32827 U32827 g1574350 Haemophilus influenzae Rd 71421 -11538099 6500734241 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1505 HI1505 Haemophilus influenzae 727 -11538099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892420	15954	38110	408	135

Description

5000695668 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1506 HI1506 Haemophilus influenzae 727 -11538100 111745 hi1506 (de:hypothetical protein hi1506) (db:swissprot) YF06_HAEIN P44228 HAEMOPHILUS INFLUENZAE 727 -11538100 166805 hypothetical protein hi1506 (db:pir2.dat) D64033 D64033 Haemophilus influenzae 727 -11538100 7500923215 hi1506 h. influenzae predicted coding region hi1506 (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4205) (re:4462) (di:direct) U32827 U32827 g1574351 Haemophilus influenzae Rd 71421 -11538100 6500734242 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1506 HI1506 Haemophilus influenzae 727 -11538100

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892427	15955	38111	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892430	15956	38112	1095	364

Description

5000695669 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1507 HI1507 Haemophilus influenzae 727 -11538101 111746 hi1507 (de:hypothetical protein hi1507) (db:swissprot) YF07_HAEIN P44229 HAEMOPHILUS INFLUENZAE 727 -11538101 166806 hypothetical protein hi1507 (db:pir2.dat) E64033 E64033 Haemophilus influenzae 727 -11538101 7500923216 hi1507 h. influenzae predicted coding region hi1507 (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4474) (re:4590) (di:direct) U32827 U32827 g1574352 Haemophilus influenzae Rd 71421 -11538101 6500734243 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1507 HI1507 Haemophilus influenzae 727 -11538101

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892431	15957	38113	807	268

Description

5000695670 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1508 HI1508 Haemophilus influenzae 727 -11538102 111747 hi1508 (de:hypothetical protein hi1508) (db:swissprot) YF08_HAEIN P44230 HAEMOPHILUS INFLUENZAE 727 -11538102 166807 hypothetical protein hi1508 (db:pir2.dat) F64033 F64033 Haemophilus influenzae 727 -11538102 7500923217 hi1508 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to pid:2353778 percent ident: 80.53;) (le:4593) (re:5018) (di:direct) U32827 U32827 g1574353 Haemophilus influenzae Rd 71421 -11538102 6500734244 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1508 HI1508 Haemophilus influenzae 727 -11538102

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892440	15958	38114	486	161

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892451	15959	38115	1416	471

Description

5000695671 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1509 HI1509 Haemophilus influenzae 727 -11538103 111748 hi1509 (de:hypothetical protein hi1509) (db:swissprot) YF09_HAEIN P44231 HAEMOPHILUS INFLUENZAE 727 -11538103 166808 hypothetical protein hi1509 (db:pir2.dat) G64033 G64033 Haemophilus influenzae 727 -11538103 7500923218 hi1509 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to pid:2353777 percent ident: 79.75;) (le:4985) (re:5569) (di:direct) U32827 U32827 g1574354 Haemophilus influenzae Rd 71421 -11538103 6500734245 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1509 HI1509 Haemophilus influenzae 727 -11538103

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892453	15960	38116	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892469	15961	38117	276	91

Description

5000695672 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1510 HI1510 Haemophilus influenzae 727 -11538104 111749 hi1510 (de:hypothetical protein hi1510) (db:swissprot) YF10_HAEIN P44232 HAEMOPHILUS INFLUENZAE 727 -11538104 166809 hypothetical protein hi1510 (db:pir2.dat) H64033 H64033 Haemophilus influenzae 727 -11538104 7500923219 hi1510 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to gp:1834290 percent ident: 44.64;) (le:5582) (re:5773) (di:direct) U32827 U32827 g1574355 Haemophilus influenzae Rd 71421 -11538104 6500734246 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1510 HI1510 Haemophilus influenzae 727 -11538104

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892482	15962	38118	414	137

Description

5000695673 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1511 HI1511 Haemophilus influenzae 727 -11538105 111750 hi1511 (de:hypothetical protein hi1511) (db:swissprot) YF11_HAEIN P44233 HAEMOPHILUS INFLUENZAE 727 -11538105 166810 hypothetical protein hi1511 (db:pir2.dat) I64033 I64033 Haemophilus influenzae 727 -11538105 7500923220 hi1511 sheath protein gpl mul (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to pid:1834291 percent ident: 46.44;) (le:5773) (re:7236) (di:direct) U32827 U32827 g1574356 Haemophilus influenzae Rd 71421 -11538105 6500734247 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1511 HI1511 Haemophilus influenzae 727 -11538105

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892501	15963	38119	549	182

Description

5000695674 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1512 HI1512 Haemophilus influenzae 727 -11538106 111752 hi1512 (de:hypothetical protein hi1512) (db:swissprot) YF12_HAEIN P44234 HAEMOPHILUS INFLUENZAE 727 -11538106 166811 hypothetical protein hi1512 (db:pir2.dat) A64034 A64034 Haemophilus influenzae 727 -11538106 7500923221 hi1512 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to pid:1834292 percent ident: 38.79;) (le:7246) (re:7602) (di:direct) U32827 U32827 g1574357 Haemophilus influenzae Rd 71421 -11538106 6500734248 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1512 HI1512 Haemophilus influenzae 727 -11538106

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892508	15964	38120	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892509	15965	38121	210	69

Description

5000695675 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1513 HI1513 Haemophilus influenzae 727 -11538107 111753 hi1513 (de:hypothetical protein hi1513) (db:swissprot) YF13_HAEIN P44235 HAEMOPHILUS INFLUENZAE 727 -11538107 166812 hypothetical protein hi1513 (db:pir2.dat) B64034 B64034 Haemophilus influenzae 727 -11538107 7500923222 hi1513 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to pid:1834293 percent ident: 50.89;) (le:7615) (re:7998) (di:direct) U32827 U32827 g1574358 Haemophilus influenzae Rd 71421 -11538107 6500734249 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1513 HI1513 Haemophilus influenzae 727 -11538107

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892514	15966	38122	261	86

Description

GTC ORF with score 300 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1750.) (nt:similar to saccharomyces cerevisiae succinate) (le:<1) (re:1465) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892516	15967	38123	297	99

Description

5000695676 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1514 HI1514 Haemophilus influenzae 727 -11538108 111755 hi1514 (de:hypothetical protein hi1514) (db:swissprot) YF14_HAEIN P44236 HAEMOPHILUS INFLUENZAE 727 -11538108 166813 hypothetical protein hi1514 (db:pir2.dat) C64034 C64034 Haemophilus influenzae 727 -11538108 7500923223 hi1514 h. influenzae predicted coding region hi1514 (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8079) (re:9974) (di:direct) U32827 U32827 g1574347 Haemophilus influenzae Rd 71421 -11538108 6500734250 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1514 HI1514 Haemophilus influenzae 727 -11538108

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892519	15968	38124	1485	494

Description

5000695677 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1517 HI1517 Haemophilus influenzae 727 -11538109 111756 hi1517 (de:hypothetical protein hi1517) (db:swissprot) YF17_HAEIN P44237 HAEMOPHILUS INFLUENZAE 727 -11538109 166814 hypothetical protein hi1517 (db:pir2.dat) D64034 D64034 Haemophilus influenzae 727 -11538109 6500734251 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1517 HI1517 Haemophilus influenzae 727 -11538109

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892522	15969	38125	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892528	15970	38126	1473	490

Description

5000695678 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1518 HI1518 Haemophilus influenzae 727 -11538110 111758 hi1518 (de:hypothetical protein hi1518) (db:swissprot) YF18_HAEIN P44238 HAEMOPHILUS INFLUENZAE 727 -11538110 166815 hypothetical protein hi1518 (db:pir2.dat) E64034 E64034 Haemophilus influenzae 727 -11538110 7500923224 hi1518 h. influenzae predicted coding region hi1518 (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:12638) (re:13186) (di:direct) U32827 U32827 g1574349 Haemophilus influenzae Rd 71421 -11538110 6500734252 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1518 HI1518 Haemophilus influenzae 727 -11538110

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892531	15971	38127	894	297

Description

5000695679 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1519 HI1519 Haemophilus influenzae 727 -11538111 111759 hi1519 (de:hypothetical protein hi1519) (db:swissprot) YF19_HAEIN P44239 HAEMOPHILUS INFLUENZAE 727 -11538111 166816 hypothetical protein hi1519 (db:pir2.dat) F64034 F64034 Haemophilus influenzae 727 -11538111 7500923225 hi1519 h. influenzae predicted coding region hi1519 (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:13195) (re:13602) (di:direct) U32827 U32827 g1574360 Haemophilus influenzae Rd 71421 -11538111 6500734253 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1519 HI1519 Haemophilus influenzae 727 -11538111

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892535	15972	38128	624	207

Description

5000695680 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1520 HI1520 Haemophilus influenzae 727 -11538112 111760 hi1520 (de:hypothetical protein hi1520) (db:swissprot) YF20_HAEIN P44240 HAEMOPHILUS INFLUENZAE 727 -11538112 166817 hypothetical protein hi1520 (db:pir2.dat) G64034 G64034 Haemophilus influenzae 727 -11538112 7500923228 hi1520 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 142 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787398 percent ident:) (le:13602) (re:14669) (di:direct) U32827 U32827 g1574361 Haemophilus influenzae Rd 71421 -11538112 6500734254 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1520 HI1520 Haemophilus influenzae 727 -11538112

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892536	15973	38129	309	102

Description

5000695681 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1521 HI1521 Haemophilus influenzae 727 -11538113 111761 hi1521 (de:hypothetical protein hi1521) (db:swissprot) YF21_HAEIN P44241 HAEMOPHILUS INFLUENZAE 727 -11538113 166818 hypothetical protein hi1521 (db:pir2.dat) H64034 H64034 Haemophilus influenzae 727 -11538113 7500923229 hi1521 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787399 percent ident:) (le:73) (re:579) (di:direct) U32828 U32828 g1574373 Haemophilus influenzae Rd 71421 -11538113 6500734255 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1521 HI1521 Haemophilus influenzae 727 -11538113

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892546	15974	38130	1008	335

Description

5000695682 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1522 HI1522 Haemophilus influenzae 727 -11538114 111762 hi1522 (de:hypothetical protein hi1522) (db:swissprot) YF22_HAEIN P44242 HAEMOPHILUS INFLUENZAE 727 -11538114 166819 hypothetical protein hi1522 (db:pir2.dat) I64034 I64034 Haemophilus influenzae 727 -11538114 7500923230 hi1522 h. influenzae predicted coding region hi1522 (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:579) (re:2450) (di:direct) U32828 U32828 g1574363 Haemophilus influenzae Rd 71421 -11538114 6500734256 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1522 HI1522 Haemophilus influenzae 727 -11538114

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892549	15975	38131	540	179

Description

GTC ORF with score 139 to: (sr:human) (db:genpept) (de:homo sapiens s164 gene, partial cds; ps1 and hypothetical proteingenes, complete cds; and s171 gene, partial cds.) (nt:unknown; intron-exon boundaries defined by ests) (le:<1465:5979:14890:17363) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892556	15976	38132	498	165

Description

6500734257 hi1522:hin_1499 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_1499 HIN_1499 Haemophilus influenzae 727 -11538115 7500976293 hi1522.1 h. influenzae predicted coding region hi1522.1 (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2934) (re:3053) (di:direct) U32828 U32828 g1574364 Haemophilus influenzae Rd 71421 -11538115 5000695683 (de:(hin149911) (pn:hypothetical) (gn:hi1522) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN149911 HIN149911 Haemophilus influenzae 727 10126722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892561	15977	38133	600	199

Description

5000695684 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1523 HI1523 Haemophilus influenzae 727 -11538116 111763 hi1523 (de:hypothetical protein hi1523) (db:swissprot) YF23_HAEIN P44243 HAEMOPHILUS INFLUENZAE 727 -11538116 166820 hypothetical protein hi1523 (db:pir2.dat) A64035 A64035 Haemophilus influenzae 727 -11538116 7500923234 hi1523 h. influenzae predicted coding region hi1523 (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3064) (re:3954) (di:direct) U32828 U32828 g1574365 Haemophilus influenzae Rd 71421 -11538116 6500734258 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1523 HI1523 Haemophilus influenzae 727 -11538116

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892566	15978	38134	321	106

Description

5000695685 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1524 HI1524 Haemophilus influenzae 727 -11538117 111764 hi1524 (de:hypothetical protein hi1524) (db:swissprot) YF24_HAEIN P44244 HAEMOPHILUS INFLUENZAE 727 -11538117 166821 hypothetical protein hi1524 (db:pir2.dat) B64035 B64035 Haemophilus influenzae 727 -11538117 7500923235 hi1524 h. influenzae predicted coding region hi1524 (db:genpept-bct1) (de:haemophilus influenzae rd section 143 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4118) (re:4270) (di:direct) U32828 U32828 g1574374 Haemophilus influenzae Rd 71421 -11538117 6500734259 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1524 HI1524 Haemophilus influenzae 727 -11538117

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892593	15979	38135	2025	674

Description

5000695686 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1534 HI1534 Haemophilus influenzae 727 -11538118 111767 hi1534 (de:hypothetical protein hi1534) (db:swissprot) YF34_HAEIN P44245 HAEMOPHILUS INFLUENZAE 727 -11538118 166822 hypothetical protein hi1534 (db:pir2.dat) C64035 C64035 Haemophilus influenzae 727 -11538118 7500923237 hi1534 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:ae000783 percent ident: 32.57;) (le:1788) (re:2330) (di:direct) U32829 U32829 g1574387 Haemophilus influenzae Rd 71421 -11538118 6500734260 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1534 HI1534 Haemophilus influenzae 727 -11538118

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892608	15980	38136	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892612	15981	38137	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892614	15982	38138	1383	460

Description

GTC ORF with score 127 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t23e7.) (nt:coded for by c. elegans cdna yk35g10.5; coded for) (le:9863:11265:11487) (re:9974:11329:11588) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892617	15983	38139	1065	354

Description

5000695687 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1535 HI1535 Haemophilus influenzae 727 -11538119 111768 hi1535 (de:hypothetical protein hi1535) (db:swissprot) YF35_HAEIN P44246 HAEMOPHILUS INFLUENZAE 727 -11538119 166823 hypothetical protein hi1535 (db:pir2.dat) D64035 D64035 Haemophilus influenzae 727 -11538119 7500923238 hi1535 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788664 percent ident:) (le:2311) (re:3483) (di:direct) U32829 U32829 g1574378 Haemophilus influenzae Rd 71421 -11538119 6500734261 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1535 HI1535 Haemophilus influenzae 727 -11538119

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892623	15984	38140	240	79

Description

5000695688 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1536 HI1536 Haemophilus influenzae 727 -11538120 111769 hi1536 (de:hypothetical protein hi1536) (db:swissprot) YF36_HAEIN P44247 HAEMOPHILUS INFLUENZAE 727 -11538120 166824 hypothetical protein hi1536 (db:pir2.dat) E64035 E64035 Haemophilus influenzae 727 -11538120 7500923239 hi1536 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788664 percent ident:) (le:3453) (re:3800) (di:direct) U32829 U32829 g1574388 Haemophilus influenzae Rd 71421 -11538120 6500734262 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1536 HI1536 Haemophilus influenzae 727 -11538120

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892629	15985	38141	240	79

Description

5000695689 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1543 HI1543 Haemophilus influenzae 727 -11538121 111770 hi1543 (de:hypothetical protein hi1543) (db:swissprot) YCDY_HAEIN P44248 HAEMOPHILUS INFLUENZAE 727 -11538121 166826 ycdy protein homolog hi1543 (cl:escherichia coli ycdy protein) (db:pir2.dat) F64035 F64035 Haemophilus influenzae 727 -11538121 7500921663 hi1543 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75915 pid:1787272 percent) (le:9813) (re:10367) (di:complement) U32829 U32829 g1574385 Haemophilus influenzae Rd 71421 -11538121 6500734263 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1543 HI1543 Haemophilus influenzae 727 -11538121

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892635	15986	38142	369	123

Description

5000695690 hypothetical symporter hi1545 (gtcfc:12.6) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1545 HI1545 Haemophilus influenzae 727 -11538122 112434 hi1545 (de:hypothetical symporter hi1545) (db:swissprot) YGJU_HAEIN P45246 HAEMOPHILUS INFLUENZAE 727 -11538122 166036 hypothetical protein hi1545 (db:pir2.dat) H64128 H64128 Haemophilus influenzae 727 -11538122 7500924309 hi1545 sod:dicarboxylate symporter protein (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to pid:1125827 percent ident: 27.20;) (le:91) (re:1335) (di:complement) U32830 U32830 g1574390 Haemophilus influenzae Rd 71421 -11538122 6500734264 hypothetical symporter hi1545 (gtcfc:12.6) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1545 HI1545 Haemophilus influenzae 727 -11538122

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892641	15987	38143	636	211

Description

5000695691 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1546 HI1546 Haemophilus influenzae 727 -11538123 111772 hi1546 (de:hypothetical protein hi1546) (db:swissprot) YF46_HAEIN P44249 HAEMOPHILUS INFLUENZAE 727 -11538123 166827 hypothetical protein hi1546 (db:pir2.dat) G64035 G64035 Haemophilus influenzae 727 -11538123 7500923247 hi1546 impa protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to percent ident: 34.26; identified by) (le:1620) (re:2042) (di:direct) U32830 U32830 g1574391 Haemophilus influenzae Rd 71421 -11538123 6500734265 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1546 HI1546 Haemophilus influenzae 727 -11538123

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892642	15988	38144	573	190

Description

5000695692 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1548 HI1548 Haemophilus influenzae 727 -11538124 111773 hi1548 (de:hypothetical protein hi1548) (db:swissprot) YCFW_HAEIN P44250 HAEMOPHILUS INFLUENZAE 727 -11538124 166828 probable permease hi1548 (db:pir2.dat) H64035 H64035 Haemophilus influenzae 727 -11538124 7500921766 hi1548 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75958 pid:1787362 percent) (le:3437) (re:4687) (di:complement) U32830 U32830 g1574393 Haemophilus influenzae Rd 71421 -11538124 6500734266 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1548 HI1548 Haemophilus influenzae 727 -11538124

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892647	15989	38145	3624	1207

Description

5000695693 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1552 HI1552 Haemophilus influenzae 727 -11538125 111774 hi1552 (de:hypothetical protein hi1552) (db:swissprot) YF52_HAEIN P44251 HAEMOPHILUS INFLUENZAE 727 -11538125 166829 hypothetical protein hi1552 (db:pir2.dat) I64035 I64035 Haemophilus influenzae 727 -11538125 7500923254 hi1552 h. influenzae predicted coding region hi1552 (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6872) (re:7519) (di:complement) U32830 U32830 g1574405 Haemophilus influenzae Rd 71421 -11538125 6500734267 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1552 HI1552 Haemophilus influenzae 727 -11538125

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892659	15990	38146	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892665	15991	38147	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892674	15992	38148	510	169

Description

5000695694 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1555 HI1555 Haemophilus influenzae 727 -11538126 111775 hi1555 (de:hypothetical protein hi1555) (db:swissprot) YCFU_HAEIN P44252 HAEMOPHILUS INFLUENZAE 727 -11538126 166830 hypothetical protein hi1555 (cl:hypothetical protein hi1555) (db:pir2.dat) A64036 A64036 Haemophilus influenzae 727 -11538126 7500921763 hi1555 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75956 pid:1787360 percent) (le:9991) (re:11172) (di:complement) U32830 U32830 g1574399 Haemophilus influenzae Rd 71421 -11538126 6500734268 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1555 HI1555 Haemophilus influenzae 727 -11538126

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892704	15993	38149	1035	344

Description

5000695695 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1560 HI1560 Haemophilus influenzae 727 -11538127 111777 hi1560 (de:hypothetical protein hi1560) (db:swissprot) YF60_HAEIN P44253 HAEMOPHILUS INFLUENZAE 727 -11538127 166832 hypothetical protein hi1560 (db:pir2.dat) B64036 B64036 Haemophilus influenzae 727 -11538127 7500923268 hi1560 h. influenzae predicted coding region hi1560 (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:14729) (re:15199) (di:complement) U32830 U32830 g1574406 Haemophilus influenzae Rd 71421 -11538127 6500734269 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1560 HI1560 Haemophilus influenzae 727 -11538127

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892705	15994	38150	1116	371

Description

GTC ORF with score 149 to: (sr:pyrococcus horikoshii (strain:ot3) dna) (db:genpept-bct1) (de:pyrococcus horikoshii ot3 genomic dna, 1485001-1738505 nt. position(7/7).) (nt:similar to pir:a64505 percent identity: 33.508 in) (le:78059) (re:81598) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892727	15995	38151	1257	418

Description

5000695696 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1562 HI1562 Haemophilus influenzae 727 -11538128 111778 hi1562 (de:hypothetical protein hi1562) (db:swissprot) YF62_HAEIN P44254 HAEMOPHILUS INFLUENZAE 727 -11538128 166833 hypothetical protein hi1562 (db:pir2.dat) C64036 C64036 Haemophilus influenzae 727 -11538128 7500923269 hi1562 h. influenzae predicted coding region hi1562 (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:84) (re:242) (di:complement) U32831 U32831 g1574414 Haemophilus influenzae Rd 71421 -11538128 6500734270 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1562 HI1562 Haemophilus influenzae 727 -11538128

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892743	15996	38152	414	137

Description

5000695697 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1563 HI1563 Haemophilus influenzae 727 -11538129 111779 hi1563 (de:hypothetical protein hi1563) (db:swissprot) YF63_HAEIN P44255 HAEMOPHILUS INFLUENZAE 727 -11538129 166834 hypothetical protein hi1563 (db:pir2.dat) D64036 D64036 Haemophilus influenzae 727 -11538129 7500923270 hi1563 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788666 percent ident:) (le:495) (re:1031) (di:complement) U32831 U32831 g1574415 Haemophilus influenzae Rd 71421 -11538129 6500734271 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1563 HI1563 Haemophilus influenzae 727 -11538129

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892750	15997	38153	429	142

Description

5000695698 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1564 HI1564 Haemophilus influenzae 727 -11538130 166835 hypothetical protein hi1564 (db:pir2.dat) E64036 E64036 Haemophilus influenzae 727 -11538130 111780 hi1564 (de:hypothetical protein hi1564) (db:swissprot) YF64_HAEIN P44256 HAEMOPHILUS INFLUENZAE 727 -11538130 6500734272 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1564 HI1564 Haemophilus influenzae 727 -11538130

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892751	15998	38154	627	208

Description

5000695699 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1566 HI1566 Haemophilus influenzae 727 -11538131 111781 hi1566 (de:hypothetical protein hi1566 precursor) (db:swissprot) YF66_HAEIN P44257 HAEMOPHILUS INFLUENZAE 727 -11538131 166836 hypothetical protein hi1566 (db:pir2.dat) F64036 F64036 Haemophilus influenzae 727 -11538131 6500734273 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1566 HI1566 Haemophilus influenzae 727 -11538131

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892766	15999	38155	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892779	16000	38156	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892787	16001	38157	579	193

Description

5000695700 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1569 HI1569 Haemophilus influenzae 727 -11538132 111783 hi1569 (de:hypothetical protein hi1569) (db:swissprot) YF69_HAEIN P44258 HAEMOPHILUS INFLUENZAE 727 -11538132 166837 hypothetical protein hi1569 (db:pir2.dat) G64036 G64036 Haemophilus influenzae 727 -11538132 7500923288 hi1569 h. influenzae predicted coding region hi1569 (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5268) (re:5420) (di:complement) U32831 U32831 g1574418 Haemophilus influenzae Rd 71421 -11538132 6500734274 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1569 HI1569 Haemophilus influenzae 727 -11538132

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892792	16002	38158	1461	487

Description

GTC ORF with score 165 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f59a6.) (nt:similar to glycoproteins) (le:13300:13899:15490:15579) (re:13615:15440:15533:15701) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892799	16003	38159	939	312

Description

5000695701 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1570 HI1570 Haemophilus influenzae 727 -11538133 111784 hi1570 (de:hypothetical protein hi1570) (db:swissprot) YF70_HAEIN P44259 HAEMOPHILUS INFLUENZAE 727 -11538133 166838 hypothetical protein hi1570 (db:pir2.dat) H64036 H64036 Haemophilus influenzae 727 -11538133 7500923289 hi1570 h. influenzae predicted coding region hi1570 (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5417) (re:5926) (di:complement) U32831 U32831 g1574419 Haemophilus influenzae Rd 71421 -11538133 6500734275 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1570 HI1570 Haemophilus influenzae 727 -11538133

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892801	16004	38160	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892802	16005	38161	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892834	16006	38162	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892838	16007	38163	363	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892842	16008	38164	1602	533

Description

5000695702 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1571 HI1571 Haemophilus influenzae 727 -11538134 166839 hypothetical protein hi1571 (db:pir2.dat) I64036 I64036 Haemophilus influenzae 727 -11538134 111785 hi1571 (de:hypothetical protein hi1571) (db:swissprot) YF71_HAEIN P44260 HAEMOPHILUS INFLUENZAE 727 -11538134 6500734276 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1571 HI1571 Haemophilus influenzae 727 -11538134

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892850	16009	38165	546	181

Description

5000695703 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1581 HI1581 Haemophilus influenzae 727 -11538135 166840 hypothetical protein hi1581 (db:pir2.dat) A64037 A64037 Haemophilus influenzae 727 -11538135 7500960693 hi1581 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to pid:1204257 sp:p52008 gb:u00096) (le:2576) (re:2749) (di:complement) U32832 U32832 g1574430 Haemophilus influenzae Rd 71421 -11538135 6500734277 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1581 HI1581 Haemophilus influenzae 727 -11538135 111517 yecl_haein (de:hypothetical protein hi1581.) P44261 P44261 Haemophilus influenzae 727 -11538135

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892875	16010	38166	726	241

Description

5000695704 h (gtcfc:14.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1582 HI1582 Haemophilus influenzae 727 -11538136 166841 hypothetical protein hi1582 (db:pir2.dat) B64037 B64037 Haemophilus influenzae 727 -11538136 7500960694 hi1582 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to pid:1204257 sp:p52008 gb:u00096) (le:2737) (re:3156) (di:complement) U32832 U32832 g1574431 Haemophilus influenzae Rd 71421 -11538136 6500734278 h (gtcfc:14.2) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1582 HI1582 Haemophilus influenzae 727 -11538136

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892880	16011	38167	933	310

Description

5000695705 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1586 HI1586 Haemophilus influenzae 727 -11538137 111787 hi1586 (de:hypothetical protein hi1586) (db:swissprot) YF86_HAEIN P44263 HAEMOPHILUS INFLUENZAE 727 -11538137 166842 hypothetical protein hi1586 (db:pir2.dat) C64037 C64037 Haemophilus influenzae 727 -11538137 7500923297 hi1586 conserved hypothetical integral membrane (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to gb:ae000511 pid:2314087 percent) (le:7741) (re:9300) (di:complement) U32832 U32832 g1574427 Haemophilus influenzae Rd 71421 -11538137 6500734279 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1586 HI1586 Haemophilus influenzae 727 -11538137

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892885	16012	38168	1533	510

Description

5000695706 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1593 HI1593 Haemophilus influenzae 727 -11538138 111788 hi1593 (de:hypothetical protein hi1593) (db:swissprot) YF93_HAEIN P44264 HAEMOPHILUS INFLUENZAE 727 -11538138 166845 hypothetical protein hi1593 (db:pir2.dat) D64037 D64037 Haemophilus influenzae 727 -11538138 7500923301 hi1593 h. influenzae predicted coding region hi1593 (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5888) (re:6043) (di:complement) U32833 U32833 g1574442 Haemophilus influenzae Rd 71421 -11538138 6500734280 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1593 HI1593 Haemophilus influenzae 727 -11538138

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892907	16013	38169	234	77

Description

5000695707 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1594 HI1594 Haemophilus influenzae 727 -11538139 111789 hi1594 (de:hypothetical protein hi1594) (db:swissprot) YF94_HAEIN P44265 HAEMOPHILUS INFLUENZAE 727 -11538139 166846 hypothetical protein hi1594 (db:pir2.dat) E64037 E64037 Haemophilus influenzae 727 -11538139 7500923305 hi1594 h. influenzae predicted coding region hi1594 (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6078) (re:6749) (di:complement) U32833 U32833 g1574443 Haemophilus influenzae Rd 71421 -11538139 6500734281 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1594 HI1594 Haemophilus influenzae 727 -11538139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892908	16014	38170	1329	442

Description

5000695708 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1595 HI1595 Haemophilus influenzae 727 -11538140 111790 hi1595 (de:hypothetical protein hi1595) (db:swissprot) YF95_HAEIN P44266 HAEMOPHILUS INFLUENZAE 727 -11538140 166847 hypothetical protein hi1595 (db:pir2.dat) F64037 F64037 Haemophilus influenzae 727 -11538140 7500923306 hi1595 h. influenzae predicted coding region hi1595 (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6763) (re:7086) (di:complement) U32833 U32833 g1574438 Haemophilus influenzae Rd 71421 -11538140 6500734282 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1595 HI1595 Haemophilus influenzae 727 -11538140

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892911	16015	38171	384	127

Description

5000695709 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1599 HI1599 Haemophilus influenzae 727 -11538141 111791 hi1599 (de:hypothetical protein hi1599) (db:swissprot) YF99_HAEIN P44267 HAEMOPHILUS INFLUENZAE 727 -11538141 166849 hypothetical protein hi1599 (db:pir2.dat) G64037 G64037 Haemophilus influenzae 727 -11538141 7500923307 hi1599 h. influenzae predicted coding region hi1599 (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:186) (re:902) (di:complement) U32834 U32834 g1574455 Haemophilus influenzae Rd 71421 -11538141 6500734283 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1599 HI1599 Haemophilus influenzae 727 -11538141

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892922	16016	38172	507	168

Description

5000695710 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1600 HI1600 Haemophilus influenzae 727 -11538142 112034 hi1600 (de:hypothetical protein hi1600) (db:swissprot) YG00_HAEIN P44268 HAEMOPHILUS INFLUENZAE 727 -11538142 166850 hypothetical protein hi1600 (db:pir2.dat) H64037 H64037 Haemophilus influenzae 727 -11538142 7500923601 hi1600 h. influenzae predicted coding region hi1600 (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:892) (re:1845) (di:complement) U32834 U32834 g1574456 Haemophilus influenzae Rd 71421 -11538142 6500734284 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1600 HI1600 Haemophilus influenzae 727 -11538142

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892934	16017	38173	1683	560

Description

5000695711 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1601 HI1601 Haemophilus influenzae 727 -11538143 112035 hi1601 (de:hypothetical protein hi1601 precursor) (db:swissprot) YG01_HAEIN P44269 HAEMOPHILUS INFLUENZAE 727 -11538143 166851 hypothetical protein hi1601 (db:pir2.dat) I64037 I64037 Haemophilus influenzae 727 -11538143 7500923602 hi1601 h. influenzae predicted coding region hi1601 (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1875) (re:2162) (di:complement) U32834 U32834 g1574457 Haemophilus influenzae Rd 71421 -11538143 6500734285 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1601 HI1601 Haemophilus influenzae 727 -11538143

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892935	16018	38174	642	213

Description

5000695712 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1602 HI1602 Haemophilus influenzae 727 -11538144 112036 hi1602 (de:hypothetical protein hi1602) (db:swissprot) YG02_HAEIN P44270 HAEMOPHILUS INFLUENZAE 727 -11538144 166852 hypothetical protein hi1602 (db:pir2.dat) A64038 A64038 Haemophilus influenzae 727 -11538144 7500923603 hi1602 h. influenzae predicted coding region hi1602 (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2201) (re:2656) (di:complement) U32834 U32834 g1574445 Haemophilus influenzae Rd 71421 -11538144 6500734286 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1602 HI1602 Haemophilus influenzae 727 -11538144

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892940	16019	38175	540	179

Description

5000695713 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1603 HI1603 Haemophilus influenzae 727 -11538145 112037 hi1603 (de:hypothetical protein hi1603) (db:swissprot) YG03_HAEIN P44271 HAEMOPHILUS INFLUENZAE 727 -11538145 166853 hypothetical protein hi1603 (db:pir2.dat) B64038 B64038 Haemophilus influenzae 727 -11538145 7500923604 hi1603 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:similar to gb:ae000782 percent ident: 28.84;) (le:2864) (re:3544) (di:direct) U32834 U32834 g1574458 Haemophilus influenzae Rd 71421 -11538145 6500734287 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1603 HI1603 Haemophilus influenzae 727 -11538145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892956	16020	38176	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892960	16021	38177	723	241

Description

GTC ORF with score 161 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892967	16022	38178	564	187

Description

GTC ORF with score 111 to: (db:genpept-bct2) (de:acinetobacter sp. adp1 vanillate demethylase region, vanillatedemethylase (vanb) and vanillate demethylase (vana) genes, completecds.) (nt:similar to salicylate hydroxylase; orf7) (le:10288) (re:11433) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892973	16023	38179	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892989	16024	38180	921	306

Description

5000695714 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1620 HI1620 Haemophilus influenzae 727 -11538146 112071 hi1620 (de:hypothetical protein hi1620) (db:swissprot) YG20_HAEIN P44273 HAEMOPHILUS INFLUENZAE 727 -11538146 166858 hypothetical protein hi1620 (db:pir2.dat) D64038 D64038 Haemophilus influenzae 727 -11538146 7500923680 hi1620 h. influenzae predicted coding region hi1620 (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6793) (re:7296) (di:complement) U32835 U32835 g1574469 Haemophilus influenzae Rd 71421 -11538146 6500734288 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1620 HI1620 Haemophilus influenzae 727 -11538146

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501892996	16025	38181	1752	583

Description

5000695715 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1621 HI1621 Haemophilus influenzae 727 -11538147 112072 hi1621 (de:hypothetical protein hi1621) (db:swissprot) YG21_HAEIN P44274 HAEMOPHILUS INFLUENZAE 727 -11538147 166859 hypothetical protein hi1621 (db:pir2.dat) E64038 E64038 Haemophilus influenzae 727 -11538147 7500923681 hi1621 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:similar to pid:1001613 pid:1001653 percent) (le:7296) (re:7916) (di:complement) U32835 U32835 g1574470 Haemophilus influenzae Rd 71421 -11538147 6500734289 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1621 HI1621 Haemophilus influenzae 727 -11538147

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893003	16026	38182	267	88

Description

5000695716 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1622 HI1622 Haemophilus influenzae 727 -11538148 112074 hi1622 (de:hypothetical protein hi1622 precursor) (db:swissprot) YG22_HAEIN P44275 HAEMOPHILUS INFLUENZAE 727 -11538148 166860 hypothetical protein hi1622 (db:pir2.dat) F64038 F64038 Haemophilus influenzae 727 -11538148 7500923684 hi1622 h. influenzae predicted coding region hi1622 (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7916) (re:8401) (di:complement) U32835 U32835 g1574471 Haemophilus influenzae Rd 71421 -11538148 6500734290 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1622 HI1622 Haemophilus influenzae 727 -11538148

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893024	16027	38183	990	329

Description

5000695717 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1624 HI1624 Haemophilus influenzae 727 -11538149 112077 hi1624 (de:hypothetical protein hi1624 precursor) (db:swissprot) YG24_HAEIN P44276 HAEMOPHILUS INFLUENZAE 727 -11538149 166861 hypothetical protein hi1624 (db:pir2.dat) G64038 G64038 Haemophilus influenzae 727 -11538149 7500923689 hi1624 h. influenzae predicted coding region hi1624 (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8414) (re:9097) (di:complement) U32835 U32835 g1574472 Haemophilus influenzae Rd 71421 -11538149 6500734291 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1624 HI1624 Haemophilus influenzae 727 -11538149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893033	16028	38184	663	221

Description

5000695718 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1625 HI1625 Haemophilus influenzae 727 -11538150 112079 hi1625 (de:hypothetical protein hi1625) (db:swissprot) YG25_HAEIN P44277 HAEMOPHILUS INFLUENZAE 727 -11538150 166862 hypothetical protein hi1625 (db:pir2.dat) H64038 H64038 Haemophilus influenzae 727 -11538150 7500923692 hi1625 h. influenzae predicted coding region hi1625 (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9654) (re:10151) (di:complement) U32835 U32835 g1574466 Haemophilus influenzae Rd 71421 -11538150 6500734292 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1625 HI1625 Haemophilus influenzae 727 -11538150

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893045	16029	38185	2097	698

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893057	16030	38186	1107	369

Description

GTC ORF with score 148 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone c1241.) (le:17874:18336) (re:18224:18719) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893071	16031	38187	3261	1086

Description

5000695719 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1626 HI1626 Haemophilus influenzae 727 -11538151 112081 hi1626 (de:hypothetical protein hi1626) (db:swissprot) YG26_HAEIN P44278 HAEMOPHILUS INFLUENZAE 727 -11538151 166863 hypothetical protein hi1626 (db:pir2.dat) I64038 I64038 Haemophilus influenzae 727 -11538151 7500923695 hi1626 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:similar to sp:p46909 pid:971339 gb:al009126 percent) (le:10152) (re:10868) (di:complement) U32835 U32835 g1574467 Haemophilus influenzae Rd 71421 -11538151 6500734293 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1626 HI1626 Haemophilus influenzae 727 -11538151

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893117	16032	38188	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893120	16033	38189	1452	483

Description

5000695720 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1631 HI1631 Haemophilus influenzae 727 -11538152 112113 hi1631 (de:hypothetical protein hi1631 precursor) (db:swissprot) YG31_HAEIN P44279 HAEMOPHILUS INFLUENZAE 727 -11538152 166866 hypothetical protein hi1631 (db:pir2.dat) A64039 A64039 Haemophilus influenzae 727 -11538152 7500923751 hi1631 h. influenzae predicted coding region hi1631 (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2125) (re:2697) (di:complement) U32836 U32836 g1574483 Haemophilus influenzae Rd 71421 -11538152 6500734294 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1631 HI1631 Haemophilus influenzae 727 -11538152

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893129	16034	38190	2376	791

Description

5000695721 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1637 HI1637 Haemophilus influenzae 727 -11538153 112125 hi1637 (de:hypothetical protein hi1637) (db:swissprot) YCJX_HAEIN P44280 HAEMOPHILUS INFLUENZAE 727 -11538153 166867 hypothetical protein hi1637 (db:pir2.dat) B64039 B64039 Haemophilus influenzae 727 -11538153 7500921881 hi1637 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787581 percent ident:) (le:10458) (re:11870) (di:complement) U32836 U32836 g1574484 Haemophilus influenzae Rd 71421 -11538153 6500734295 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1637 HI1637 Haemophilus influenzae 727 -11538153

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893136	16035	38191	1440	479

Description

5000695722 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1650 HI1650 Haemophilus influenzae 727 -11538154 112191 hi1650 (de:hypothetical protein hi1650) (db:swissprot) YG50_HAEIN P44281 HAEMOPHILUS INFLUENZAE 727 -11538154 166871 hypothetical protein hi1650 (db:pir2.dat) C64039 C64039 Haemophilus influenzae 727 -11538154 7500923879 hi1650 h. influenzae predicted coding region hi1650 (db:genpept-bct1) (de:haemophilus influenzae rd section 153 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2259) (re:2369) (di:direct) U32838 U32838 g1574499 Haemophilus influenzae Rd 71421 -11538154 6500734296 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1650 HI1650 Haemophilus influenzae 727 -11538154

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893148	16036	38192	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893187	16037	38193	198	65

Description

5000695723 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1651 HI1651 Haemophilus influenzae 727 -11538155 112192 hi1651 (de:hypothetical protein hi1651) (db:swissprot) YG51_HAEIN P44282 HAEMOPHILUS INFLUENZAE 727 -11538155 166872 hypothetical protein hi1651 (db:pir2.dat) D64039 D64039 Haemophilus influenzae 727 -11538155 7500923880 hi1651 h. influenzae predicted coding region hi1651 (db:genpept-bct1) (de:haemophilus influenzae rd section 153 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2484) (re:2762) (di:complement) U32838 U32838 g1574500 Haemophilus influenzae Rd 71421 -11538155 6500734297 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1651 HI1651 Haemophilus influenzae 727 -11538155

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893195	16038	38194	558	185

Description

5000695724 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1665 HI1665 Haemophilus influenzae 727 -11538156 112229 hi1665 (de:hypothetical protein hi1665) (db:swissprot) YG65_HAEIN P44283 HAEMOPHILUS INFLUENZAE 727 -11538156 166880 hypothetical protein hi1665 (db:pir2.dat) E64039 E64039 Haemophilus influenzae 727 -11538156 7500923953 hi1665 h. influenzae predicted coding region hi1665 (db:genpept-bct1) (de:haemophilus influenzae rd section 154 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9650) (re:9772) (di:complement) U32839 U32839 g1574516 Haemophilus influenzae Rd 71421 -11538156 6500734298 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1665 HI1665 Haemophilus influenzae 727 -11538156

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893196	16039	38195	606	201

Description

5000695725 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1666 HI1666 Haemophilus influenzae 727 -11538157 112231 hi1666 (de:hypothetical protein hi1666) (db:swissprot) YCBK_HAEIN P44284 HAEMOPHILUS INFLUENZAE 727 -11538157 166881 hypothetical protein hi1666 (db:pir2.dat) F64039 F64039 Haemophilus influenzae 727 -11538157 7500921576 hi1666 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 154 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75848 pid:1787157 percent) (le:9826) (re:10209) (di:complement) U32839 U32839 g1574517 Haemophilus influenzae Rd 71421 -11538157 6500734299 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1666 HI1666 Haemophilus influenzae 727 -11538157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893198	16040	38196	372	123

Description

GTC ORF with score 130 to: (db:genpept-bct1) (de:bacillus licheniformis bacitracin synthetase operon includingbacitracin synthetase 1 (baca), 2 (bacb) and 3 (bacc) genes,complete cds.) (nt:peptide synthetase; ba3; bacc) (le:24119) (re:43198) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893209	16041	38197	867	289

Description

5000695726 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1667 HI1667 Haemophilus influenzae 727 -11538158 112233 hi1667 (de:hypothetical protein hi1667) (db:swissprot) YCBB_HAEIN P44285 HAEMOPHILUS INFLUENZAE 727 -11538158 166882 hypothetical protein hi1667 (db:pir2.dat) G64039 G64039 Haemophilus influenzae 727 -11538158 7500921567 hi1667 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 154 of 163 of the completegenome.) (nt:similar to sp:p22525 gb:x57550 pid:42044 gb:u00096) (le:10225) (re:11694) (di:complement) U32839 U32839 g1574515 Haemophilus influenzae Rd 71421 -11538158 6500734300 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1667 HI1667 Haemophilus influenzae 727 -11538158

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893222	16042	38198	330	109

Description

5000695727 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1669 HI1669 Haemophilus influenzae 727 -11538159 111492 hi1669 (de:hypothetical protein hi1669) (db:swissprot) YEBJ_HAEIN P44286 HAEMOPHILUS INFLUENZAE 727 -11538159 166883 hypothetical protein hi1669 (cl:hypothetical protein hi1669) (db:pir2.dat) H64039 H64039 Haemophilus influenzae 727 -11538159 7500922924 hi1669 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to sp:p45577 gb:u00096 percent ident:) (le:2176) (re:2301) (di:complement) U32840 U32840 g1574520 Haemophilus influenzae Rd 71421 -11538159 6500734301 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1669 HI1669 Haemophilus influenzae 727 -11538159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893229	16043	38199	672	223

Description

5000695728 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1680 HI1680 Haemophilus influenzae 727 -11538160 112776 hi1680 (de:hypothetical protein hi1680) (db:swissprot) YCCS_HAEIN P44289 HAEMOPHILUS INFLUENZAE 727 -11538160 166888 hypothetical protein hi1680 (cl:hypothetical protein hi1680) (db:pir2.dat) B64040 B64040 Haemophilus influenzae 727 -11538160 7500921631 hi1680 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787194 percent ident:) (le:2187) (re:4343) (di:complement) U32841 U32841 g1574532 Haemophilus influenzae Rd 71421 -11538160 6500734302 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1680 HI1680 Haemophilus influenzae 727 -11538160

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893230	16044	38200	213	70

Description

GTC ORF with score 257 to: (db:genpept-pln2) (de:botryotinia fuckeliana monoubiquitin/carboxy extension proteinfusion (ubi1cep79) gene, complete cds.) (nt:similar to neurospora crassa ubiquitin/ribosomal) (le:190:618) (re:564:710) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893256	16045	38201	621	206

Description

6500734303 hi1683:hin_1656 hypothetical (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HIN_1656 HIN_1656 Haemophilus influenzae 727 -11538161 7500976299 hi1683 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787914 percent ident:) (le:6617) (re:7195) (di:direct) U32841 U32841 g1574535 Haemophilus influenzae Rd 71421 -11538161 5000695729 (de:(hin165611) (pn:hypothetical) (gn:hi1683) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-haemophilus influenzae)) HIN165611 HIN165611 Haemophilus influenzae 727 10126726

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893260	16046	38202	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893268	16047	38203	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893271	16048	38204	534	177

Description

GTC ORF with score 342 to: (fn:mge1p is an essential protein involved in) (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae s288c mge1p gene, complete cds.) (nt:n-terminus has a leader sequence with features) (le:160) (re:846) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893273	16049	38205	600	199

Description

5000695730 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1687 HI1687 Haemophilus influenzae 727 -11538162 112239 hi1687 (de:hypothetical protein hi1687) (db:swissprot) YG87_HAEIN P44291 HAEMOPHILUS INFLUENZAE 727 -11538162 166891 hypothetical protein hi1687 (cl:hypothetical protein hi1687) (db:pir2.dat) D64040 D64040 Haemophilus influenzae 727 -11538162 7500923984 hi1687 nitrogen fixation protein rnfg (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to pid:1905812 percent ident: 47.34;) (le:11405) (re:12028) (di:direct) U32841 U32841 g1574539 Haemophilus influenzae Rd 71421 -11538162 6500734304 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1687 HI1687 Haemophilus influenzae 727 -11538162

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893298	16050	38206	414	137

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893300	16051	38207	495	164

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893309	16052	38208	1230	409

Description

5000695731 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1701 HI1701 Haemophilus influenzae 727 -11538163 112565 hi1701 (de:hypothetical protein hi1701) (db:swissprot) YH01_HAEIN P44292 HAEMOPHILUS INFLUENZAE 727 -11538163 166893 hypothetical protein hi1701 (db:pir2.dat) E64040 E64040 Haemophilus influenzae 727 -11538163 7500936669 hi1701 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 158 of 163 of the completegenome.) (nt:similar to pid:1652989 percent ident: 33.19;) (le:93) (re:836) (di:direct) U32843 U32843 g1574555 Haemophilus influenzae Rd 71421 -11538163 6500734305 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1701 HI1701 Haemophilus influenzae 727 -11538163

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893313	16053	38209	306	101

Description

5000695732 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1709 HI1709 Haemophilus influenzae 727 -11538164 112404 hi1709 (de:hypothetical protein hi1709 precursor) (db:swissprot) YGIW_HAEIN P44293 HAEMOPHILUS INFLUENZAE 727 -11538164 166896 hypothetical protein hi1709 (db:pir2.dat) F64040 F64040 Haemophilus influenzae 727 -11538164 7500924274 hi1709 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:similar to pid:882554 sp:p52083 gb:u00096) (le:62) (re:427) (di:complement) U32844 U32844 g1574564 Haemophilus influenzae Rd 71421 -11538164 6500734306 hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1709 HI1709 Haemophilus influenzae 727 -11538164

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893319	16054	38210	507	168

Description

5000695733 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1710 HI1710 Haemophilus influenzae 727 -11538165 112573 hi1710 (de:hypothetical protein hi1710) (db:swissprot) YH10_HAEIN P44294 HAEMOPHILUS INFLUENZAE 727 -11538165 166897 hypothetical protein hi1710 (db:pir2.dat) G64040 G64040 Haemophilus influenzae 727 -11538165 7500936678 hi1710 h. influenzae predicted coding region hi1710 (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:542) (re:682) (di:complement) U32844 U32844 g1574565 Haemophilus influenzae Rd 71421 -11538165 6500734307 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1710 HI1710 Haemophilus influenzae 727 -11538165

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893331	16055	38211	426	141

Description

5000695734 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1717 HI1717 Haemophilus influenzae 727 -11538166 112580 hi1717 (de:hypothetical protein hi1717) (db:swissprot) YH17_HAEIN P44295 HAEMOPHILUS INFLUENZAE 727 -11538166 166900 hypothetical protein hi1717 (db:pir2.dat) H64040 H64040 Haemophilus influenzae 727 -11538166 7500936686 hi1717 h. influenzae predicted coding region hi1717 (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6944) (re:7042) (di:complement) U32844 U32844 g1574573 Haemophilus influenzae Rd 71421 -11538166 6500734308 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1717 HI1717 Haemophilus influenzae 727 -11538166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893332	16056	38212	1095	364

Description

5000695735 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1718 HI1718 Haemophilus influenzae 727 -11538167 112582 hi1718 (de:hypothetical protein hi1718) (db:swissprot) YH18_HAEIN P44296 HAEMOPHILUS INFLUENZAE 727 -11538167 166901 hypothetical protein hi1718 (db:pir2.dat) I64040 I64040 Haemophilus influenzae 727 -11538167 7500936690 hi1718 h. influenzae predicted coding region hi1718 (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7176) (re:7961) (di:complement) U32844 U32844 g1574574 Haemophilus influenzae Rd 71421 -11538167 6500734309 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1718 HI1718 Haemophilus influenzae 727 -11538167

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893337	16057	38213	327	108

Description

5000695736 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1724 HI1724 Haemophilus influenzae 727 -11538168 166905 hypothetical protein hi1724 (cl:hypothetical protein hi1724) (db:pir2.dat) A64041 A64041 Haemophilus influenzae 727 -11538168 7500960703 hi1724 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to sp:p45567 gb:u00096 pid:1786310 percent) (le:2751) (re:3149) (di:direct) U32845 U32845 g1574580 Haemophilus influenzae Rd 71421 -11538168 6500734310 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1724 HI1724 Haemophilus influenzae 727 -11538168

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893342	16058	38214	546	181

Description

5000695737 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1730 HI1730 Haemophilus influenzae 727 -11538169 112590 hi1730 (de:hypothetical protein hi1730) (db:swissprot) YBGK_HAEIN P44298 HAEMOPHILUS INFLUENZAE 727 -11538169 166906 hypothetical protein hi1730 (cl:hypothetical protein hi1730) (db:pir2.dat) B64041 B64041 Haemophilus influenzae 727 -11538169 7500896750 hi1730 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75745 pid:1786930 percent) (le:10068) (re:10997) (di:complement) U32845 U32845 g1574586 Haemophilus influenzae Rd 71421 -11538169 6500734311 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1730 HI1730 Haemophilus influenzae 727 -11538169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893344	16059	38215	516	171

Description

5000695738 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1731 HI1731 Haemophilus influenzae 727 -11538170 112591 hi1731 (de:hypothetical protein hi1731) (db:swissprot) YBGJ_HAEIN P44299 HAEMOPHILUS INFLUENZAE 727 -11538170 166907 hypothetical protein hi1731 (cl:hypothetical protein hi1731) (db:pir2.dat) C64041 C64041 Haemophilus influenzae 727 -11538170 7500896748 hi1731 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75744 pid:1786929 percent) (le:10994) (re:11635) (di:complement) U32845 U32845 g1574587 Haemophilus influenzae Rd 71421 -11538170 6500734312 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1731 HI1731 Haemophilus influenzae 727 -11538170

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893349	16060	38216	468	155

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893350	16061	38217	384	127

Description

5000695739 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1736 HI1736 Haemophilus influenzae 727 -11538171 112592 hi1736 (de:hypothetical protein hi1736) (db:swissprot) YH36_HAEIN P44300 HAEMOPHILUS INFLUENZAE 727 -11538171 166908 hypothetical protein hi1736 (db:pir2.dat) D64041 D64041 Haemophilus influenzae 727 -11538171 7500936702 hi1736 h. influenzae predicted coding region hi1736 (db:genpept-bct1) (de:haemophilus influenzae rd section 161 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9164) (re:9397) (di:complement) U32846 U32846 g1574594 Haemophilus influenzae Rd 71421 -11538171 6500734313 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1736 HI1736 Haemophilus influenzae 727 -11538171

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893373	16062	38218	2730	909

Description

GTC ORF with score 123 to: (fn:transcriptional regulation) (db:genpept-vrl) (de:human herpesvirus 6 replication origin-binding protein (hdrfo),partial cds, helicase-primase component (hdrf1), virion protein(hdlf1), putative helicase (hdrf2), putative ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893379	16063	38219	933	310

Description

5000695740 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1737 HI1737 Haemophilus influenzae 727 -11538172 112593 hi1737 (de:hypothetical protein hi1737) (db:swissprot) YH37_HAEIN P44301 HAEMOPHILUS INFLUENZAE 727 -11538172 166909 branched-chain amino acid transport protein azlD homolog hi1737 (cl:branched-chain amino acid transport protein azlD) (db:pir2.dat) E64041 E64041 Haemophilus influenzae 727 -11538172 7500936703 hi1737 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 161 of 163 of the completegenome.) (nt:similar to gb:al009126 percent ident: 53.70;) (le:9500) (re:9829) (di:complement) U32846 U32846 g1574595 Haemophilus influenzae Rd 71421 -11538172 6500734314 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1737 HI1737 Haemophilus influenzae 727 -11538172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893385	16064	38220	1773	590

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893394	16065	38221	453	150

Description

GTC ORF with score 105 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t22d1.) (nt:contains similarity to helicases; coded for by c.) (le:1986:2958:3083:3966) (re:2645:3032:3451:4135) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893399	16066	38222	528	175

Description

5000695741 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1738 HI1738 Haemophilus influenzae 727 -11538173 112594 hi1738 (de:hypothetical protein hi1738) (db:swissprot) YH38_HAEIN P44302 HAEMOPHILUS INFLUENZAE 727 -11538173 166910 hypothetical protein hi1738 (cl:hypothetical protein b2682) (db:pir2.dat) F64041 F64041 Haemophilus influenzae 727 -11538173 7500936704 hi1738 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 161 of 163 of the completegenome.) (nt:similar to gb:al009126 percent ident: 51.29;) (le:9826) (re:10560) (di:complement) U32846 U32846 g1574596 Haemophilus influenzae Rd 71421 -11538173 6500734315 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (db:gtc-haemophilus influenzae) HI1738 HI1738 Haemophilus influenzae 727 -11538173

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893409	16067	38223	393	130

Description

5000694979 gb:l10328_61:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0003 HI0003 Haemophilus influenzae 727 -11538174 108331 hi0003 (de:hypothetical protein hi0003) (db:swissprot) Y003_HAEIN P44447 HAEMOPHILUS INFLUENZAE 727 -11538174 166236 hypothetical protein hi0003 (db:pir2.dat) I64139 I64139 Haemophilus influenzae 727 -11538174 7500894506 hi0003 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p09997 pid:290545 pid:41648) (le:3050) (re:3838) (di:complement) U32686 U32686 g1572947 Haemophilus influenzae Rd 71421 -11538174 6500734316 gb:l10328_61:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0003 HI0003 Haemophilus influenzae 727 -11538174

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893412	16068	38224	348	115

Description

5000694980 gb:u00016_19:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0004 HI0004 Haemophilus influenzae 727 -11538175 4000708183 hi0004 (de:hypothetical protein hi0004) (db:swissprot) YBEY_HAEIN P71335 HAEMOPHILUS INFLUENZAE 727 -11538175 166237 conserved hypothetical protein hi0004 (db:pir2.dat) A64140 A64140 Haemophilus influenzae 727 -11538175 7500896709 hi0004 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77385 pid:1778578) (le:3854) (re:4318) (di:complement) U32686 U32686 g1572948 Haemophilus influenzae Rd 71421 -11538175 6500734317 gb:u00016_19:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0004 HI0004 Haemophilus influenzae 727 -11538175

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893415	16069	38225	297	98

Description

5000694981 gb:u14003_282:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0012 HI0012 Haemophilus influenzae 727 -11538176 113862 hi0012 (de:hypothetical protein hi0012) (db:swissprot) YJJT_HAEIN P44453 HAEMOPHILUS INFLUENZAE 727 -11538176 166238 hypothetical protein hi0012 (db:pir2.dat) B64140 B64140 Haemophilus influenzae 727 -11538176 7500938129 hi0012 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39406 pid:537211 gb:u00096) (le:83) (re:1075) (di:direct) U32687 U32687 g1572956 Haemophilus influenzae Rd 71421 -11538176 6500734318 gb:u14003_282:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0012 HI0012 Haemophilus influenzae 727 -11538176

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893424	16070	38226	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893425	16071	38227	357	119

Description

5000694982 sp:p33633:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0017 HI0017 Haemophilus influenzae 727 -11538177 111936 hi0017 (de:hypothetical protein hi0017) (db:swissprot) YFID_HAEIN P44455 HAEMOPHILUS INFLUENZAE 727 -11538177 166239 probable glycyl radical protein hi0017:hypothetical protein hi0017 (cl:probable glycyl radical protein yfid:glycyl radical homology) (db:pir1.dat) C64140 C64140 Haemophilus influenzae 727 -11538177 7500923516 hi0017 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to sp:p33633 gb:u00096 pid:1788933 percent) (le:5751) (re:6134) (di:complement) U32687 U32687 g1572961 Haemophilus influenzae Rd 71421 -11538177 6500734319 sp:p33633:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0017 HI0017 Haemophilus influenzae 727 -11538177

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893432	16072	38228	189	62

Description

5000694983 pir:s49379:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0019 HI0019 Haemophilus influenzae 727 -11538178 121749 hi0019 (de:hypothetical protein hi0019) (db:swissprot) YLEA_HAEIN Q57163 HAEMOPHILUS INFLUENZAE 727 -11538178 166240 conserved hypothetical protein hi0019 (cl:conserved hypothetical protein hi0019) (db:pir2.dat) D64140 D64140 Haemophilus influenzae 727 -11538178 7500950959 hi0019 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77645 pid:1778580) (le:7121) (re:8545) (di:complement) U32687 U32687 g1572963 Haemophilus influenzae Rd 71421 -11538178 6500734320 pir:s49379:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0019 HI0019 Haemophilus influenzae 727 -11538178

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893442	16073	38229	453	150

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893445	16074	38230	471	157

Description

6500734321 citg:hi0021 hypothetical protein:gp:x79817_5:protein homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0021 HI0021 Haemophilus influenzae 727 -11538179 64703 citg:hi0021 (de:citg protein) (db:swissprot) CITG_HAEIN P44458 HAEMOPHILUS INFLUENZAE 727 -11538179 166241 hypothetical protein hi0021 (db:pir2.dat) E64140 E64140 Haemophilus influenzae 727 -11538179 7500878779 hi0021 citg protein citg (db:genpept-bct1) (de:haemophilus influenzae rd section 2 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77231 pid:1778530) (le:10405) (re:11655) (di:complement) U32687 U32687 g1572965 Haemophilus influenzae Rd 71421 -11538179 5000694984 (de:(hi0021) (pn:protein homolog:hypothetical protein:x79817_5) (gn:citg) (gtcfc:13.7:14.1) (ec:) (citg_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0021 HI0021 Haemophilus influenzae 727 10007365

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893467	16075	38231	234	77

Description

5000694985 gb:l07636_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0028 HI0028 Haemophilus influenzae 727 -11538180 110247 hi0028 (de:hypothetical protein hi0028) (db:swissprot) YBED_HAEIN P44465 HAEMOPHILUS INFLUENZAE 727 -11538180 166242 hypothetical protein hi0028 (cl:ybed protein) (db:pir2.dat) F64140 F64140 Haemophilus influenzae 727 -11538180 7500896666 hi0028 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to gb:l07636 sp:p30977 pid:146621 gb:u00096) (le:5822) (re:6100) (di:complement) U32688 U32688 g1572973 Haemophilus influenzae Rd 71421 -11538180 6500734322 gb:l07636_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0028 HI0028 Haemophilus influenzae 727 -11538180

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893473	16076	38232	1374	457

Description

5000694986 sp:p05850:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0033 HI0033 Haemophilus influenzae 727 -11538181 110242 hi0033 (de:hypothetical protein hi0033) (db:swissprot) YBEA_HAEIN P44470 HAEMOPHILUS INFLUENZAE 727 -11538181 157262 ybea protein homolog hi0033 (cl:conserved hypothetical protein hi0033) (db:pir2.dat) G64140 G64140 Haemophilus influenzae 727 -11538181 7500896662 hi0033 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to sp:p05850 gb:x04516 pid:581174 gb:u00096) (le:11349) (re:11816) (di:complement) U32688 U32688 g1572978 Haemophilus influenzae Rd 71421 -11538181 6500734323 sp:p05850:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0033 HI0033 Haemophilus influenzae 727 -11538181

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893477	16077	38233	255	84

Description

5000694987 sp:p05848:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0034 HI0034 Haemophilus influenzae 727 -11538182 110244 hi0034 (de:hypothetical protein hi0034) (db:swissprot) YBEB_HAEIN P44471 HAEMOPHILUS INFLUENZAE 727 -11538182 157258 ybeb protein homolog hi0034 (cl:escherichia coli ybeb protein) (db:pir2.dat) H64140 H64140 Haemophilus influenzae 727 -11538182 7500896663 hi0034 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to sp:p05848 gb:x04516 pid:42314 gb:u00096) (le:11870) (re:12178) (di:complement) U32688 U32688 g1572979 Haemophilus influenzae Rd 71421 -11538182 6500734324 sp:p05848:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0034 HI0034 Haemophilus influenzae 727 -11538182

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893498	16078	38234	423	140

Description

5000694988 gb:l10328_50:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0035 HI0035 Haemophilus influenzae 727 -11538183 113210 hi0035 (de:hypothetical protein hi0035) (db:swissprot) YIDE_HAEIN P44472 HAEMOPHILUS INFLUENZAE 727 -11538183 166243 hypothetical protein hi0035 (db:pir2.dat) I64140 I64140 Haemophilus influenzae 727 -11538183 7500937364 hi0035 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p29211 gb:m94104 pid:290534) (le:93) (re:1748) (di:complement) U32689 U32689 g1572981 Haemophilus influenzae Rd 71421 -11538183 6500734325 gb:l10328_50:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0035 HI0035 Haemophilus influenzae 727 -11538183

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893524	16079	38235	1638	545

Description

5000694989 sp:p39219:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0042 HI0042 Haemophilus influenzae 727 -11538184 108492 hi0042 (de:hypothetical protein hi0042) (db:swissprot) Y042_HAEIN P43930 HAEMOPHILUS INFLUENZAE 727 -11538184 166245 hypothetical protein hi0042 (db:pir2.dat) B64000 B64000 Haemophilus influenzae 727 -11538184 7500894578 hi0042 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to sp:p39219 gb:u00096 pid:1786244 percent) (le:8228) (re:8902) (di:complement) U32689 U32689 g1572988 Haemophilus influenzae Rd 71421 -11538184 6500734326 sp:p39219:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0042 HI0042 Haemophilus influenzae 727 -11538184

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893527	16080	38236	429	142

Description

5000694990 sp:p06967:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0044 HI0044 Haemophilus influenzae 727 -11538185 110622 hi0044 (de:hypothetical protein hi0044) (db:swissprot) YCCA_HAEIN P44477 HAEMOPHILUS INFLUENZAE 727 -11538185 166247 probable glutamte receptor hi0044 (db:pir2.dat) A64141 A64141 Haemophilus influenzae 727 -11538185 7500921616 hi0044 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 4 of 163 of the complete genome.) (nt:similar to sp:p06967 gb:x00547 pid:41284 gb:u00096) (le:10026) (re:10688) (di:complement) U32689 U32689 g1572990 Haemophilus influenzae Rd 71421 -11538185 6500734327 sp:p06967:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0044 HI0044 Haemophilus influenzae 727 -11538185

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893529	16081	38237	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893535	16082	38238	549	182

Description

5000694991 hypothetical protein:gb:u14003_128:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0045 HI0045 Haemophilus influenzae 727 -11538186 116406 hi0045 (de:hypothetical protein hi0045 precursor) (db:swissprot) YTFJ_HAEIN P44478 HAEMOPHILUS INFLUENZAE 727 -11538186 166248 hypothetical protein hi0045 (db:pir2.dat) B64141 B64141 Haemophilus influenzae 727 -11538186 7500952762 hi0045 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39187 pid:471102) (le:267) (re:821) (di:complement) U32690 U32690 g1572992 Haemophilus influenzae Rd 71421 -11538186 6500734328 hypothetical protein:gb:u14003_128:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0045 HI0045 Haemophilus influenzae 727 -11538186

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893541	16083	38239	579	192

Description

5000694992 sp:p37675:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0050 HI0050 Haemophilus influenzae 727 -11538187 108530 hi0050 (de:hypothetical protein hi0050) (db:swissprot) Y050_HAEIN P44483 HAEMOPHILUS INFLUENZAE 727 -11538187 166249 hypothetical protein hi0050 (cl:conserved hypothetical protein hi1029) (db:pir2.dat) C64141 C64141 Haemophilus influenzae 727 -11538187 7500894589 hi0050 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to sp:p37675 pid:466716 gb:u00096) (le:3781) (re:4986) (di:complement) U32690 U32690 g1572997 Haemophilus influenzae Rd 71421 -11538187 6500734329 sp:p37675:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0050 HI0050 Haemophilus influenzae 727 -11538187

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893542	16084	38240	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893544	16085	38241	540	179

Description

5000694993 sp:p37674:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0051 HI0051 Haemophilus influenzae 727 -11538188 108531 hi0051 (de:hypothetical protein hi0051) (db:swissprot) Y051_HAEIN P44484 HAEMOPHILUS INFLUENZAE 727 -11538188 166250 hypothetical protein hi0051 (db:pir2.dat) D64141 D64141 Haemophilus influenzae 727 -11538188 7500894593 hi0051 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to sp:p37674 pid:466715 gb:u00096) (le:5061) (re:5558) (di:complement) U32690 U32690 g1572998 Haemophilus influenzae Rd 71421 -11538188 6500734330 sp:p37674:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0051 HI0051 Haemophilus influenzae 727 -11538188

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893548	16086	38242	192	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893556	16087	38243	510	169

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893570	16088	38244	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893576	16089	38245	342	113

Description

5000694994 sp:p37676:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0052 HI0052 Haemophilus influenzae 727 -11538189 4000709709 hi0052 (de:hypothetical protein hi0052 precursor) (db:swissprot) Y052_HAEIN P71336 HAEMOPHILUS INFLUENZAE 727 -11538189 166251 hypothetical protein hi0052 (db:pir2.dat) E64141 E64141 Haemophilus influenzae 727 -11538189 7500894594 hi0052 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to sp:p37676 pid:466717 gb:u00096) (le:5597) (re:6583) (di:complement) U32690 U32690 g1572999 Haemophilus influenzae Rd 71421 -11538189 6500734331 sp:p37676:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0052 HI0052 Haemophilus influenzae 727 -11538189

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893577	16090	38246	276	91

Description

5000694995 hypothetical protein orf18:gp:d21242_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0056 HI0056 Haemophilus influenzae 727 -11538190 108541 hi0056 (de:hypothetical protein hi0056) (db:swissprot) YGDQ_HAEIN P43932 HAEMOPHILUS INFLUENZAE 727 -11538190 166253 hypothetical protein hi0056 (cl:conserved hypothetical protein hi0056) (db:pir2.dat) D64000 D64000 Haemophilus influenzae 727 -11538190 7500924097 hi0056 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to pid:882725 gb:u00096 pid:1789197 percent) (le:9813) (re:10526) (di:complement) U32690 U32690 g1573003 Haemophilus influenzae Rd 71421 -11538190 6500734332 hypothetical protein orf18:gp:d21242_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0056 HI0056 Haemophilus influenzae 727 -11538190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893578	16091	38247	474	157

Description

5000694996 sp:p27300:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0059 HI0059 Haemophilus influenzae 727 -11538191 110567 lpxk:hi0059 (ec:2.7.1.130) (de:tetraacyldisaccharide 4'-kinase, (lipid a 4'-kinase)) (db:swissprot) LPXK_HAEIN P44491 HAEMOPHILUS INFLUENZAE 727 -11538191 166254 hypothetical protein hi0059 (db:pir2.dat) G64141 G64141 Haemophilus influenzae 727 -11538191 7500885153 hi0059 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 6 of 163 of the complete genome.) (nt:similar to sp:p27300 gb:z11796 pid:42024 gb:u00096) (le:2745) (re:3743) (di:complement) U32691 U32691 g1573007 Haemophilus influenzae Rd 71421 -11538191 6500734333 sp:p27300:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0059 HI0059 Haemophilus influenzae 727 -11538191

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893592	16092	38248	312	103

Description

5000694997 hypothetical protein:sp:p31805:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0065 HI0065 Haemophilus influenzae 727 -11538192 113686 hi0065 (de:hypothetical protein hi0065 precursor) (db:swissprot) YJEE_HAEIN P44492 HAEMOPHILUS INFLUENZAE 727 -11538192 166255 hypothetical protein hi0065 (cl:hypothetical protein hi0065) (db:pir2.dat) H64141 H64141 Haemophilus influenzae 727 -11538192 7500937955 hi0065 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 7 of 163 of the complete genome.) (nt:similar to sp:p31805 pid:304913 pid:537009) (le:68) (re:544) (di:direct) U32692 U32692 g1573014 Haemophilus influenzae Rd 71421 -11538192 6500734334 hypothetical protein:sp:p31805:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0065 HI0065 Haemophilus influenzae 727 -11538192

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893596	16093	38249	204	67

Description

5000694998 sp:p37768:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0072 HI0072 Haemophilus influenzae 727 -11538193 111971 hi0072 (de:hypothetical protein hi0072) (db:swissprot) YFJB_HAEIN P44497 HAEMOPHILUS INFLUENZAE 727 -11538193 7500923542 hi0072 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 7 of 163 of the complete genome.) (nt:similar to sp:p46140 pid:1033111 gb:u00096) (le:9539) (re:10324) (di:complement) U32692 U32692 g1573020 Haemophilus influenzae Rd 71421 -11538193 6500734335 sp:p37768:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0072 HI0072 Haemophilus influenzae 727 -11538193

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893604	16094	38250	297	98

Description

5000694999 gb:u14003_289:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0081 HI0081 Haemophilus influenzae 727 -11538194 113865 hi0081 (de:hypothetical protein hi0081) (db:swissprot) YJJV_HAEIN P44500 HAEMOPHILUS INFLUENZAE 727 -11538194 166261 hypothetical protein hi0081 (db:pir2.dat) A64142 A64142 Haemophilus influenzae 727 -11538194 7500938131 hi0081 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39408 pid:537218 gb:u00096) (le:8459) (re:9247) (di:direct) U32693 U32693 g1573029 Haemophilus influenzae Rd 71421 -11538194 6500734336 gb:u14003_289:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0081 HI0081 Haemophilus influenzae 727 -11538194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893608	16095	38251	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893626	16096	38252	915	304

Description

5000695000 sp:p24562:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0090 HI0090 Haemophilus influenzae 727 -11538195 112354 hi0090 (de:hypothetical protein hi0090) (db:swissprot) YGGS_HAEIN P44506 HAEMOPHILUS INFLUENZAE 727 -11538195 166264 hypothetical protein hi0090 (cl:conserved hypothetical protein hi0090) (db:pir2.dat) B64142 B64142 Haemophilus influenzae 727 -11538195 7500924201 hi0090 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 9 of 163 of the complete genome.) (nt:similar to pid:882480 sp:p52054 gb:u00096) (le:8104) (re:8817) (di:direct) U32694 U32694 g1573041 Haemophilus influenzae Rd 71421 -11538195 6500734337 sp:p24562:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0090 HI0090 Haemophilus influenzae 727 -11538195

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893628	16097	38253	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893637	16098	38254	1341	446

Description

5000695001 gb:d90212_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0091 HI0091 Haemophilus influenzae 727 -11538196 112607 hi0091 (de:hypothetical protein hi0091) (db:swissprot) YHAD_HAEIN P44507 HAEMOPHILUS INFLUENZAE 727 -11538196 166265 conserved hypothetical protein hi0091 (cl:yhad protein) (db:pir2.dat) C64142 C64142 Haemophilus influenzae 727 -11538196 7500936741 hi0091 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 9 of 163 of the complete genome.) (nt:similar to sp:p42100 pid:563934 pid:904179) (le:8857) (re:9993) (di:complement) U32694 U32694 g1573042 Haemophilus influenzae Rd 71421 -11538196 6500734338 gb:d90212_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0091 HI0091 Haemophilus influenzae 727 -11538196

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893655	16099	38255	411	136

Description

5000695002 gb:u14003_233:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0092 HI0092 Haemophilus influenzae 727 -11538197 4000708214 hi0092 (de:hypothetical protein hi0092) (db:swissprot) Y092_HAEIN Q57493 HAEMOPHILUS INFLUENZAE 727 -11538197 166266 hypothetical protein hi0092 (db:pir2.dat) D64142 D64142 Haemophilus influenzae 727 -11538197 7500894670 hi0092 h. influenzae predicted coding region hi0092 (db:genpept-bct1) (de:haemophilus influenzae rd section 9 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10002) (re:11261) (di:complement) U32694 U32694 g1573043 Haemophilus influenzae Rd 71421 -11538197 6500734339 gb:u14003_233:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0092 HI0092 Haemophilus influenzae 727 -11538197

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893656	16100	38256	198	65

Description

5000695003 sp:p37047:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0093 HI0093 Haemophilus influenzae 727 -11538198 109690 hi0093 (de:hypothetical protein hi0093) (db:swissprot) YAEG_HAEIN P44509 HAEMOPHILUS INFLUENZAE 727 -11538198 166267 hypothetical protein hi0093 (cl:hypothetical protein hi0093) (db:pir2.dat) E64142 E64142 Haemophilus influenzae 727 -11538198 7500896092 hi0093 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:similar to sp:p37047 gb:u00096 pid:1552740) (le:91) (re:1197) (di:complement) U32695 U32695 g1573045 Haemophilus influenzae Rd 71421 -11538198 6500734340 sp:p37047:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0093 HI0093 Haemophilus influenzae 727 -11538198

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893664	16101	38257	906	302

Description

5000695004 sp:p24178:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0103 HI0103 Haemophilus influenzae 727 -11538199 111874 hi0103 (de:hypothetical protein hi0103) (db:swissprot) YFFB_HAEIN P44515 HAEMOPHILUS INFLUENZAE 727 -11538199 166272 hypothetical protein hi0103 (db:pir2.dat) F64142 F64142 Haemophilus influenzae 727 -11538199 7500923434 hi0103 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 10 of 163 of the complete genome.) (nt:similar to sp:p24178 gb:x57403 pid:41233 gb:u00096) (le:9462) (re:9806) (di:complement) U32695 U32695 g1573052 Haemophilus influenzae Rd 71421 -11538199 6500734341 sp:p24178:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0103 HI0103 Haemophilus influenzae 727 -11538199

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893677	16102	38258	498	165

Description

5000695005 gb:l01112_7:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0105 HI0105 Haemophilus influenzae 727 -11538200 5500686479 hi0105 (de:hypothetical protein hi0105) (db:swissprot) YBGI_HAEIN Q57354 HAEMOPHILUS INFLUENZAE 727 -11538200 166273 conserved hypothetical protein hi0105 (db:pir2.dat) G64142 G64142 Haemophilus influenzae 727 -11538200 7500896746 hi0105 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 11 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p75743 pid:1786928 percent) (le:139) (re:978) (di:direct) U32696 U32696 g1573058 Haemophilus influenzae Rd 71421 -11538200 6500734342 gb:l01112_7:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0105 HI0105 Haemophilus influenzae 727 -11538200

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893681	16103	38259	702	233

Description

5000695006 gb:u14003_130:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0107 HI0107 Haemophilus influenzae 727 -11538201 166274 hypothetical protein hi0107 (cl:hypothetical protein hi0107) (db:pir2.dat) H64142 H64142 Haemophilus influenzae 727 -11538201 7500894713 hi0107 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 11 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788966 percent identity:) (le:2755) (re:3966) (di:direct) U32696 U32696 g1573060 Haemophilus influenzae Rd 71421 -11538201 4000708211 hi0107 (de:hypothetical protein hi0107) (db:swissprot) Y107_HAEIN Q57017 HAEMOPHILUS INFLUENZAE 727 -11538201 6500734343 gb:u14003_130:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0107 HI0107 Haemophilus influenzae 727 -11538201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893683	16104	38260	204	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893689	16105	38261	468	155

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893690	16106	38262	822	273

Description

5000695007 gb:u14003_278:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0108 HI0108 Haemophilus influenzae 727 -11538202 113857 hi0108 (de:hypothetical protein hi0108) (db:swissprot) YJJP_HAEIN P44520 HAEMOPHILUS INFLUENZAE 727 -11538202 166275 hypothetical protein hi0108 (db:pir2.dat) I64142 I64142 Haemophilus influenzae 727 -11538202 7500938126 hi0108 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 11 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39402 pid:537207 gb:u00096) (le:4095) (re:4988) (di:direct) U32696 U32696 g1573061 Haemophilus influenzae Rd 71421 -11538202 6500734344 gb:u14003_278:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0108 HI0108 Haemophilus influenzae 727 -11538202

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893694	16107	38263	852	283

Description

5000695008 gb:u09558_1:hypothetical protein:insertion element is1223 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0112 HI0112 Haemophilus influenzae 727 -11538203 7000687067 hi0112 (de:hypothetical protein hi0112) (db:swissprot) Y112_HAEIN P71339 HAEMOPHILUS INFLUENZAE 727 -11538203 166277 hypothetical protein hi0112 (db:pir2.dat) A64143 A64143 Haemophilus influenzae 727 -11538203 7500894720 hi0112 h. influenzae predicted coding region hi0112 (db:genpept-bct1) (de:haemophilus influenzae rd section 11 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7850) (re:8146) (di:complement) U32696 U32696 g1573064 Haemophilus influenzae Rd 71421 -11538203 6500734345 gb:u09558_1:hypothetical protein:insertion element is1223 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0112 HI0112 Haemophilus influenzae 727 -11538203

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893695	16108	38264	924	307

Description

5000695009 gb:x73124_20:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0115 HI0115 Haemophilus influenzae 727 -11538204 166279 hypothetical protein hi0115 (db:pir2.dat) B64143 B64143 Haemophilus influenzae 727 -11538204 6500734346 gb:x73124_20:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0115 HI0115 Haemophilus influenzae 727 -11538204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893701	16109	38265	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893702	16110	38266	1110	369

Description

5000695010 sp:p37773:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0121 HI0121 Haemophilus influenzae 727 -11538205 113717 mpl:hi0121 (ec:6.3.2.-) (de:ligase,) (db:swissprot) MPL_HAEIN P43948 HAEMOPHILUS INFLUENZAE 727 -11538205 166283 hypothetical protein hi0121 (db:pir2.dat) B64002 B64002 Haemophilus influenzae 727 -11538205 7500885844 hi0121 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p37773 pid:537075 gb:u00096) (le:3850) (re:5211) (di:complement) U32698 U32698 g1573076 Haemophilus influenzae Rd 71421 -11538205 6500734347 sp:p37773:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0121 HI0121 Haemophilus influenzae 727 -11538205

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893717	16111	38267	471	157

Description

5000695011 sp:p32702:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0125 HI0125 Haemophilus influenzae 727 -11538206 113643 hi0125 (de:hypothetical protein hi0125) (db:swissprot) YJCD_HAEIN P44530 HAEMOPHILUS INFLUENZAE 727 -11538206 166284 hypothetical protein hi0125 (cl:conserved hypothetical protein hi0125) (db:pir2.dat) C64143 C64143 Haemophilus influenzae 727 -11538206 7500937902 hi0125 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the complete genome.) (nt:similar to sp:p32702 pid:396399 gb:u00096) (le:8950) (re:10266) (di:direct) U32698 U32698 g1573080 Haemophilus influenzae Rd 71421 -11538206 6500734348 sp:p32702:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0125 HI0125 Haemophilus influenzae 727 -11538206

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893721	16112	38268	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893722	16113	38269	777	258

Description

5000695012 hypothetical protein:sp:p37009:hypothetical abc transporter atp-binding protein hi0126 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0126 HI0126 Haemophilus influenzae 727 -11538207 109748 afuc:hi0126 (de:putative ferric transport atp-binding protein afuc) (db:swissprot) AFUC_HAEIN P44531 HAEMOPHILUS INFLUENZAE 727 -11538207 166285 probable abc-type transport protein hi0126:hypothetical protein hi0126 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) D64143 D64143 Haemophilus influenzae 727 -11538207 7500876647 hi0126 ferric abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the complete genome.) (nt:similar to pid:1469284 pid:1477453 percent) (le:10424) (re:11410) (di:complement) U32698 U32698 g1573081 Haemophilus influenzae Rd 71421 -11538207 6500734349 hypothetical protein:sp:p37009:hypothetical abc transporter atp-binding protein hi0126 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0126 HI0126 Haemophilus influenzae 727 -11538207

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893723	16114	38270	660	219

Description

GTC ORF with score 168 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0216 gene, complete cds.) (nt:similar to myosin heavy chain: containing) (le:485) (re:5230) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893728	16115	38271	597	198

Description

5000695013 sp:p31122:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0135 HI0135 Haemophilus influenzae 727 -11538208 111282 hi0135 (de:hypothetical protein hi0135) (db:swissprot) YDEA_HAEIN P44535 HAEMOPHILUS INFLUENZAE 727 -11538208 166290 chloramphenicol resistance protein homolog hi0135 (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) E64143 E64143 Haemophilus influenzae 727 -11538208 7500922240 hi0135 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:similar to gb:ae000511 pid:2314345 percent) (le:3923) (re:5113) (di:direct) U32699 U32699 g1573088 Haemophilus influenzae Rd 71421 -11538208 6500734350 sp:p31122:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0135 HI0135 Haemophilus influenzae 727 -11538208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893753	16116	38272	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893757	16117	38273	390	129

Description

5000695014 hypothetical protein:gb:u00021_5:hypothetical gtp-binding protein hi0136 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0136 HI0136 Haemophilus influenzae 727 -11538209 108844 hi0136 (de:hypothetical gtp-binding protein hi0136) (db:swissprot) YFGK_HAEIN P44536 HAEMOPHILUS INFLUENZAE 727 -11538209 166291 hypothetical protein hi0136 (cl:translation elongation factor tu homology) (db:pir2.dat) F64143 F64143 Haemophilus influenzae 727 -11538209 7500894771 hi0136 gtp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788858 percent identity:) (le:5193) (re:6707) (di:complement) U32699 U32699 g1573089 Haemophilus influenzae Rd 71421 -11538209 6500734351 hypothetical protein:gb:u00021_5:hypothetical gtp-binding protein hi0136 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0136 HI0136 Haemophilus influenzae 727 -11538209

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893759	16118	38274	510	169

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893761	16119	38275	471	156

Description

5000695015 gb:m81878_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0143 HI0143 Haemophilus influenzae 727 -11538210 108868 hi0143 (de:hypothetical protein hi0143) (db:swissprot) Y143_HAEIN P44540 HAEMOPHILUS INFLUENZAE 727 -11538210 7500894776 hi0143 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the complete genome.) (nt:similar to gb:m81878 sp:p26833 pid:144859 percent) (le:3533) (re:4399) (di:complement) U32700 U32700 g1573099 Haemophilus influenzae Rd 71421 -11538210 6500734352 gb:m81878_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0143 HI0143 Haemophilus influenzae 727 -11538210

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893763	16120	38276	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893767	16121	38277	357	118

Description

5000695016 hypothetical protein:sp:p37676:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0146 HI0146 Haemophilus influenzae 727 -11538211 108876 hi0146 (de:hypothetical protein hi0146 precursor) (db:swissprot) Y146_HAEIN P44542 HAEMOPHILUS INFLUENZAE 727 -11538211 166293 hypothetical protein hi0146 (db:pir2.dat) H64143 H64143 Haemophilus influenzae 727 -11538211 7500894785 hi0146 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the complete genome.) (nt:similar to sp:p37676 pid:466717 gb:u00096) (le:6376) (re:7365) (di:direct) U32700 U32700 g1573102 Haemophilus influenzae Rd 71421 -11538211 6500734353 hypothetical protein:sp:p37676:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0146 HI0146 Haemophilus influenzae 727 -11538211

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893770	16122	38278	2871	956

Description

5000695017 sp:p37675:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0147 HI0147 Haemophilus influenzae 727 -11538212 108879 hi0147 (de:hypothetical protein hi0147) (db:swissprot) Y147_HAEIN P44543 HAEMOPHILUS INFLUENZAE 727 -11538212 166294 hypothetical protein hi0147 (db:pir2.dat) I64143 I64143 Haemophilus influenzae 727 -11538212 7500894790 hi0147 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the complete genome.) (nt:similar to sp:p37675 pid:466716 gb:u00096) (le:7376) (re:9277) (di:direct) U32700 U32700 g1573103 Haemophilus influenzae Rd 71421 -11538212 6500734354 sp:p37675:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0147 HI0147 Haemophilus influenzae 727 -11538212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893776	16123	38279	450	149

Description

5000695018 gb:u14003_222:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0148 HI0148 Haemophilus influenzae 727 -11538213 113809 hi0148 (de:hypothetical protein hi0148) (db:swissprot) YJHT_HAEIN P44544 HAEMOPHILUS INFLUENZAE 727 -11538213 166295 hypothetical protein hi0148 (db:pir2.dat) A64144 A64144 Haemophilus influenzae 727 -11538213 7500938069 hi0148 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39371 pid:537151 gb:u00096) (le:9441) (re:10580) (di:direct) U32700 U32700 g1573104 Haemophilus influenzae Rd 71421 -11538213 6500734355 gb:u14003_222:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0148 HI0148 Haemophilus influenzae 727 -11538213

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893778	16124	38280	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893802	16125	38281	495	164

Description

GTC ORF with score 386 to: (sr:porphyridium purpureum (strain:iam-r1) cdna to mrna) (db:genpept-pln1) (ec:4.2.1.1) (de:porphyridium purpureum mrna for carbonic anhydrase, complete cds.) (nt:n-terminal half and c-terminal half of the putative) (le:91) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893806	16126	38282	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893808	16127	38283	375	124

Description

GTC ORF with score 107 to: (sr:porphyridium purpureum (strain:iam-r1) cdna to mrna) (db:genpept-pln1) (ec:4.2.1.1) (de:porphyridium purpureum mrna for carbonic anhydrase, complete cds.) (nt:n-terminal and c-terminal halves of the putaive) (le:31) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893814	16128	38284	336	111

Description

GTC ORF with score 121 to: (sr:neurospora crassa (individual_isolate ic3, strain 74a) (library) (db:genpept-pln1) (ec:4.1.1.17) (de:neurospora crassa ornithine decarboxylase gene, complete cds.) (nt:putative) (le:2577:2981) (re:2910:4101) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893815	16129	38285	756	251

Description

5000695019 hypothetical protein:gb:u20229_3:hypothetical lipoprotein hi0162 precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0162 HI0162 Haemophilus influenzae 727 -11538214 109811 hi0162 (de:hypothetical lipoprotein hi0162 precursor) (db:swissprot) YAJG_HAEIN P43782 HAEMOPHILUS INFLUENZAE 727 -11538214 166298 hypothetical protein hi0162 (db:pir2.dat) B64144 B64144 Haemophilus influenzae 727 -11538214 241609 unknown (db:genpept-bct1) (de:haemophilus influenzae bola (bola), glutathione reductase (gor),phosphatidylserine decarboxylase (psd), 30k protein (rpmf), genes,complete cds.) (nt:orf199) (le:924) (re:1523) (di:direct) HIU20229 U20229 g644853 Haemophilus influenzae 727 -11538214 7500896233 hi0162 lipoprotein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1773118 pid:1786637) (le:1671) (re:2270) (di:complement) U32702 U32702 g1573120 Haemophilus influenzae Rd 71421 -11538214 6500734356 hypothetical protein:gb:u20229_3:hypothetical lipoprotein hi0162 precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0162 HI0162 Haemophilus influenzae 727 -11538214

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893819	16130	38286	498	165

Description

5000695020 sp:p33943:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0172 HI0172 Haemophilus influenzae 727 -11538215 115266 apbe:hi0172 (de:thiamine biosynthesis lipoprotein apbe precursor) (db:swissprot) APBE_HAEIN P44550 HAEMOPHILUS INFLUENZAE 727 -11538215 166304 hypothetical protein hi0172 (cl:hypothetical protein hi0172) (db:pir2.dat) C64144 C64144 Haemophilus influenzae 727 -11538215 7500952115 hi0172 lipoprotein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to sp:p33943 pid:405940 gb:u00096) (le:8892) (re:9932) (di:direct) U32702 U32702 g1573128 Haemophilus influenzae Rd 71421 -11538215 6500734357 sp:p33943:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0172 HI0172 Haemophilus influenzae 727 -11538215

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893825	16131	38287	414	137

Description

5000695021 sp:p25745:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0174 HI0174 Haemophilus influenzae 727 -11538216 110748 trmu:hi0174 (ec:2.1.1.61) (de:(ec 2.1.1.61)) (db:swissprot) TRMU_HAEIN P44551 HAEMOPHILUS INFLUENZAE 727 -11538216 166306 probable atpase hi0174 (cl:probable membrane protein ydl033c) (db:pir2.dat) D64144 D64144 Haemophilus influenzae 727 -11538216 7500893414 hi0174 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to sp:p25745 pid:42583 gb:u00096) (le:10207) (re:11463) (di:direct) U32702 U32702 g1573129 Haemophilus influenzae Rd 71421 -11538216 6500734358 sp:p25745:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0174 HI0174 Haemophilus influenzae 727 -11538216

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893833	16132	38288	426	141

Description

5000695022 sp:p33644:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0175 HI0175 Haemophilus influenzae 727 -11538217 111947 hi0175 (de:hypothetical protein hi0175) (db:swissprot) YFIH_HAEIN P44552 HAEMOPHILUS INFLUENZAE 727 -11538217 166307 hypothetical protein hi0175 (db:pir2.dat) E64144 E64144 Haemophilus influenzae 727 -11538217 7500923524 hi0175 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to sp:p33644 gb:m29364 pid:1236632) (le:11507) (re:12241) (di:complement) U32702 U32702 g1573130 Haemophilus influenzae Rd 71421 -11538217 6500734359 sp:p33644:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0175 HI0175 Haemophilus influenzae 727 -11538217

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893836	16133	38289	2850	949

Description

5000695023 sp:p33643:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0176 HI0176 Haemophilus influenzae 727 -11538218 111952 rlud:sfhb:hi0176 (ec:4.2.1.70) (de:(pseudouridylate synthase) (uracil hydrolyase)) (db:swissprot) RLUD_HAEIN P44445 HAEMOPHILUS INFLUENZAE 727 -11538218 166308 hypothetical protein hi0176 (cl:conserved hypothetical protein hi0176) (db:pir2.dat) F64144 F64144 Haemophilus influenzae 727 -11538218 7500891567 hi0176 sfhb protein sfhb (db:genpept-bct1) (de:haemophilus influenzae rd section 17 of 163 of the complete genome.) (nt:similar to sp:p33643 pid:1236631 gb:u00096) (le:12243) (re:13217) (di:complement) U32702 U32702 g1573131 Haemophilus influenzae Rd 71421 -11538218 6500734360 sp:p33643:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0176 HI0176 Haemophilus influenzae 727 -11538218

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893838	16134	38290	675	224

Description

5000695024 sp:p33641:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0177 HI0177 Haemophilus influenzae 727 -11538219 108942 hi0177 (de:hypothetical protein hi0177) (db:swissprot) Y177_HAEIN P44553 HAEMOPHILUS INFLUENZAE 727 -11538219 166309 hypothetical protein hi0177 (cl:conserved hypothetical protein hi0177) (db:pir2.dat) G64144 G64144 Haemophilus influenzae 727 -11538219 7500894823 hi0177 lipoprotein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 18 of 163 of the complete genome.) (nt:similar to pid:1107833 percent identity: 32.93;) (le:84) (re:872) (di:direct) U32703 U32703 g1573134 Haemophilus influenzae Rd 71421 -11538219 6500734361 sp:p33641:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0177 HI0177 Haemophilus influenzae 727 -11538219

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893839	16135	38291	240	79

Description

5000695025 sp:p30143:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0183 HI0183 Haemophilus influenzae 727 -11538220 109504 hi0183 (de:hypothetical protein hi0183) (db:swissprot) YAAJ_HAEIN P44555 HAEMOPHILUS INFLUENZAE 727 -11538220 166312 probable amino acid transport protein hi0183:sodium-dependent (cl:sodium-dependent d-alanine/glycine transport protein) (db:pir2.dat) I64144 I64144 Haemophilus influenzae 727 -11538220 7500895973 hi0183 amino acid carrier protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 18 of 163 of the complete genome.) (nt:similar to pid:757741 sp:q45068 pid:1405464) (le:7132) (re:8577) (di:direct) U32703 U32703 g1573139 Haemophilus influenzae Rd 71421 -11538220 6500734362 sp:p30143:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0183 HI0183 Haemophilus influenzae 727 -11538220

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893840	16136	38292	462	153

Description

5000695026 gb:m87049_61:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0187 HI0187 Haemophilus influenzae 727 -11538221 166314 hypothetical protein hi0187 (cl:conserved hypothetical secreted protein hp0320) (db:pir2.dat) B64145 B64145 Haemophilus influenzae 727 -11538221 6500734363 gb:m87049_61:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0187 HI0187 Haemophilus influenzae 727 -11538221

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893887	16137	38293	486	161

Description

5000695027 sp:p27857:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0188 HI0188 Haemophilus influenzae 727 -11538222 113305 tatc:hi0188 (de:sec-independent protein translocase protein tatc) (db:swissprot) TATC_HAEIN P44560 HAEMOPHILUS INFLUENZAE 727 -11538222 166315 hypothetical protein hi0188 (cl:conserved hypothetical protein hi0188) (db:pir2.dat) C64145 C64145 Haemophilus influenzae 727 -11538222 7500937464 hi0188 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 19 of 163 of the complete genome.) (nt:similar to sp:p27857 gb:m87049 pid:148238) (le:1520) (re:2290) (di:direct) U32704 U32704 g1573146 Haemophilus influenzae Rd 71421 -11538222 6500734364 sp:p27857:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0188 HI0188 Haemophilus influenzae 727 -11538222

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893896	16138	38294	1206	402

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893907	16139	38295	990	329

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893910	16140	38296	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893912	16141	38297	1914	638

Description

5000695028 sp:p14008:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0198 HI0198 Haemophilus influenzae 727 -11538223 111825 hi0198 (de:hypothetical protein hi0198) (db:swissprot) YFCA_HAEIN P46490 HAEMOPHILUS INFLUENZAE 727 -11538223 7500923364 hi0198 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:similar to sp:p14008 pid:41996 gb:u00096) (le:951) (re:1718) (di:direct) U32705 U32705 g1573158 Haemophilus influenzae Rd 71421 -11538223 6500734365 sp:p14008:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0198 HI0198 Haemophilus influenzae 727 -11538223

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893925	16142	38298	462	153

Description

5000695029 sp:p21504:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0203 HI0203 Haemophilus influenzae 727 -11538224 111968 rimm:hi0203 (de:16s rrna processing protein rimm) (db:swissprot) RIMM_HAEIN P44568 HAEMOPHILUS INFLUENZAE 727 -11538224 166317 hypothetical protein hi0203 (db:pir2.dat) D64145 D64145 Haemophilus influenzae 727 -11538224 7500889792 hi0203 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:similar to sp:p21504 gb:u00096 pid:1788960 percent) (le:5093) (re:5629) (di:complement) U32705 U32705 g1573163 Haemophilus influenzae Rd 71421 -11538224 6500734366 sp:p21504:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0203 HI0203 Haemophilus influenzae 727 -11538224

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893956	16143	38299	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893962	16144	38300	1257	418

Description

5000695030 gb:s68137_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0219 HI0219 Haemophilus influenzae 727 -11538225 108990 hi0219 (de:hypothetical protein hi0219) (db:swissprot) YKGB_HAEIN P44577 HAEMOPHILUS INFLUENZAE 727 -11538225 166321 hypothetical protein hi0219 (cl:conserved hypothetical protein hi0219) (db:pir2.dat) E64145 E64145 Haemophilus influenzae 727 -11538225 7500938486 hi0219 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 22 of 163 of the complete genome.) (nt:similar to gb:s68137 sp:p46928 pid:469476 percent) (le:3337) (re:3978) (di:complement) U32707 U32707 g1573181 Haemophilus influenzae Rd 71421 -11538225 6500734367 gb:s68137_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0219 HI0219 Haemophilus influenzae 727 -11538225

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893963	16145	38301	315	104

Description

5000695031 gb:u18997_150:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0227 HI0227 Haemophilus influenzae 727 -11538226 112680 hi0227 (de:hypothetical protein hi0227) (db:swissprot) YHCH_HAEIN P44583 HAEMOPHILUS INFLUENZAE 727 -11538226 166322 hypothetical protein hi0227 (cl:hypothetical protein hi0227) (db:pir2.dat) F64145 F64145 Haemophilus influenzae 727 -11538226 7500936812 hi0227 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 24 of 163 of the complete genome.) (nt:similar to sp:p37673 pid:466714 gb:u00096) (le:1542) (re:2009) (di:complement) U32709 U32709 g1573192 Haemophilus influenzae Rd 71421 -11538226 6500734368 gb:u18997_150:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0227 HI0227 Haemophilus influenzae 727 -11538226

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893965	16146	38302	729	242

Description

5000695032 gb:u18997_93:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0230 HI0230 Haemophilus influenzae 727 -11538227 112641 hi0230 (de:hypothetical protein hi0230) (db:swissprot) YHBM_HAEIN P44585 HAEMOPHILUS INFLUENZAE 727 -11538227 166324 hypothetical protein hi0230 (cl:hypothetical protein hi0230:tetratricopeptide repeat homology) (db:pir2.dat) G64145 G64145 Haemophilus influenzae 727 -11538227 7500936774 hi0230 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 24 of 163 of the complete genome.) (nt:similar to sp:p39833 pid:606103 pid:1128971) (le:4969) (re:5913) (di:direct) U32709 U32709 g1573194 Haemophilus influenzae Rd 71421 -11538227 6500734369 gb:u18997_93:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0230 HI0230 Haemophilus influenzae 727 -11538227

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893981	16147	38303	1284	427

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893982	16148	38304	426	141

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893990	16149	38305	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501893993	16150	38306	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894006	16151	38307	1104	367

Description

5000695033 sp:p30135:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0232 HI0232 Haemophilus influenzae 727 -11538228 111907 hi0232 (de:hypothetical protein hi0232) (db:swissprot) YFHD_HAEIN P44587 HAEMOPHILUS INFLUENZAE 727 -11538228 166325 hypothetical protein hi0232 (cl:hypothetical protein hi0232) (db:pir2.dat) H64145 H64145 Haemophilus influenzae 727 -11538228 7500923482 hi0232 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 24 of 163 of the complete genome.) (nt:similar to sp:p30135 gb:x72336 pid:1033147) (le:8053) (re:9441) (di:direct) U32709 U32709 g1573196 Haemophilus influenzae Rd 71421 -11538228 6500734370 sp:p30135:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0232 HI0232 Haemophilus influenzae 727 -11538228

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894021	16152	38308	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894025	16153	38309	1152	384

Description

5000695034 gb:l29458_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0235 HI0235 Haemophilus influenzae 727 -11538229 112725 hi0235 (de:hypothetical protein hi0235) (db:swissprot) YHDL_HAEIN P44588 HAEMOPHILUS INFLUENZAE 727 -11538229 166328 hypothetical protein hi0235 (db:pir2.dat) I64145 I64145 Haemophilus influenzae 727 -11538229 7500936841 hi0235 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:similar to gb:l29458 sp:p36675 pid:473421 percent) (le:134) (re:343) (di:complement) U32710 U32710 g1573201 Haemophilus influenzae Rd 71421 -11538229 6500734371 gb:l29458_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0235 HI0235 Haemophilus influenzae 727 -11538229

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894039	16154	38310	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894063	16155	38311	1476	491

Description

5000695035 gb:m63939_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0241 HI0241 Haemophilus influenzae 727 -11538230 109804 hi0241 (de:hypothetical protein hi0241) (db:swissprot) YAJC_HAEIN P44592 HAEMOPHILUS INFLUENZAE 727 -11538230 166331 yajc protein homolog hi0241 (cl:yajc protein) (db:pir2.dat) A64146 A64146 Haemophilus influenzae 727 -11538230 7500896230 hi0241 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:similar to pid:599589 percent identity: 62.37;) (le:4908) (re:5201) (di:complement) U32710 U32710 g1573206 Haemophilus influenzae Rd 71421 -11538230 6500734372 gb:m63939_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0241 HI0241 Haemophilus influenzae 727 -11538230

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894078	16156	38312	2475	825

Description

5000695036 sp:p33014:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0242 HI0242 Haemophilus influenzae 727 -11538231 109011 hi0242 (de:hypothetical protein hi0242) (db:swissprot) Y242_HAEIN P44593 HAEMOPHILUS INFLUENZAE 727 -11538231 166332 hypothetical protein hi0242 (db:pir2.dat) B64146 B64146 Haemophilus influenzae 727 -11538231 7500894944 hi0242 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 25 of 163 of the complete genome.) (nt:similar to gb:l77117 sp:q58397 pid:1591652 percent) (le:5309) (re:5530) (di:complement) U32710 U32710 g1573207 Haemophilus influenzae Rd 71421 -11538231 6500734373 sp:p33014:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0242 HI0242 Haemophilus influenzae 727 -11538231

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894079	16157	38313	1935	644

Description

5000695037 gb:u00014_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0260 HI0260 Haemophilus influenzae 727 -11538232 112359 hi0260 (de:hypothetical protein hi0260) (db:swissprot) YGGV_HAEIN P44598 HAEMOPHILUS INFLUENZAE 727 -11538232 166338 hypothetical protein hi0260 (cl:methanococcus jannaschii conserved hypothetical protein mj0226) (db:pir2.dat) D64146 D64146 Haemophilus influenzae 727 -11538232 7500924205 hi0260 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 27 of 163 of the complete genome.) (nt:similar to pid:882483 sp:p52061 gb:u00096) (le:69) (re:656) (di:complement) U32712 U32712 g1573226 Haemophilus influenzae Rd 71421 -11538232 6500734374 gb:u00014_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0260 HI0260 Haemophilus influenzae 727 -11538232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894081	16158	38314	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894083	16159	38315	579	192

Description

5000695038 sp:p31056:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0266 HI0266 Haemophilus influenzae 727 -11538233 112396 hi0266 (de:hypothetical protein hi0266) (db:swissprot) YGIH_HAEIN P44603 HAEMOPHILUS INFLUENZAE 727 -11538233 166339 hypothetical protein hi0266 (cl:escherichia coli ygih protein) (db:pir2.dat) E64146 E64146 Haemophilus influenzae 727 -11538233 7500924258 hi0266 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 28 of 163 of the complete genome.) (nt:similar to sp:p31056 pid:882581 gb:u00096) (le:72) (re:671) (di:direct) U32713 U32713 g1573232 Haemophilus influenzae Rd 71421 -11538233 6500734375 sp:p31056:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0266 HI0266 Haemophilus influenzae 727 -11538233

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894102	16160	38316	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894116	16161	38317	342	113

Description

5000695039 sp:p33371:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0270 HI0270 Haemophilus influenzae 727 -11538234 115248 hi0270 (de:hypothetical protein hi0270) (db:swissprot) YOHI_HAEIN P44606 HAEMOPHILUS INFLUENZAE 727 -11538234 166340 hypothetical protein hi0270 (db:pir2.dat) F64146 F64146 Haemophilus influenzae 727 -11538234 7500952103 hi0270 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 28 of 163 of the complete genome.) (nt:similar to sp:p33371 pid:405871 gb:u00096) (le:4462) (re:5394) (di:complement) U32713 U32713 g1573236 Haemophilus influenzae Rd 71421 -11538234 6500734376 sp:p33371:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0270 HI0270 Haemophilus influenzae 727 -11538234

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894117	16162	38318	222	73

Description

5000695040 sp:p31680:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0271 HI0271 Haemophilus influenzae 727 -11538235 109546 djla:hi0271 (de:dnaj-like protein djla) (db:swissprot) DJLA_HAEIN P44607 HAEMOPHILUS INFLUENZAE 727 -11538235 166341 yabh protein homolog hi0271 (cl:dnaj amino-terminal homology) (db:pir2.dat) G64146 G64146 Haemophilus influenzae 727 -11538235 7500880347 hi0271 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 28 of 163 of the complete genome.) (nt:similar to sp:p31680 gb:u00096 pid:1786241 percent) (le:5394) (re:6260) (di:complement) U32713 U32713 g1573237 Haemophilus influenzae Rd 71421 -11538235 6500734377 sp:p31680:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0271 HI0271 Haemophilus influenzae 727 -11538235

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894132	16163	38319	180	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894133	16164	38320	471	156

Description

5000695041 gb:l19201_29:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0276 HI0276 Haemophilus influenzae 727 -11538236 113341 rbn:hi0276 (ec:3.1.-.-) (de:ribonuclease bn, (rnase bn)) (db:swissprot) RBN_HAEIN P44608 HAEMOPHILUS INFLUENZAE 727 -11538236 166343 hypothetical protein hi0276 (db:pir2.dat) H64146 H64146 Haemophilus influenzae 727 -11538236 7500889462 hi0276 ribonuclease bn rbn (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32146 pid:304990 gb:u00096) (le:1769) (re:2578) (di:complement) U32714 U32714 g1573242 Haemophilus influenzae Rd 71421 -11538236 6500734378 gb:l19201_29:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0276 HI0276 Haemophilus influenzae 727 -11538236

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894135	16165	38321	222	73

Description

5000695042 sp:p38481:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0277 HI0277 Haemophilus influenzae 727 -11538237 110790 hi0277 (de:hypothetical protein hi0277) (db:swissprot) YCHJ_HAEIN P44609 HAEMOPHILUS INFLUENZAE 727 -11538237 166344 hypothetical protein hi0277 (cl:hypothetical protein hi0277) (db:pir2.dat) I64146 I64146 Haemophilus influenzae 727 -11538237 7500921818 hi0277 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:similar to gb:l20251 sp:p37052 pid:410154 gb:u00096) (le:2575) (re:3060) (di:complement) U32714 U32714 g1573243 Haemophilus influenzae Rd 71421 -11538237 6500734379 sp:p38481:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0277 HI0277 Haemophilus influenzae 727 -11538237

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894143	16166	38322	360	119

Description

5000695043 hypothetical protein:sp:p37643:hypothetical metabolite transport protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0281 HI0281 Haemophilus influenzae 727 -11538238 109044 hi0281 (de:hypothetical metabolite transport protein hi0281) (db:swissprot) Y281_HAEIN P44610 HAEMOPHILUS INFLUENZAE 727 -11538238 166347 hypothetical protein hi0281 (cl:citrate utilization determinant) (db:pir2.dat) A64147 A64147 Haemophilus influenzae 727 -11538238 7500895062 hi0281 transport protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:similar to sp:p37643 pid:466660 gb:u00096) (le:4945) (re:6261) (di:complement) U32714 U32714 g1573246 Haemophilus influenzae Rd 71421 -11538238 6500734380 hypothetical protein:sp:p37643:hypothetical metabolite transport protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0281 HI0281 Haemophilus influenzae 727 -11538238

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894147	16167	38323	1305	434

Description

5000695044 gb:l35030_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0282 HI0282 Haemophilus influenzae 727 -11538239 111814 hi0282 (de:hypothetical protein hi0282) (db:swissprot) YFBB_HAEIN P44611 HAEMOPHILUS INFLUENZAE 727 -11538239 166348 hypothetical protein hi0282 (cl:hypothetical protein hi0282) (db:pir2.dat) B64147 B64147 Haemophilus influenzae 727 -11538239 7500923337 hi0282 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:similar to gb:l35030 sp:p37355 pid:516608 gb:u00096) (le:6317) (re:7060) (di:complement) U32714 U32714 g1573247 Haemophilus influenzae Rd 71421 -11538239 6500734381 gb:l35030_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0282 HI0282 Haemophilus influenzae 727 -11538239

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894150	16168	38324	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894171	16169	38325	1137	378

Description

5000695045 sp:p37912:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0303 HI0303 Haemophilus influenzae 727 -11538240 112346 hi0303 (de:hypothetical protein hi0303) (db:swissprot) YGGJ_HAEIN P44627 HAEMOPHILUS INFLUENZAE 727 -11538240 166352 hypothetical protein hi0303 (db:pir2.dat) D64147 D64147 Haemophilus influenzae 727 -11538240 7500924196 hi0303 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to sp:p37912 pid:882475 gb:u00096) (le:3776) (re:4513) (di:direct) U32716 U32716 g1573272 Haemophilus influenzae Rd 71421 -11538240 6500734382 sp:p37912:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0303 HI0303 Haemophilus influenzae 727 -11538240

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894173	16170	38326	351	116

Description

5000695046 sp:p36767:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0306 HI0306 Haemophilus influenzae 727 -11538241 109780 hi0306 (de:hypothetical protein hi0306) (db:swissprot) YAID_HAEIN P44628 HAEMOPHILUS INFLUENZAE 727 -11538241 166355 hypothetical protein hi0306 (db:pir2.dat) E64147 E64147 Haemophilus influenzae 727 -11538241 7500896200 hi0306 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to sp:p36767 gb:x76979 pid:440403 gb:u00096) (le:5539) (re:6447) (di:complement) U32716 U32716 g1573275 Haemophilus influenzae Rd 71421 -11538241 6500734383 sp:p36767:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0306 HI0306 Haemophilus influenzae 727 -11538241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894174	16171	38327	639	212

Description

5000695047 gb:z37966_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0308 HI0308 Haemophilus influenzae 727 -11538242 109068 hi0308 (de:hypothetical protein hi0308) (db:swissprot) YFHS_HAEIN P44629 HAEMOPHILUS INFLUENZAE 727 -11538242 166356 hypothetical protein hi0308 (cl:conserved hypothetical protein hi0308) (db:pir2.dat) F64147 F64147 Haemophilus influenzae 727 -11538242 7500923492 hi0308 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to gb:z37966 pid:550599 gb:u00096 sp:q47142) (le:7328) (re:8494) (di:direct) U32716 U32716 g1573277 Haemophilus influenzae Rd 71421 -11538242 6500734384 gb:z37966_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0308 HI0308 Haemophilus influenzae 727 -11538242

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894180	16172	38328	381	127

Description

5000695048 gb:d10165_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0315 HI0315 Haemophilus influenzae 727 -11538243 111483 hi0315 (de:hypothetical protein hi0315) (db:swissprot) YEBC_HAEIN P44634 HAEMOPHILUS INFLUENZAE 727 -11538243 166359 hypothetical protein hi0315 (cl:hypothetical protein mg332) (db:pir2.dat) G64147 G64147 Haemophilus influenzae 727 -11538243 7500922915 hi0315 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:d10165 sp:p24237 pid:216652 pid:42173) (le:681) (re:1421) (di:complement) U32717 U32717 g1573285 Haemophilus influenzae Rd 71421 -11538243 6500734385 gb:d10165_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0315 HI0315 Haemophilus influenzae 727 -11538243

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894182	16173	38329	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894197	16174	38330	474	157

Description

5000695049 gb:u06949_6:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0323 HI0323 Haemophilus influenzae 727 -11538244 109084 gloa:hi0323 (ec:4.4.1.5) (de:(s-d-lactoylglutathione methylglyoxal lyase)) (db:swissprot) LGUL_HAEIN P44638 HAEMOPHILUS INFLUENZAE 727 -11538244 166363 gloa lactoylglutathione lyase::conserved hypothetical protein hi0323 (ec:4.4.1.5) (db:pir2.dat) I64147 I64147 Haemophilus influenzae 727 -11538244 7500885002 hi0323 lactoylglutathione lyase gloa (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:q59384 pid:1354845) (le:6158) (re:6565) (di:direct) U32717 U32717 g1573292 Haemophilus influenzae Rd 71421 -11538244 6500734386 gb:u06949_6:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0323 HI0323 Haemophilus influenzae 727 -11538244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894203	16175	38331	516	171

Description

5000695050 gb:u06949_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0325 HI0325 Haemophilus influenzae 727 -11538245 109086 hi0325 (de:hypothetical protein hi0325) (db:swissprot) Y325_HAEIN P44640 HAEMOPHILUS INFLUENZAE 727 -11538245 166364 hypothetical protein hi0325 (cl:conserved integral membrane protein hp0758) (db:pir2.dat) A64148 A64148 Haemophilus influenzae 727 -11538245 7500895129 hi0325 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:al009126 percent identity: 52.27;) (le:7642) (re:8994) (di:direct) U32717 U32717 g1573294 Haemophilus influenzae Rd 71421 -11538245 6500734387 gb:u06949_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0325 HI0325 Haemophilus influenzae 727 -11538245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894210	16176	38332	264	87

Description

5000695051 gb:u14003_61:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0329 HI0329 Haemophilus influenzae 727 -11538246 113694 hi0329 (de:hypothetical protein hi0329) (db:swissprot) YJEK_HAEIN P44641 HAEMOPHILUS INFLUENZAE 727 -11538246 166366 hypothetical protein hi0329 (cl:conserved hypothetical protein yodo) (db:pir2.dat) B64148 B64148 Haemophilus influenzae 727 -11538246 7500937961 hi0329 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 32 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39280 pid:536990 gb:u00096) (le:10568) (re:11584) (di:direct) U32717 U32717 g1573296 Haemophilus influenzae Rd 71421 -11538246 6500734388 gb:u14003_61:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0329 HI0329 Haemophilus influenzae 727 -11538246

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894212	16177	38333	1668	555

Description

6500734389 mog:hi0336 molybdopeterin biosynthesis mog protein:sp:p28694:molybdopterin biosynthesis protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0336 HI0336 Haemophilus influenzae 727 -11538247 84006 mog:hi0336 (de:molybdopterin biosynthesis mog protein) (db:swissprot) MOG_HAEIN P44645 HAEMOPHILUS INFLUENZAE 727 -11538247 166368 molybdopterin biosynthesis protein:protein hi0336 (db:pir2.dat) D64148 D64148 Haemophilus influenzae 727 -11538247 7500885766 hi0336 molybdopeterin biosynthesis protein mog (db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the complete genome.) (nt:similar to sp:p28694 pid:41755 gb:u00096) (le:6631) (re:7224) (di:direct) U32718 U32718 g1573305 Haemophilus influenzae Rd 71421 -11538247 5000695052 (de:(hi0336) (pn:molybdopterin biosynthesis protein:molybdopeterin biosynthesis mog protein:p28694) (gn:mog) (gtcfc:13.7:14.1) (ec:) (mog_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0336 HI0336 Haemophilus influenzae 727 10026212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894225	16178	38334	555	184

Description

5000695053 gb:u00039_28:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0338 HI0338 Haemophilus influenzae 727 -11538248 112836 hi0338 (de:hypothetical protein hi0338) (db:swissprot) YHHT_HAEIN P44646 HAEMOPHILUS INFLUENZAE 727 -11538248 166369 hypothetical protein hi0338 (cl:conserved hypothetical protein hi0338) (db:pir2.dat) E64148 E64148 Haemophilus influenzae 727 -11538248 7500936957 hi0338 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1787885 percent identity:) (le:7564) (re:8610) (di:direct) U32718 U32718 g1573307 Haemophilus influenzae Rd 71421 -11538248 6500734390 gb:u00039_28:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0338 HI0338 Haemophilus influenzae 727 -11538248

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894243	16179	38335	1356	451

Description

5000695054 sp:p32049:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0340 HI0340 Haemophilus influenzae 727 -11538249 112344 hi0340 (de:hypothetical protein hi0340) (db:swissprot) YGGH_HAEIN P44648 HAEMOPHILUS INFLUENZAE 727 -11538249 166370 hypothetical protein hi0340 (cl:hypothetical protein hi0340) (db:pir2.dat) F64148 F64148 Haemophilus influenzae 727 -11538249 7500924195 hi0340 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p32049 gb:m59471 pid:882489) (le:72) (re:812) (di:direct) U32719 U32719 g1573311 Haemophilus influenzae Rd 71421 -11538249 6500734391 sp:p32049:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0340 HI0340 Haemophilus influenzae 727 -11538249

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894244	16180	38336	483	160

Description

5000695055 sp:p38521:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0341 HI0341 Haemophilus influenzae 727 -11538250 112348 hi0341 (de:hypothetical protein hi0341) (db:swissprot) YGGL_HAEIN P44649 HAEMOPHILUS INFLUENZAE 727 -11538250 166371 hypothetical protein hi0341 (db:pir2.dat) G64148 G64148 Haemophilus influenzae 727 -11538250 7500924197 hi0341 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p38521 pid:882488 gb:u00096) (le:897) (re:1241) (di:direct) U32719 U32719 g1573312 Haemophilus influenzae Rd 71421 -11538250 6500734392 sp:p38521:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0341 HI0341 Haemophilus influenzae 727 -11538250

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894247	16181	38337	477	158

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894282	16182	38338	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894284	16183	38339	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894290	16184	38340	333	110

Description

6500734393 napf:hi0342 hypothetical protein:sp:p33939:ferredoxin-type protein homolog (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0342 HI0342 Haemophilus influenzae 727 -11538251 85227 napf:hi0342 (de:ferredoxin-type protein napf homolog) (db:swissprot) NAPF_HAEIN P44650 HAEMOPHILUS INFLUENZAE 727 -11538251 166372 hypothetical protein hi0342 (db:pir2.dat) H64148 H64148 Haemophilus influenzae 727 -11538251 7500886293 hi0342 ferredoxin-type protein napf (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p33939 pid:453990 gb:u00096) (le:1447) (re:1788) (di:direct) U32719 U32719 g1573313 Haemophilus influenzae Rd 71421 -11538251 5000695056 (de:(hi0342) (pn:ferredoxin-type protein homolog:hypothetical protein:p33939) (gn:napf) (gtcfc:13.7:14.1) (ec:) (napf_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0342 HI0342 Haemophilus influenzae 727 10027408

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894291	16185	38341	279	92

Description

5000695057 sp:p33938:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0343 HI0343 Haemophilus influenzae 727 -11538252 115262 napd:hi0343 (de:napd protein) (db:swissprot) NAPD_HAEIN P44651 HAEMOPHILUS INFLUENZAE 727 -11538252 166373 hypothetical protein hi0343 (cl:hypothetical protein hi0343) (db:pir2.dat) I64148 I64148 Haemophilus influenzae 727 -11538252 7500886292 hi0343 napd protein napd (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p33938 pid:405935 gb:u00096) (le:1969) (re:2250) (di:direct) U32719 U32719 g1573314 Haemophilus influenzae Rd 71421 -11538252 6500734394 sp:p33938:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0343 HI0343 Haemophilus influenzae 727 -11538252

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894297	16186	38342	846	281

Description

6500734395 napg:hi0345 hypothetical protein:sp:p33936:ferredoxin-type protein homolog (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0345 HI0345 Haemophilus influenzae 727 -11538253 85229 napg:hi0345 (de:ferredoxin-type protein napg homolog) (db:swissprot) NAPG_HAEIN P44652 HAEMOPHILUS INFLUENZAE 727 -11538253 166374 hypothetical protein hi0345 (cl:conserved hypothetical protein hi0345) (db:pir2.dat) A64149 A64149 Haemophilus influenzae 727 -11538253 7500886295 hi0345 ferredoxin-type protein napg (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p33936 pid:405930 pid:405931) (le:4826) (re:5665) (di:direct) U32719 U32719 g1573315 Haemophilus influenzae Rd 71421 -11538253 5000695058 (de:(hi0345) (pn:ferredoxin-type protein homolog:hypothetical protein:p33936) (gn:napg) (gtcfc:13.7:14.1) (ec:) (napg_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0345 HI0345 Haemophilus influenzae 727 10027410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894300	16187	38343	504	167

Description

6500734396 naph:hi0346 hypothetical protein:sp:p33934:ferredoxin-type protein homolog (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0346 HI0346 Haemophilus influenzae 727 -11538254 85231 naph:hi0346 (de:ferredoxin-type protein naph homolog) (db:swissprot) NAPH_HAEIN P44653 HAEMOPHILUS INFLUENZAE 727 -11538254 166375 hypothetical protein hi0346 (cl:hypothetical protein hi0346) (db:pir2.dat) B64149 B64149 Haemophilus influenzae 727 -11538254 7500886297 hi0346 ferredoxin-type protein naph (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p33934 pid:405929 gb:u00096) (le:5665) (re:6528) (di:direct) U32719 U32719 g1573316 Haemophilus influenzae Rd 71421 -11538254 5000695059 (de:(hi0346) (pn:ferredoxin-type protein homolog:hypothetical protein:p33934) (gn:naph) (gtcfc:13.7:14.1) (ec:) (naph_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0346 HI0346 Haemophilus influenzae 727 10027412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894308	16188	38344	546	181

Description

5000695060 sp:p24326:hypothetical protein:orf3 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0350 HI0350 Haemophilus influenzae 727 -11538255 6500734397 hi0350 (de:hypothetical protein hi0350 (orf3)) (db:swissprot) Y350_HAEIN P24326 HAEMOPHILUS INFLUENZAE 727 -11538255 166376 hypothetical protein hi0350 (db:pir2.dat) D64149 D64149 Haemophilus influenzae 727 -11538255 7500895171 hi0350 permease:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p36670 pid:1773117) (le:8483) (re:9760) (di:complement) U32719 U32719 g1573320 Haemophilus influenzae Rd 71421 -11538255 109106 hi0350 (de:hypothetical protein hi0350 (orf3)) (db:swissprot) Y350_HAEIN P24326 HAEMOPHILUS INFLUENZAE 727 -11538255

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894315	16189	38345	597	198

Description

GTC ORF with score 155 to: (sr:saccharomyces cerevisiae (library: lambda yes by s. elledge) cdn) (db:genpept-pln1) (de:saccharomyces cerevisiae putative malr homologue mrna, partial cds.) (nt:sequence similarity to yeast malr protein,) (le:6) (re:392) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894324	16190	38346	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894330	16191	38347	675	224

Description

5000695061 sp:p24324:hypothetical protein:orf1 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0352 HI0352 Haemophilus influenzae 727 -11538256 6500734398 hi0352 (de:hypothetical protein hi0352 (orf1)) (db:swissprot) Y352_HAEIN P24324 HAEMOPHILUS INFLUENZAE 727 -11538256 166377 hypothetical protein hi0352 (db:pir2.dat) E64149 E64149 Haemophilus influenzae 727 -11538256 7500895174 hi0352 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to sp:p24324 gb:x57315 pid:43588 percent) (le:117) (re:812) (di:complement) U32720 U32720 g1573333 Haemophilus influenzae Rd 71421 -11538256 109108 hi0352 (de:hypothetical protein hi0352 (orf1)) (db:swissprot) Y352_HAEIN P24324 HAEMOPHILUS INFLUENZAE 727 -11538256

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894337	16192	38348	456	152

Description

GTC ORF with score 206 to: (de:(yhr020w) (pn:putative prolyl-trna synthetase yhr020w:proline--trna ligase:prors:strong similarity to human glutamyl-prolyl-trna synthetase and fruit fly multifunctional aminoacyl-trna synthetase) (gtcfc:5.10:10.6) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894339	16193	38349	1047	348

Description

5000695062 gb:l16808_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0355 HI0355 Haemophilus influenzae 727 -11538257 5500686315 hi0355 (de:hypothetical abc transporter permease protein hi0355) (db:swissprot) Y355_HAEIN Q57306 HAEMOPHILUS INFLUENZAE 727 -11538257 7500895181 hi0355 abc transporter:permease protein (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to gb:l16808 sp:p40401 pid:438473) (le:2247) (re:2984) (di:direct) U32720 U32720 g1573324 Haemophilus influenzae Rd 71421 -11538257 6500734399 gb:l16808_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0355 HI0355 Haemophilus influenzae 727 -11538257

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894340	16194	38350	429	142

Description

5000695063 gb:l34630_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0359 HI0359 Haemophilus influenzae 727 -11538258 109114 hi0359 (de:hypothetical protein hi0359) (db:swissprot) Y359_HAEIN P44660 HAEMOPHILUS INFLUENZAE 727 -11538258 166379 hypothetical protein hi0359 (cl:conserved hypothetical protein hi0360) (db:pir2.dat) G64149 G64149 Haemophilus influenzae 727 -11538258 7500895188 hi0359 iron chelated abc transporter:permease (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to pid:1245464 sp:q56955 pid:1245467) (le:4707) (re:5522) (di:complement) U32720 U32720 g1573327 Haemophilus influenzae Rd 71421 -11538258 6500734400 gb:l34630_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0359 HI0359 Haemophilus influenzae 727 -11538258

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894358	16195	38351	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894376	16196	38352	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894377	16197	38353	723	240

Description

5000695064 sp:p36979:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0365 HI0365 Haemophilus influenzae 727 -11538259 111891 hi0365 (de:hypothetical protein hi0365) (db:swissprot) YFGB_HAEIN P44665 HAEMOPHILUS INFLUENZAE 727 -11538259 166381 hypothetical protein hi0365 (cl:conserved hypothetical protein hi0365) (db:pir2.dat) I64149 I64149 Haemophilus influenzae 727 -11538259 7500923458 hi0365 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 35 of 163 of the complete genome.) (nt:similar to sp:p36979 gb:u02965 pid:493519 gb:u00096) (le:9637) (re:10809) (di:direct) U32720 U32720 g1573332 Haemophilus influenzae Rd 71421 -11538259 6500734401 sp:p36979:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0365 HI0365 Haemophilus influenzae 727 -11538259

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894380	16198	38354	429	142

Description

5000695065 sp:p27434:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0367 HI0367 Haemophilus influenzae 727 -11538260 5500686316 hi0367 (de:hypothetical protein hi0367) (db:swissprot) Y367_HAEIN Q57065 HAEMOPHILUS INFLUENZAE 727 -11538260 166383 hypothetical protein hi0367 (db:pir2.dat) A64150 A64150 Haemophilus influenzae 727 -11538260 7500895197 hi0367 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to sp:p27434 gb:d21149 gb:u02965 gb:x64451) (le:692) (re:1603) (di:direct) U32721 U32721 g1573336 Haemophilus influenzae Rd 71421 -11538260 6500734402 sp:p27434:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0367 HI0367 Haemophilus influenzae 727 -11538260

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894386	16199	38355	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894391	16200	38356	678	225

Description

5000695066 sp:p37096:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0371 HI0371 Haemophilus influenzae 727 -11538261 111915 hi0371 (de:hypothetical protein hi0371) (db:swissprot) YFHJ_HAEIN P44668 HAEMOPHILUS INFLUENZAE 727 -11538261 166385 hypothetical protein hi0371 (db:pir2.dat) B64150 B64150 Haemophilus influenzae 727 -11538261 7500923487 hi0371 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to sp:p37096 gb:u00096 pid:1788873 percent) (le:4682) (re:4876) (di:complement) U32721 U32721 g1573340 Haemophilus influenzae Rd 71421 -11538261 6500734403 sp:p37096:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0371 HI0371 Haemophilus influenzae 727 -11538261

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894400	16201	38357	813	270

Description

5000695067 sp:p37003:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0374 HI0374 Haemophilus influenzae 727 -11538262 110271 hi0374 (de:hypothetical protein hi0374) (db:swissprot) YBFG_HAEIN P44670 HAEMOPHILUS INFLUENZAE 727 -11538262 166386 hypothetical protein hi0374 (db:pir2.dat) C64150 C64150 Haemophilus influenzae 727 -11538262 7500896718 hi0374 h. influenzae predicted coding region hi0374 (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7135) (re:7821) (di:complement) U32721 U32721 g1573343 Haemophilus influenzae Rd 71421 -11538262 6500734404 sp:p37003:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0374 HI0374 Haemophilus influenzae 727 -11538262

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894408	16202	38358	459	152

Description

5000695068 sp:p36540:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0375 HI0375 Haemophilus influenzae 727 -11538263 4000707877 hscb:hi0375 (de:chaperone protein hscb (hsc20)) (db:swissprot) HSCB_HAEIN Q57006 HAEMOPHILUS INFLUENZAE 727 -11538263 166387 hypothetical protein hi0375 (db:pir2.dat) D64150 D64150 Haemophilus influenzae 727 -11538263 7500883561 hi0375 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to sp:p36540 gb:u01827 pid:402674 gb:u00096) (le:7872) (re:8396) (di:complement) U32721 U32721 g1573344 Haemophilus influenzae Rd 71421 -11538263 6500734405 sp:p36540:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0375 HI0375 Haemophilus influenzae 727 -11538263

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894415	16203	38359	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894419	16204	38360	1446	481

Description

5000695069 sp:p36539:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0376 HI0376 Haemophilus influenzae 727 -11538264 111910 hi0376 (de:hypothetical protein hi0376) (db:swissprot) YFHF_HAEIN P44672 HAEMOPHILUS INFLUENZAE 727 -11538264 166388 hypothetical protein hi0376 (cl:conserved hypothetical protein hi0376) (db:pir2.dat) E64150 E64150 Haemophilus influenzae 727 -11538264 7500923484 hi0376 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to sp:p36539 percent identity: 63.55;) (le:8409) (re:8732) (di:complement) U32721 U32721 g1573345 Haemophilus influenzae Rd 71421 -11538264 6500734406 sp:p36539:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0376 HI0376 Haemophilus influenzae 727 -11538264

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894423	16205	38361	240	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894441	16206	38362	684	228

Description

5000695070 hypothetical protein rrf2:sp:p33395:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0379 HI0379 Haemophilus influenzae 727 -11538265 109129 hi0379 (de:hypothetical protein hi0379) (db:swissprot) Y379_HAEIN P44675 HAEMOPHILUS INFLUENZAE 727 -11538265 166389 hypothetical protein hi0379 (cl:hypothetical protein b2531) (db:pir2.dat) F64150 F64150 Haemophilus influenzae 727 -11538265 7500895215 hi0379 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788880 percent identity:) (le:61) (re:513) (di:complement) U32722 U32722 g1573349 Haemophilus influenzae Rd 71421 -11538265 6500734407 hypothetical protein rrf2:sp:p33395:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0379 HI0379 Haemophilus influenzae 727 -11538265

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894451	16207	38363	2163	720

Description

5000695071 gb:u14003_314:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0380 HI0380 Haemophilus influenzae 727 -11538266 81524 hi0380 (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase hi0380,) (db:swissprot) Y380_HAEIN P44676 HAEMOPHILUS INFLUENZAE 727 -11538266 166390 hypothetical protein hi0380 (cl:conserved hypothetical protein mth1849) (db:pir2.dat) G64150 G64150 Haemophilus influenzae 727 -11538266 7500884813 hi0380 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788881 percent identity:) (le:566) (re:1291) (di:complement) U32722 U32722 g1573350 Haemophilus influenzae Rd 71421 -11538266 6500734408 gb:u14003_314:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0380 HI0380 Haemophilus influenzae 727 -11538266

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894463	16208	38364	639	212

Description

5000695072 sp:p08999:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0386 HI0386 Haemophilus influenzae 727 -11538267 110287 hi0386 (de:hypothetical protein hi0386) (db:swissprot) YBGC_HAEIN P44679 HAEMOPHILUS INFLUENZAE 727 -11538267 154835 conserved hypothetical protein hi0386 (cl:15.5k protein (tolab operon 5' region)) (db:pir2.dat) H64150 H64150 Haemophilus influenzae 727 -11538267 7500896739 hi0386 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 37 of 163 of the complete genome.) (nt:similar to sp:p08999 pid:1128977 gb:u00096) (le:5871) (re:6281) (di:complement) U32722 U32722 g1573356 Haemophilus influenzae Rd 71421 -11538267 6500734409 sp:p08999:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0386 HI0386 Haemophilus influenzae 727 -11538267

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894476	16209	38365	567	188

Description

5000695073 hypothetical protein:sp:p31216:probable gtp-binding protein hi0393 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0393 HI0393 Haemophilus influenzae 727 -11538268 166395 probable gtp-binding protein hi0393 (cl:yeast probable purine nucleotide-binding protein ybr025c) (db:pir2.dat) I64150 I64150 Haemophilus influenzae 727 -11538268 7500960725 hi0393 conserved hypothetical gtp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to sp:p31216 gb:u02423 gb:x61941 pid:311421) (le:1195) (re:2286) (di:complement) U32723 U32723 g1573365 Haemophilus influenzae Rd 71421 -11538268 6500734410 hypothetical protein:sp:p31216:probable gtp-binding protein hi0393 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0393 HI0393 Haemophilus influenzae 727 -11538268

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894487	16210	38366	189	62

Description

GTC ORF with score 130 to: (sr:human) (db:genpept-pri3) (de:homo sapiens chromosome 19, cosmid r32611, complete sequence.) (nt:hypothetical human partial protein; most similar to) (le:27810:28534:28782) (re:27841:28627:28865) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894491	16211	38367	393	130

Description

5000695074 sp:p27431:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0396 HI0396 Haemophilus influenzae 727 -11538269 110752 hi0396 (de:hypothetical protein hi0396) (db:swissprot) YCFD_HAEIN P44683 HAEMOPHILUS INFLUENZAE 727 -11538269 166397 hypothetical protein hi0396 (db:pir2.dat) A64151 A64151 Haemophilus influenzae 727 -11538269 7500921728 hi0396 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to sp:p27431 gb:u00096 pid:1787373 percent) (le:3397) (re:4611) (di:direct) U32723 U32723 g1573367 Haemophilus influenzae Rd 71421 -11538269 6500734411 sp:p27431:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0396 HI0396 Haemophilus influenzae 727 -11538269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894492	16212	38368	237	78

Description

5000695075 sp:p36651:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0398 HI0398 Haemophilus influenzae 727 -11538270 115957 hi0398 (de:hypothetical protein hi0398) (db:swissprot) YQIE_HAEIN P44684 HAEMOPHILUS INFLUENZAE 727 -11538270 166398 hypothetical protein hi0398 (db:pir2.dat) B64151 B64151 Haemophilus influenzae 727 -11538270 7500952503 hi0398 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to sp:p36651 pid:882564 gb:u00096) (le:6109) (re:6762) (di:direct) U32723 U32723 g1573369 Haemophilus influenzae Rd 71421 -11538270 6500734412 sp:p36651:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0398 HI0398 Haemophilus influenzae 727 -11538270

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894509	16213	38369	753	250

Description

5000695076 gb:l19201_64:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0400 HI0400 Haemophilus influenzae 727 -11538271 113362 hi0400 (de:hypothetical protein hi0400) (db:swissprot) Y400_HAEIN P44686 HAEMOPHILUS INFLUENZAE 727 -11538271 166399 c4-dicarboxylate transport protein homolog hi0400 (cl:c4-dicarboxylate carrier protein) (db:pir2.dat) C64151 C64151 Haemophilus influenzae 727 -11538271 7500895244 hi0400 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1788685 percent ident:) (le:7694) (re:7981) (di:complement) U32723 U32723 g1573371 Haemophilus influenzae Rd 71421 -11538271 6500734413 gb:l19201_64:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0400 HI0400 Haemophilus influenzae 727 -11538271

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894511	16214	38370	2283	760

Description

6500734414 mesj:hi0404 hypothetical protein:gb:d26185_130:cell cycle protein homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0404 HI0404 Haemophilus influenzae 727 -11538272 83523 mesj:hi0404 (de:cell cycle protein mesj homolog) (db:swissprot) MESJ_HAEIN P44689 HAEMOPHILUS INFLUENZAE 727 -11538272 166400 hypothetical protein hi0404 (cl:hypothetical protein hi0404) (db:pir2.dat) D64151 D64151 Haemophilus influenzae 727 -11538272 7500885509 hi0404 cell cycle protein mesj (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1552765 pid:1786386) (le:10848) (re:12140) (di:complement) U32723 U32723 g1573375 Haemophilus influenzae Rd 71421 -11538272 5000695077 (de:(hi0404) (pn:cell cycle protein homolog:hypothetical protein:gb:d26185_130) (gn:mesj) (gtcfc:13.7:14.1) (ec:) (mesj_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0404 HI0404 Haemophilus influenzae 727 10025737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894534	16215	38371	624	207

Description

5000695078 gb:u11243_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0405 HI0405 Haemophilus influenzae 727 -11538273 111858 pdxy:hi0405 (ec:2.7.1.35) (de:pyridoxamine kinase, (pm kinase)) (db:swissprot) PDXY_HAEIN P44690 HAEMOPHILUS INFLUENZAE 727 -11538273 166401 probable pyridoxal kinase:hi0405:protein hi0405 (ec:2.7.1.35) (db:pir2.dat) E64151 E64151 Haemophilus influenzae 727 -11538273 7500887785 hi0405 pyridoxine kinase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 38 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1787924 sp:p77150) (le:12140) (re:13006) (di:complement) U32723 U32723 g1573376 Haemophilus influenzae Rd 71421 -11538273 6500734415 gb:u11243_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0405 HI0405 Haemophilus influenzae 727 -11538273

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894543	16216	38372	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894551	16217	38373	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894552	16218	38374	291	96

Description

5000695079 gb:m77039_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0409 HI0409 Haemophilus influenzae 727 -11538274 111480 hi0409 (de:hypothetical protein hi0409) (db:swissprot) YEBA_HAEIN P44693 HAEMOPHILUS INFLUENZAE 727 -11538274 166402 hypothetical protein hi0409 (cl:hypothetical protein hi0409) (db:pir2.dat) F64151 F64151 Haemophilus influenzae 727 -11538274 7500922914 hi0409 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 39 of 163 of the complete genome.) (nt:similar to gb:m77039 sp:p24204 pid:146890) (le:2867) (re:4294) (di:direct) U32724 U32724 g1573382 Haemophilus influenzae Rd 71421 -11538274 6500734416 gb:m77039_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0409 HI0409 Haemophilus influenzae 727 -11538274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894554	16219	38375	243	80

Description

5000695080 sp:p23851:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0412 HI0412 Haemophilus influenzae 727 -11538275 110661 rluc:hi0412 (ec:4.2.1.70) (de:(pseudouridylate synthase) (uracil hydrolyase)) (db:swissprot) RLUC_HAEIN P44433 HAEMOPHILUS INFLUENZAE 727 -11538275 166403 hypothetical protein hi0412 (db:pir2.dat) G64151 G64151 Haemophilus influenzae 727 -11538275 7500921677 hi0412 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 39 of 163 of the complete genome.) (nt:similar to sp:p23851 gb:m62747 pid:146050) (le:5828) (re:6796) (di:complement) U32724 U32724 g1573385 Haemophilus influenzae Rd 71421 -11538275 6500734417 sp:p23851:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0412 HI0412 Haemophilus influenzae 727 -11538275

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894559	16220	38376	525	174

Description

5000695081 gb:x73124_26:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0415 HI0415 Haemophilus influenzae 727 -11538276 1500687061 thim:hi0415 (ec:2.7.1.50) (de:hydroxyethylthiazole kinase) (thz kinase) (th kinase)) (db:swissprot) THIM_HAEIN Q57233 HAEMOPHILUS INFLUENZAE 727 -11538276 166404 hydroxyethylthiazole kinase::hypothetical protein hi0415 (cl:hydroxyethylthiazole kinase:hydroxyethylthiazole kinase homology) (ec:2.7.1.50) (db:pir2.dat) H64151 H64151 Haemophilus influenzae 727 -11538276 7500893076 hi0415 hydroxyethylthiazole kinase (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:similar to gb:x73124 sp:p39593 pid:413949) (le:682) (re:1479) (di:direct) U32725 U32725 g1573389 Haemophilus influenzae Rd 71421 -11538276 6500734418 gb:x73124_26:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0415 HI0415 Haemophilus influenzae 727 -11538276

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894570	16221	38377	1014	337

Description

GTC ORF with score 127 to: (sr:mus musculus (sub_species:domesticus, strain:balb/c) testis cdna t) (db:genpept-rod) (de:mus musculus mrna for hepatoma-derived growth factor, complete cds,strain:balb/c.) (nt:hdgf; this protein has a domain of about 90 ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894577	16222	38378	549	182

Description

5000695082 gb:x73124_53:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0416 HI0416 Haemophilus influenzae 727 -11538277 109154 thid:hi0416 (ec:2.7.4.7) (de:(hmp-p kinase)) (db:swissprot) THID_HAEIN P44697 HAEMOPHILUS INFLUENZAE 727 -11538277 166405 hypothetical protein hi0416 (cl:phosphomethylpyrimidine phosphate kinase) (db:pir2.dat) I64151 I64151 Haemophilus influenzae 727 -11538277 7500893058 hi0416 phosphomethylpyrimidine kinase thid (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:similar to gb:ae000511 pid:2313975 percent) (le:1472) (re:2281) (di:direct) U32725 U32725 g1573390 Haemophilus influenzae Rd 71421 -11538277 6500734419 gb:x73124_53:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0416 HI0416 Haemophilus influenzae 727 -11538277

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894591	16223	38379	5025	1675

Description

5000695083 gb:x73124_27:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0417 HI0417 Haemophilus influenzae 727 -11538278 5500686062 thie:hi0417 (ec:2.5.1.3) (de:pyrophosphorylase) (tmp-ppase) (thiamin-phosphate synthase)) (db:swissprot) THIE_HAEIN P71350 HAEMOPHILUS INFLUENZAE 727 -11538278 166406 probable thiamin-phosphate pyrophosphorylase::hypothetical protein hi0417 (cl:thie protein:thiamin-phosphate pyrophosphorylase homology) (ec:2.5.1.3) (db:pir2.dat) A64152 A64152 Haemophilus influenzae 727 -11538278 7500893061 hi0417 thiamin-phosphate pyrophosphorylase (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:similar to gb:ae000511 pid:2313974 percent) (le:2292) (re:2972) (di:direct) U32725 U32725 g1573391 Haemophilus influenzae Rd 71421 -11538278 6500734420 gb:x73124_27:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0417 HI0417 Haemophilus influenzae 727 -11538278

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894621	16224	38380	1458	485

Description

GTC ORF with score 273 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t18e12 genomic sequence,complete sequence.) (nt:unknown protein) (le:73497:73771:73948) (re:73586:73848:74084) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894640	16225	38381	1251	416

Description

5000695084 hypothetical protein:sp:p37643:hypothetical metabolite transport protein hi0418 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0418 HI0418 Haemophilus influenzae 727 -11538279 109155 hi0418 (de:hypothetical metabolite transport protein hi0418) (db:swissprot) Y418_HAEIN P44699 HAEMOPHILUS INFLUENZAE 727 -11538279 166407 conserved hypothetical protein hi0418 (cl:citrate utilization determinant) (db:pir2.dat) B64152 B64152 Haemophilus influenzae 727 -11538279 7500895263 hi0418 transport protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:similar to gb:l42023 sp:p44610 pid:1003458) (le:2917) (re:4260) (di:direct) U32725 U32725 g1573392 Haemophilus influenzae Rd 71421 -11538279 6500734421 hypothetical protein:sp:p37643:hypothetical metabolite transport protein hi0418 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0418 HI0418 Haemophilus influenzae 727 -11538279

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894657	16226	38382	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894675	16227	38383	282	94

Description

5000695085 sp:p31825:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0423 HI0423 Haemophilus influenzae 727 -11538280 111933 hi0423 (de:hypothetical protein hi0423) (db:swissprot) YFIC_HAEIN P44702 HAEMOPHILUS INFLUENZAE 727 -11538280 166410 hypothetical protein hi0423 (cl:hypothetical protein hi0423) (db:pir2.dat) C64152 C64152 Haemophilus influenzae 727 -11538280 7500923513 hi0423 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:similar to sp:p31825 gb:u00096 pid:1788929 percent) (le:8316) (re:9038) (di:direct) U32725 U32725 g1573395 Haemophilus influenzae Rd 71421 -11538280 6500734422 sp:p31825:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0423 HI0423 Haemophilus influenzae 727 -11538280

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894685	16228	38384	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894689	16229	38385	372	123

Description

5000695086 sp:p33635:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0424 HI0424 Haemophilus influenzae 727 -11538281 111942 hi0424 (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase hi0424,) (db:swissprot) YFIF_HAEIN P44703 HAEMOPHILUS INFLUENZAE 727 -11538281 166411 hypothetical protein hi0424 (cl:hypothetical protein hi0424) (db:pir2.dat) D64152 D64152 Haemophilus influenzae 727 -11538281 7500923520 hi0424 rrna methylase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 40 of 163 of the complete genome.) (nt:similar to sp:p33635 gb:u00096 pid:1788935 percent) (le:9071) (re:10126) (di:complement) U32725 U32725 g1573396 Haemophilus influenzae Rd 71421 -11538281 6500734423 sp:p33635:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0424 HI0424 Haemophilus influenzae 727 -11538281

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894693	16230	38386	369	122

Description

5000695087 sp:p32680:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0431 HI0431 Haemophilus influenzae 727 -11538282 113601 hi0431 (de:hypothetical protein hi0431) (db:swissprot) YJAG_HAEIN P44709 HAEMOPHILUS INFLUENZAE 727 -11538282 166412 hypothetical protein hi0431 (db:pir2.dat) E64152 E64152 Haemophilus influenzae 727 -11538282 7500937848 hi0431 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to sp:p32680 pid:396338 gb:u00096) (le:6863) (re:7453) (di:complement) U32726 U32726 g1573406 Haemophilus influenzae Rd 71421 -11538282 6500734424 sp:p32680:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0431 HI0431 Haemophilus influenzae 727 -11538282

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894695	16231	38387	234	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894703	16232	38388	495	164

Description

5000695088 sp:p32664:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0432 HI0432 Haemophilus influenzae 727 -11538283 113597 hi0432 (de:hypothetical protein hi0432) (db:swissprot) YJAD_HAEIN P44710 HAEMOPHILUS INFLUENZAE 727 -11538283 166413 hypothetical protein hi0432 (cl:hypothetical protein hi0432:mutt domain homology) (db:pir2.dat) F64152 F64152 Haemophilus influenzae 727 -11538283 7500937846 hi0432 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to sp:p32664 pid:396335 gb:u00096) (le:7489) (re:8283) (di:complement) U32726 U32726 g1573407 Haemophilus influenzae Rd 71421 -11538283 6500734425 sp:p32664:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0432 HI0432 Haemophilus influenzae 727 -11538283

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894711	16233	38389	474	157

Description

5000695089 transformation:com locus protein:gb:m62809_10:hypothetical 21 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0433 HI0433 Haemophilus influenzae 727 -11538284 112807 hi0433 (de:(orfg)) (db:swissprot) YHGI_HAEIN P31774 HAEMOPHILUS INFLUENZAE 727 -11538284 167211 transformation locus protein hi0433:com locus protein hi0433:hypothetical protein g (db:pir2.dat) F64067 F64067 Haemophilus influenzae 727 -11538284 241252 (sr:h.influenzae dna) (db:genpept-bct1) (de:h.influenzae com101a gene, orf1, orf3 and orf1r, complete cds.) (nt:orf 3) (le:1919) (re:2515) (di:direct) HEACOM101 M59751 g148877 Haemophilus influenzae 727 -11538284 7500936940 hi0433 orfg protein (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:m62809 sp:p31774 pid:1573408 percent) (le:8350) (re:8946) (di:complement) U32726 U32726 g1573408 Haemophilus influenzae Rd 71421 -11538284 6500734426 transformation:com locus protein:gb:m62809_10:hypothetical 21 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0433 HI0433 Haemophilus influenzae 727 -11538284

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894736	16234	38390	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894739	16235	38391	636	212

Description

5000695090 transformation:com locus protein:gb:m62809_1:hypothetical protein:orfj (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0441 HI0441 Haemophilus influenzae 727 -11538285 112878 hi0441 (de:hypothetical protein hi0441 (orfj)) (db:swissprot) YHIR_HAEIN P31777 HAEMOPHILUS INFLUENZAE 727 -11538285 167217 comj transformation competence-related protein comj (db:pir2.dat) E64068 E64068 Haemophilus influenzae 727 -11538285 241337 (sr:haemophilus influenzae rd dna) (db:genpept-bct1) (de:haemophilus influenzae transformation gene cluster dna.) (nt:the predicted molecular weight and pi of orf j are) (le:135) (re:980) (di:complement) HEATRANS M62809 g148991 Haemophilus influenzae 727 -11538285 7500936995 hi0441 orfj protein (db:genpept-bct1) (de:haemophilus influenzae rd section 42 of 163 of the complete genome.) (nt:similar to gb:m62809 sp:p31777 pid:1573417 percent) (le:2762) (re:3607) (di:direct) U32727 U32727 g1573417 Haemophilus influenzae Rd 71421 -11538285 6500734427 transformation:com locus protein:gb:m62809_1:hypothetical protein:orfj (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0441 HI0441 Haemophilus influenzae 727 -11538285

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894756	16236	38392	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894762	16237	38393	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894765	16238	38394	1014	337

Description

5000695091 gb:m38777_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0442 HI0442 Haemophilus influenzae 727 -11538286 157288 hypothetical protein hi0442 (db:pir2.dat) G64152 G64152 Haemophilus influenzae 727 -11538286 7500955733 hi0442 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 42 of 163 of the complete genome.) (nt:similar to gb:m38777 sp:p17577 gb:x04487 pid:145298) (le:3724) (re:4089) (di:direct) U32727 U32727 g1573418 Haemophilus influenzae Rd 71421 -11538286 6500734428 gb:m38777_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0442 HI0442 Haemophilus influenzae 727 -11538286

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894803	16239	38395	1431	476

Description

5000695092 gb:u14003_130:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0452 HI0452 Haemophilus influenzae 727 -11538287 116409 hi0452 (de:hypothetical protein hi0452) (db:swissprot) YTFL_HAEIN P44717 HAEMOPHILUS INFLUENZAE 727 -11538287 166416 hypothetical protein hi0452 (cl:hypothetical protein hi0107) (db:pir2.dat) H64152 H64152 Haemophilus influenzae 727 -11538287 7500952765 hi0452 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39319 pid:537059 gb:u00096) (le:1236) (re:2534) (di:complement) U32728 U32728 g1573427 Haemophilus influenzae Rd 71421 -11538287 6500734429 gb:u14003_130:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0452 HI0452 Haemophilus influenzae 727 -11538287

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894810	16240	38396	885	294

Description

5000695093 gb:d26185_102:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0454 HI0454 Haemophilus influenzae 727 -11538288 110757 hi0454 (de:hypothetical protein hi0454) (db:swissprot) YCFH_HAEIN P44718 HAEMOPHILUS INFLUENZAE 727 -11538288 166418 probable metal-dependent hydrolase:hi0454 (cl:hypothetical protein hi0454) (ec:3.-.-.-) (db:pir2.dat) I64152 I64152 Haemophilus influenzae 727 -11538288 7500921731 hi0454 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to sp:p37346 gb:u00096 pid:1787342 percent) (le:3136) (re:3918) (di:complement) U32728 U32728 g1573428 Haemophilus influenzae Rd 71421 -11538288 6500734430 gb:d26185_102:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0454 HI0454 Haemophilus influenzae 727 -11538288

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894817	16241	38397	837	278

Description

5000695094 gb:l10328_10:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0467 HI0467 Haemophilus influenzae 727 -11538289 113184 hi0467 (de:hypothetical protein hi0467) (db:swissprot) YICC_HAEIN P44726 HAEMOPHILUS INFLUENZAE 727 -11538289 166422 hypothetical protein hi0467 (cl:hypothetical protein hi0467) (db:pir2.dat) C64153 C64153 Haemophilus influenzae 727 -11538289 7500937337 hi0467 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 44 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p23839 gb:x14235 pid:290494) (le:6755) (re:7618) (di:complement) U32729 U32729 g1573445 Haemophilus influenzae Rd 71421 -11538289 6500734431 gb:l10328_10:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0467 HI0467 Haemophilus influenzae 727 -11538289

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894833	16242	38398	894	297

Description

5000695095 sp:p19769:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0493 HI0493 Haemophilus influenzae 727 -11538290 7502852320 hi0493 (de:hypothetical transposase-like protein hi0493) (db:swissprot) Y493_HAEIN O05023 HAEMOPHILUS INFLUENZAE 727 -11538290 166430 hypothetical protein hi0493 (db:pir2.dat) D64153 D64153 Haemophilus influenzae 727 -11538290 7500960669 hi0493 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to gb:m29945 pid:1197032 percent ident:) (le:3765) (re:4121) (di:direct) U32731 U32731 g1573471 Haemophilus influenzae Rd 71421 -11538290 6500734432 sp:p19769:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0493 HI0493 Haemophilus influenzae 727 -11538290

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894837	16243	38399	564	187

Description

5000695096 gp:m87049_62:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0500 HI0500 Haemophilus influenzae 727 -11538291 113296 hi0500 (de:hypothetical protein hi0500) (db:swissprot) YIGN_HAEIN P44733 HAEMOPHILUS INFLUENZAE 727 -11538291 166433 hypothetical protein hi0500 (db:pir2.dat) F64153 F64153 Haemophilus influenzae 727 -11538291 7500937452 hi0500 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p27850 pid:148230 gb:u00096) (le:314) (re:1354) (di:direct) U32732 U32732 g1573481 Haemophilus influenzae Rd 71421 -11538291 6500734433 gp:m87049_62:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0500 HI0500 Haemophilus influenzae 727 -11538291

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894841	16244	38400	690	229

Description

5000695097 gb:d15061_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0510 HI0510 Haemophilus influenzae 727 -11538292 109678 hi0510 (de:hypothetical protein hi0510) (db:swissprot) YAEB_HAEIN P44740 HAEMOPHILUS INFLUENZAE 727 -11538292 166437 hypothetical protein hi0510 (db:pir2.dat) I64153 I64153 Haemophilus influenzae 727 -11538292 7500896089 hi0510 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 47 of 163 of the complete genome.) (nt:similar to gb:d15061 sp:p28634 pid:303558 gb:u00096) (le:9672) (re:10391) (di:direct) U32732 U32732 g1573491 Haemophilus influenzae Rd 71421 -11538292 6500734434 gb:d15061_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0510 HI0510 Haemophilus influenzae 727 -11538292

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894847	16245	38401	1242	413

Description

5000695098 sp:p33024:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0519 HI0519 Haemophilus influenzae 727 -11538293 111612 hi0519 (de:hypothetical protein hi0519) (db:swissprot) YEIM_HAEIN P44742 HAEMOPHILUS INFLUENZAE 727 -11538293 166438 hypothetical protein hi0519 (cl:pyrimidine nucleoside transport protein nupc) (db:pir2.dat) A64154 A64154 Haemophilus influenzae 727 -11538293 7500923054 hi0519 transport protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to gb:ae000511 pid:2314337 percent) (le:2317) (re:3570) (di:complement) U32734 U32734 g1573502 Haemophilus influenzae Rd 71421 -11538293 6500734435 sp:p33024:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0519 HI0519 Haemophilus influenzae 727 -11538293

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894853	16246	38402	1374	457

Description

5000695099 gb:u14003_290:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0520 HI0520 Haemophilus influenzae 727 -11538294 109202 hi0520 (de:hypothetical protein hi0520) (db:swissprot) Y520_HAEIN P44743 HAEMOPHILUS INFLUENZAE 727 -11538294 166439 hypothetical protein hi0520 (db:pir2.dat) B64154 B64154 Haemophilus influenzae 727 -11538294 7500895372 hi0520 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39409 pid:537219 gb:u00096) (le:3669) (re:4457) (di:complement) U32734 U32734 g1573503 Haemophilus influenzae Rd 71421 -11538294 6500734436 gb:u14003_290:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0520 HI0520 Haemophilus influenzae 727 -11538294

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894869	16247	38403	501	166

Description

5000695100 gb:u14003_291:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0521 HI0521 Haemophilus influenzae 727 -11538295 113849 hi0521 (de:hypothetical protein hi0521) (db:swissprot) YJJI_HAEIN P44744 HAEMOPHILUS INFLUENZAE 727 -11538295 166440 hypothetical protein hi0521 (db:pir2.dat) C64154 C64154 Haemophilus influenzae 727 -11538295 7500938116 hi0521 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p37342 pid:537220 gb:u00096) (le:4466) (re:6010) (di:complement) U32734 U32734 g1573504 Haemophilus influenzae Rd 71421 -11538295 6500734437 gb:u14003_291:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0521 HI0521 Haemophilus influenzae 727 -11538295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894870	16248	38404	663	221

Description

5000695101 sp:p37505:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0522 HI0522 Haemophilus influenzae 727 -11538296 5500686326 hi0522 (de:hypothetical protein hi0522) (db:swissprot) Y522_HAEIN Q57256 HAEMOPHILUS INFLUENZAE 727 -11538296 166441 hypothetical protein hi0522 (db:pir2.dat) D64154 D64154 Haemophilus influenzae 727 -11538296 7500895376 hi0522 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to gb:d26185 sp:p37505 pid:467358) (le:6223) (re:6879) (di:direct) U32734 U32734 g1573505 Haemophilus influenzae Rd 71421 -11538296 6500734438 sp:p37505:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0522 HI0522 Haemophilus influenzae 727 -11538296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894879	16249	38405	462	153

Description

GTC ORF with score 185 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f56a11.) (nt:coded for by c. elegans cdna yk171d3.5) (le:32282:33079:33163) (re:33024:33112:33414) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894898	16250	38406	1338	445

Description

5000695102 gb:m87483_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0555 HI0555 Haemophilus influenzae 727 -11538297 5500686329 hi0555 (de:hypothetical protein hi0555) (db:swissprot) Y555_HAEIN Q57409 HAEMOPHILUS INFLUENZAE 727 -11538297 7500895402 hi0555 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 52 of 163 of the complete genome.) (nt:similar to gb:m87483 sp:q02009 pid:551879 percent) (le:4243) (re:4482) (di:complement) U32737 U32737 g1573541 Haemophilus influenzae Rd 71421 -11538297 6500734439 gb:m87483_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0555 HI0555 Haemophilus influenzae 727 -11538297

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894904	16251	38407	552	183

Description

5000695103 gb:u18997_324:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0562 HI0562 Haemophilus influenzae 727 -11538298 116148 hi0562 (de:hypothetical protein hi0562) (db:swissprot) YRFH_HAEIN P44754 HAEMOPHILUS INFLUENZAE 727 -11538298 166448 hypothetical protein hi0562 (db:pir2.dat) F64154 F64154 Haemophilus influenzae 727 -11538298 7500952652 hi0562 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to sp:p45802 pid:606334 gb:u00096) (le:187) (re:582) (di:direct) U32738 U32738 g1573549 Haemophilus influenzae Rd 71421 -11538298 6500734440 gb:u18997_324:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0562 HI0562 Haemophilus influenzae 727 -11538298

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894910	16252	38408	975	324

Description

5000695104 sp:p27307:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0570 HI0570 Haemophilus influenzae 727 -11538299 113378 hi0570 (de:hypothetical protein hi0570) (db:swissprot) YIJC_HAEIN P44757 HAEMOPHILUS INFLUENZAE 727 -11538299 166450 hypothetical protein hi0570 (db:pir2.dat) H64154 H64154 Haemophilus influenzae 727 -11538299 7500937548 hi0570 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1790401 percent ident:) (le:9314) (re:9931) (di:complement) U32738 U32738 g1573557 Haemophilus influenzae Rd 71421 -11538299 6500734441 sp:p27307:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0570 HI0570 Haemophilus influenzae 727 -11538299

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894911	16253	38409	552	183

Description

6500734442 hin1693:hi0572 sp:p37687:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0572 HI0572 Haemophilus influenzae 727 -11538300 109215 hi0572 (de:hypothetical protein hi0572) (db:swissprot) Y572_HAEIN P44758 HAEMOPHILUS INFLUENZAE 727 -11538300 166451 conserved hypothetical protein hi0572 (db:pir2.dat) I64154 I64154 Haemophilus influenzae 727 -11538300 7500895409 hi0572 membrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to pid:1652858 percent ident: 56.82;) (le:92) (re:817) (di:direct) U32739 U32739 g1573561 Haemophilus influenzae Rd 71421 -11538300 5000695105 (de:(hi0572) (pn:hypothetical protein:p37687) (gn:hin1693) (gtcfc:13.7:14.1) (ec:) (y572_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0572 HI0572 Haemophilus influenzae 727 10050947

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894917	16254	38410	582	193

Description

6500734443 hypothetical protein:gb:u14003_119:probable fkbp-type peptidyl-prolyl cis-trans isomerase:ppiase:rotamase (gtcfc:14.1) (ec:5.2.1.8) (keggfc:14.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0574 HI0574 Haemophilus influenzae 727 -11538301 71788 hi0574 (ec:5.2.1.8) (de:(ec 5.2.1.8) (ppiase) (rotamase)) (db:swissprot) FKBY_HAEIN P44760 HAEMOPHILUS INFLUENZAE 727 -11538301 166452 hypothetical protein hi0574 (cl:bkbp-type peptidylprolyl isomerase homology) (db:pir2.dat) A64155 A64155 Haemophilus influenzae 727 -11538301 7500881499 hi0574 fkbp-type peptidyl-prolyl cis-trans isomerase (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to sp:p45523 sp:p39175 pid:606281) (le:1224) (re:1949) (di:direct) U32739 U32739 g1573563 Haemophilus influenzae Rd 71421 -11538301 5000695106 (de:(hi0574) (pn:probable fkbp-type peptidyl-prolyl cis-trans isomerase:ppiase:rotamase:hypothetical protein:gb:u14003_119) (gtcfc:13.7:14.1) (ec:5.2.1.8) (fkby_haein) (keggfc:11.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0574 HI0574 Haemophilus influenzae 727 10014344

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894918	16255	38411	579	192

Description

5000695107 gb:u18997_270:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0575 HI0575 Haemophilus influenzae 727 -11538302 112760 hi0575 (de:hypothetical protein hi0575) (db:swissprot) YHEO_HAEIN P44761 HAEMOPHILUS INFLUENZAE 727 -11538302 166453 hypothetical protein hi0575 (db:pir2.dat) B64155 B64155 Haemophilus influenzae 727 -11538302 7500936881 hi0575 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to sp:p45533 pid:606280 gb:u00096) (le:2038) (re:2703) (di:direct) U32739 U32739 g1573564 Haemophilus influenzae Rd 71421 -11538302 6500734444 gb:u18997_270:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0575 HI0575 Haemophilus influenzae 727 -11538302

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894923	16256	38412	432	143

Description

5000695108 gb:u18997_269:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0576 HI0576 Haemophilus influenzae 727 -11538303 112758 hi0576 (de:hypothetical protein hi0576) (db:swissprot) YHEN_HAEIN P44762 HAEMOPHILUS INFLUENZAE 727 -11538303 166454 hypothetical protein hi0576 (cl:hypothetical protein hi0576) (db:pir2.dat) C64155 C64155 Haemophilus influenzae 727 -11538303 7500936879 hi0576 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 54 of 163 of the complete genome.) (nt:similar to sp:p45532 pid:606279 gb:u00096) (le:2703) (re:3083) (di:direct) U32739 U32739 g1573565 Haemophilus influenzae Rd 71421 -11538303 6500734445 gb:u18997_269:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0576 HI0576 Haemophilus influenzae 727 -11538303

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894924	16257	38413	642	213

Description

5000695109 gp:141667_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0589 HI0589 Haemophilus influenzae 727 -11538304 109222 hi0589 (de:hypothetical protein hi0589) (db:swissprot) Y589_HAEIN P44020 HAEMOPHILUS INFLUENZAE 727 -11538304 166458 hypothetical protein hi0589 (db:pir2.dat) B64010 B64010 Haemophilus influenzae 727 -11538304 7500895420 hi0589 sigma factor regulatory protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 55 of 163 of the complete genome.) (nt:similar to sp:p46187 pid:987645 pid:1045631) (le:7374) (re:7793) (di:direct) U32740 U32740 g1573579 Haemophilus influenzae Rd 71421 -11538304 6500734446 gp:141667_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0589 HI0589 Haemophilus influenzae 727 -11538304

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894934	16258	38414	633	211

Description

5000695110 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0607 HI0607 Haemophilus influenzae 727 -11538305 111360 hi0607 (de:hypothetical protein hi0607) (db:swissprot) YDIB_HAEIN P44774 HAEMOPHILUS INFLUENZAE 727 -11538305 167156 hypothetical protein hi0607 (cl:shikimate dehydrogenase:shikimate dehydrogenase homology) (db:pir2.dat) H64080 H64080 Haemophilus influenzae 727 -11538305 7500922340 hi0607 shikimate 5-dehydrogenase-related protein (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1742758 pid:1787983) (le:1899) (re:2714) (di:direct) U32743 U32743 g1573600 Haemophilus influenzae Rd 71421 -11538305 6500734447 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0607 HI0607 Haemophilus influenzae 727 -11538305

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894940	16259	38415	723	240

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894942	16260	38416	414	137

Description

5000695111 sp:p39219:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0617 HI0617 Haemophilus influenzae 727 -11538306 109560 rlua:hi0617 (ec:4.2.1.70) (de:(pseudouridylate synthase) (uracil hydrolyase)) (db:swissprot) RLUA_HAEIN P44782 HAEMOPHILUS INFLUENZAE 727 -11538306 166464 yabo protein homolog hi0617 (db:pir2.dat) E64155 E64155 Haemophilus influenzae 727 -11538306 7500896013 hi0617 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 59 of 163 of the complete genome.) (nt:similar to sp:p39219 gb:u00096 pid:1786244 percent) (le:3842) (re:4501) (di:direct) U32744 U32744 g1573611 Haemophilus influenzae Rd 71421 -11538306 6500734448 sp:p39219:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0617 HI0617 Haemophilus influenzae 727 -11538306

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894974	16261	38417	2439	812

Description

5000695113 sp:p32695:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0634 HI0634 Haemophilus influenzae 727 -11538307 113628 hi0634 (de:hypothetical protein hi0634) (db:swissprot) YJBN_HAEIN P44794 HAEMOPHILUS INFLUENZAE 727 -11538307 166469 conserved hypothetical protein hi0634 (cl:haemophilus influenzae conserved hypothetical protein hi0634) (db:pir2.dat) H64155 H64155 Haemophilus influenzae 727 -11538307 7500937881 hi0634 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 61 of 163 of the complete genome.) (nt:similar to sp:p32695 pid:396384 gb:u00096) (le:4480) (re:5463) (di:direct) U32746 U32746 g1573630 Haemophilus influenzae Rd 71421 -11538307 6500734449 sp:p32695:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0634 HI0634 Haemophilus influenzae 727 -11538307

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894975	16262	38418	321	106

Description

5000695114 sp:p25746:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0638 HI0638 Haemophilus influenzae 727 -11538308 110750 hi0638 (de:hypothetical protein hi0638) (db:swissprot) YCFC_HAEIN P44796 HAEMOPHILUS INFLUENZAE 727 -11538308 166471 hypothetical protein hi0638 (db:pir2.dat) I64155 I64155 Haemophilus influenzae 727 -11538308 7500921727 hi0638 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the complete genome.) (nt:similar to sp:p25746 pid:581207 gb:u00096) (le:95) (re:712) (di:direct) U32747 U32747 g1573636 Haemophilus influenzae Rd 71421 -11538308 6500734450 sp:p25746:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0638 HI0638 Haemophilus influenzae 727 -11538308

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894976	16263	38419	711	236

Description

5000695115 pir:s42532:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0653 HI0653 Haemophilus influenzae 727 -11538309 109244 hi0653 (de:hypothetical protein hi0653) (db:swissprot) Y653_HAEIN P44029 HAEMOPHILUS INFLUENZAE 727 -11538309 166474 hypothetical protein hi0653 (db:pir2.dat) B64011 B64011 Haemophilus influenzae 727 -11538309 7500895439 hi0653 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to pid:1389735 percent ident: 51.43;) (le:6012) (re:6776) (di:direct) U32748 U32748 g1573652 Haemophilus influenzae Rd 71421 -11538309 6500734451 pir:s42532:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0653 HI0653 Haemophilus influenzae 727 -11538309

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501894983	16264	38420	264	87

Description

5000695116 gb:u18997_206:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0656 HI0656 Haemophilus influenzae 727 -11538310 116128 hi0656 (de:hypothetical protein hi0656) (db:swissprot) YRDC_HAEIN P44807 HAEMOPHILUS INFLUENZAE 727 -11538310 166475 hypothetical protein hi0656 (db:pir2.dat) B64156 B64156 Haemophilus influenzae 727 -11538310 7500952635 hi0656 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to sp:p45748 pid:606216 gb:u00096) (le:8149) (re:8700) (di:complement) U32748 U32748 g1573655 Haemophilus influenzae Rd 71421 -11538310 6500734452 gb:u18997_206:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0656 HI0656 Haemophilus influenzae 727 -11538310

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895003	16265	38421	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895029	16266	38422	549	182

Description

5000695117 hypothetical protein:gb:u18997_276:hypothetical abc transporter atp-binding protein hi0658 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0658 HI0658 Haemophilus influenzae 727 -11538311 112763 hi0658 (de:hypothetical abc transporter atp-binding protein hi0658) (db:swissprot) YHES_HAEIN P44808 HAEMOPHILUS INFLUENZAE 727 -11538311 166476 hypothetical protein hi0658 (cl:atp-binding cassette homology) (db:pir2.dat) C64156 C64156 Haemophilus influenzae 727 -11538311 7500936884 hi0658 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to sp:p45535 pid:606286 gb:u00096) (le:9262) (re:11178) (di:complement) U32748 U32748 g1573657 Haemophilus influenzae Rd 71421 -11538311 6500734453 hypothetical protein:gb:u18997_276:hypothetical abc transporter atp-binding protein hi0658 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0658 HI0658 Haemophilus influenzae 727 -11538311

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895032	16267	38423	897	298

Description

5000695118 gb:l19201_70:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0668 HI0668 Haemophilus influenzae 727 -11538312 113365 hi0668 (de:hypothetical protein hi0668) (db:swissprot) YIIU_HAEIN P44812 HAEMOPHILUS INFLUENZAE 727 -11538312 166482 hypothetical protein hi0668 (db:pir2.dat) D64156 D64156 Haemophilus influenzae 727 -11538312 7500937530 hi0668 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32164 pid:305031 gb:u00096) (le:111) (re:329) (di:direct) U32750 U32750 g1573669 Haemophilus influenzae Rd 71421 -11538312 6500734454 gb:l19201_70:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0668 HI0668 Haemophilus influenzae 727 -11538312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895039	16268	38424	405	134

Description

GTC ORF with score 402 to: (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe small subunit of u2af splicing factorspu2af23 gene, complete cds.) (nt:small subunit of u2af splicing factor) (le:5) (re:655) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895040	16269	38425	342	113

Description

GTC ORF with score 316 to: (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe small subunit of u2af splicing factorspu2af23 gene, complete cds.) (nt:small subunit of u2af splicing factor) (le:5) (re:655) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895046	16270	38426	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895048	16271	38427	186	60

Description

5000695119 gb:l19201_30:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0670 HI0670 Haemophilus influenzae 727 -11538313 113343 hi0670 (de:hypothetical protein hi0670) (db:swissprot) YIHZ_HAEIN P44814 HAEMOPHILUS INFLUENZAE 727 -11538313 166483 hypothetical protein hi0670 (cl:conserved hypothetical protein hi0670) (db:pir2.dat) E64156 E64156 Haemophilus influenzae 727 -11538313 7500937508 hi0670 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32147 pid:304991 gb:u00096) (le:863) (re:1297) (di:direct) U32750 U32750 g1573671 Haemophilus influenzae Rd 71421 -11538313 6500734455 gb:l19201_30:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0670 HI0670 Haemophilus influenzae 727 -11538313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895055	16272	38428	210	69

Description

5000695120 gb:l07942_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0671 HI0671 Haemophilus influenzae 727 -11538314 112266 hi0671 (de:hypothetical protein hi0671) (db:swissprot) YGBB_HAEIN P44815 HAEMOPHILUS INFLUENZAE 727 -11538314 166484 hypothetical protein hi0671 (cl:conserved hypothetical protein hi0671) (db:pir2.dat) F64156 F64156 Haemophilus influenzae 727 -11538314 7500924019 hi0671 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to pid:1151073 percent ident: 84.18;) (le:1599) (re:2075) (di:complement) U32750 U32750 g1573672 Haemophilus influenzae Rd 71421 -11538314 6500734456 gb:l07942_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0671 HI0671 Haemophilus influenzae 727 -11538314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895058	16273	38429	432	143

Description

5000695121 sp:pq06755:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0672 HI0672 Haemophilus influenzae 727 -11538315 7000687778 hi0672 (de:hypothetical protein hi0672) (db:swissprot) YGBP_HAEIN O05029 HAEMOPHILUS INFLUENZAE 727 -11538315 166485 hypothetical protein hi0672 (db:pir2.dat) G64156 G64156 Haemophilus influenzae 727 -11538315 7500924041 hi0672 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to pid:882640 gb:u00096 pid:1789104 percent) (le:2072) (re:2749) (di:complement) U32750 U32750 g1573673 Haemophilus influenzae Rd 71421 -11538315 6500734457 sp:pq06755:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0672 HI0672 Haemophilus influenzae 727 -11538315

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895061	16274	38430	189	62

Description

5000695122 gb:d26185_39:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0687 HI0687 Haemophilus influenzae 727 -11538316 166488 hypothetical protein hi0687 (db:pir2.dat) H64156 H64156 Haemophilus influenzae 727 -11538316 7500960670 hi0687 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 66 of 163 of the complete genome.) (nt:similar to gb:d26185 sp:p37511 pid:467365) (le:8064) (re:8978) (di:direct) U32751 U32751 g1573689 Haemophilus influenzae Rd 71421 -11538316 6500734458 gb:d26185_39:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0687 HI0687 Haemophilus influenzae 727 -11538316

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895065	16275	38431	552	183

Description

5000695123 sp:p35159:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0694 HI0694 Haemophilus influenzae 727 -11538317 109259 hi0694 (de:hypothetical protein hi0694) (db:swissprot) YMFC_HAEIN P44827 HAEMOPHILUS INFLUENZAE 727 -11538317 166490 probable pseudouridylate synthase hi0694 (db:pir2.dat) I64156 I64156 Haemophilus influenzae 727 -11538317 7500951317 hi0694 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 67 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p75966 pid:1787380 percent) (le:4261) (re:4983) (di:direct) U32752 U32752 g1573697 Haemophilus influenzae Rd 71421 -11538317 6500734459 sp:p35159:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0694 HI0694 Haemophilus influenzae 727 -11538317

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895068	16276	38432	1305	435

Description

5000695124 sp:p39322:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0696 HI0696 Haemophilus influenzae 727 -11538318 1500686284 hi0696 (de:hypothetical protein hi0696) (db:swissprot) YTFN_HAEIN Q57523 HAEMOPHILUS INFLUENZAE 727 -11538318 166491 hypothetical protein hi0696 (cl:ytfn protein) (db:pir2.dat) A64157 A64157 Haemophilus influenzae 727 -11538318 7500952769 hi0696 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 67 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39322 pid:537063 gb:u00096) (le:6088) (re:9984) (di:complement) U32752 U32752 g1573699 Haemophilus influenzae Rd 71421 -11538318 6500734460 sp:p39322:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0696 HI0696 Haemophilus influenzae 727 -11538318

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895070	16277	38433	1554	517

Description

5000695125 hypothetical protein:sp:p39320:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0698 HI0698 Haemophilus influenzae 727 -11538319 116411 hi0698 (de:hypothetical protein hi0698 precursor) (db:swissprot) YTFM_HAEIN P44038 HAEMOPHILUS INFLUENZAE 727 -11538319 166492 hypothetical protein hi0698 (db:pir2.dat) B64012 B64012 Haemophilus influenzae 727 -11538319 7500952767 hi0698 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 67 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39320 pid:537061 gb:u00096) (le:9994) (re:11730) (di:complement) U32752 U32752 g1573700 Haemophilus influenzae Rd 71421 -11538319 6500734461 hypothetical protein:sp:p39320:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0698 HI0698 Haemophilus influenzae 727 -11538319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895081	16278	38434	1362	453

Description

5000695126 gb:u14003_167:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0700 HI0700 Haemophilus influenzae 727 -11538320 113751 hi0700 (de:hypothetical protein hi0700) (db:swissprot) YJGD_HAEIN P44831 HAEMOPHILUS INFLUENZAE 727 -11538320 166493 hypothetical protein hi0700 (db:pir2.dat) B64157 B64157 Haemophilus influenzae 727 -11538320 7500938014 hi0700 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 68 of 163 of the complete genome.) (nt:similar to sp:p37163 gb:u14003 pid:537096 gb:u00096) (le:758) (re:1219) (di:complement) U32753 U32753 g1573703 Haemophilus influenzae Rd 71421 -11538320 6500734462 gb:u14003_167:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0700 HI0700 Haemophilus influenzae 727 -11538320

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895094	16279	38435	228	75

Description

5000695127 gb:u14003_156:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0719 HI0719 Haemophilus influenzae 727 -11538321 113754 hi0719 (de:hypothetical protein hi0719) (db:swissprot) YJGF_HAEIN P44839 HAEMOPHILUS INFLUENZAE 727 -11538321 166498 hypothetical protein hi0719 (cl:hypothetical protein hi0719) (db:pir2.dat) C64157 C64157 Haemophilus influenzae 727 -11538321 7500938015 hi0719 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 69 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39330 pid:537085 gb:u00096) (le:9681) (re:10073) (di:direct) U32754 U32754 g1573721 Haemophilus influenzae Rd 71421 -11538321 6500734463 gb:u14003_156:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0719 HI0719 Haemophilus influenzae 727 -11538321

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895103	16280	38436	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895115	16281	38437	1263	420

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895121	16282	38438	600	199

Description

5000695128 hypothetical protein:sp:p37618:hypothetical protein hi0721 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0721 HI0721 Haemophilus influenzae 727 -11538322 166499 hypothetical protein hi0721 (cl:conserved hypothetical protein hi0721) (db:pir2.dat) D64157 D64157 Haemophilus influenzae 727 -11538322 7500960672 hi0721 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 70 of 163 of the complete genome.) (nt:similar to sp:p37618 pid:466606 gb:u00096) (le:1007) (re:1288) (di:complement) U32755 U32755 g1573724 Haemophilus influenzae Rd 71421 -11538322 6500734464 hypothetical protein:sp:p37618:hypothetical protein hi0721 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0721 HI0721 Haemophilus influenzae 727 -11538322

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895128	16283	38439	333	110

Description

5000695129 sp:p32130:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0724 HI0724 Haemophilus influenzae 727 -11538323 113323 hi0724 (de:hypothetical protein hi0724) (db:swissprot) YIHI_HAEIN P44844 HAEMOPHILUS INFLUENZAE 727 -11538323 166501 hypothetical protein hi0724 (db:pir2.dat) F64157 F64157 Haemophilus influenzae 727 -11538323 7500937487 hi0724 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 70 of 163 of the complete genome.) (nt:similar to pid:1685095 percent ident: 62.11;) (le:9505) (re:10065) (di:direct) U32755 U32755 g1573727 Haemophilus influenzae Rd 71421 -11538323 6500734465 sp:p32130:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0724 HI0724 Haemophilus influenzae 727 -11538323

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895137	16284	38440	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895139	16285	38441	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895149	16286	38442	933	311

Description

5000695130 imp:osta:hi0730 hypothetical protein:sp:p31554:organic solvent tolerance protein homolog precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0730 HI0730 Haemophilus influenzae 727 -11538324 87922 imp:osta:hi0730 (de:organic solvent tolerance protein homolog precursor) (db:swissprot) OSTA_HAEIN P44846 HAEMOPHILUS INFLUENZAE 727 -11538324 166503 probable organic solvent tolerance protein precursor hi0730 (cl:organic solvent tolerance protein) (db:pir2.dat) G64157 G64157 Haemophilus influenzae 727 -11538324 7500887378 hi0730 organic solvent tolerance protein (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:similar to sp:p31554 gb:u00096 pid:1786239 percent) (le:6458) (re:8806) (di:complement) U32756 U32756 g1573734 Haemophilus influenzae Rd 71421 -11538324 6500734466 imp:osta hypothetical protein:sp:p31554:organic solvent tolerance protein homolog precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0730 HI0730 Haemophilus influenzae 727 -11538324

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895167	16287	38443	297	98

Description

GTC ORF with score 96 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid zk632, complete sequence.) (nt:cdna est ceesn66f comes from this gene; cdna est) (le:21685:22413:22621:22703) (re:21771:22536:22658:23065) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895171	16288	38444	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895172	16289	38445	621	207

Description

GTC ORF with score 252 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid zk632, complete sequence.) (nt:cdna est ceesn66f comes from this gene; cdna est) (le:21685:22413:22621:22703) (re:21771:22536:22658:23065) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895184	16290	38446	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895187	16291	38447	330	109

Description

5000695131 sp:p37688:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0744 HI0744 Haemophilus influenzae 727 -11538325 113169 hi0744 (de:hypothetical protein hi0744) (db:swissprot) YIBN_HAEIN P44854 HAEMOPHILUS INFLUENZAE 727 -11538325 166510 glpe protein homolog hi0744 (cl:glpe protein) (db:pir2.dat) A64158 A64158 Haemophilus influenzae 727 -11538325 7500937325 hi0744 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 73 of 163 of the complete genome.) (nt:similar to sp:p37688 pid:466749 gb:u00096) (le:2772) (re:3218) (di:complement) U32758 U32758 g1573751 Haemophilus influenzae Rd 71421 -11538325 6500734467 sp:p37688:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0744 HI0744 Haemophilus influenzae 727 -11538325

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895190	16292	38448	462	153

Description

5000695132 sp:p31485:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0753 HI0753 Haemophilus influenzae 727 -11538326 109275 hi0753 (de:hypothetical protein hi0753) (db:swissprot) Y753_HAEIN P44861 HAEMOPHILUS INFLUENZAE 727 -11538326 166511 hypothetical protein hi0753 (cl:hypothetical protein hi0753) (db:pir2.dat) B64158 B64158 Haemophilus influenzae 727 -11538326 7500895492 hi0753 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 74 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1787928 percent ident:) (le:7181) (re:8329) (di:direct) U32759 U32759 g1573761 Haemophilus influenzae Rd 71421 -11538326 6500734468 sp:p31485:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0753 HI0753 Haemophilus influenzae 727 -11538326

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895203	16293	38449	1293	431

Description

5000695133 sp:p37691:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0755 HI0755 Haemophilus influenzae 727 -11538327 7500976261 hi0755 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 74 of 163 of the complete genome.) (nt:similar to sp:p37691 pid:912478 gb:u00096) (le:9280) (re:9975) (di:complement) U32759 U32759 g1573763 Haemophilus influenzae Rd 71421 -11538327 6500734469 sp:p37691:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0755 HI0755 Haemophilus influenzae 727 -11538327

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895226	16294	38450	306	101

Description

5000695134 sp:p37690:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0756 HI0756 Haemophilus influenzae 727 -11538328 113171 hi0756 (de:hypothetical protein hi0756) (db:swissprot) YIBP_HAEIN P44864 HAEMOPHILUS INFLUENZAE 727 -11538328 166513 hypothetical protein hi0756 (db:pir2.dat) D64158 D64158 Haemophilus influenzae 727 -11538328 7500937327 hi0756 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to sp:p37690 pid:466751 gb:u00096) (le:104) (re:1336) (di:complement) U32760 U32760 g1573765 Haemophilus influenzae Rd 71421 -11538328 6500734470 sp:p37690:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0756 HI0756 Haemophilus influenzae 727 -11538328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895258	16295	38451	1002	333

Description

5000695135 sp:p33899:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0766 HI0766 Haemophilus influenzae 727 -11538329 113166 hi0766 (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase hi0766,) (db:swissprot) YIBK_HAEIN P44868 HAEMOPHILUS INFLUENZAE 727 -11538329 166517 hypothetical protein hi0766 (db:pir2.dat) E64158 E64158 Haemophilus influenzae 727 -11538329 7500937322 hi0766 rrna methylase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to sp:p33899 pid:466744 gb:u00096) (le:9467) (re:9949) (di:complement) U32760 U32760 g1573774 Haemophilus influenzae Rd 71421 -11538329 6500734471 sp:p33899:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0766 HI0766 Haemophilus influenzae 727 -11538329

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895263	16296	38452	486	161

Description

5000695136 sp:p10120:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0767 HI0767 Haemophilus influenzae 727 -11538330 112819 hi0767 (de:hypothetical protein hi0767) (db:swissprot) YHHF_HAEIN P44869 HAEMOPHILUS INFLUENZAE 727 -11538330 157286 hypothetical protein hi0767 (db:pir2.dat) F64158 F64158 Haemophilus influenzae 727 -11538330 7500936948 hi0767 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to sp:p10120 gb:u00039 gb:x04398 pid:41497) (le:9960) (re:10541) (di:complement) U32760 U32760 g1573775 Haemophilus influenzae Rd 71421 -11538330 6500734472 sp:p10120:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0767 HI0767 Haemophilus influenzae 727 -11538330

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895275	16297	38453	360	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895279	16298	38454	297	98

Description

5000695137 gb:u18997_325:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0810 HI0810 Haemophilus influenzae 727 -11538331 116150 hi0810 (de:hypothetical protein hi0810) (db:swissprot) YRFI_HAEIN P44877 HAEMOPHILUS INFLUENZAE 727 -11538331 166523 hypothetical protein hi0810 (db:pir2.dat) H64158 H64158 Haemophilus influenzae 727 -11538331 7500952654 hi0810 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 78 of 163 of the complete genome.) (nt:similar to sp:p45803 pid:606335 gb:u00096) (le:5563) (re:6444) (di:complement) U32763 U32763 g1573822 Haemophilus influenzae Rd 71421 -11538331 6500734473 gb:u18997_325:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0810 HI0810 Haemophilus influenzae 727 -11538331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895280	16299	38455	849	282

Description

5000695138 gb:d90281_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0817 HI0817 Haemophilus influenzae 727 -11538332 112319 hi0817 (de:hypothetical protein hi0817) (db:swissprot) YGFB_HAEIN P44882 HAEMOPHILUS INFLUENZAE 727 -11538332 166524 hypothetical protein hi0817 (db:pir2.dat) I64158 I64158 Haemophilus influenzae 727 -11538332 7500924149 hi0817 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to gb:d90281 sp:p25533 pid:216626) (le:1955) (re:2503) (di:complement) U32764 U32764 g1573830 Haemophilus influenzae Rd 71421 -11538332 6500734474 gb:d90281_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0817 HI0817 Haemophilus influenzae 727 -11538332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895288	16300	38456	198	65

Description

5000695139 sp:p21366:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0826 HI0826 Haemophilus influenzae 727 -11538333 110805 hi0826 (de:hypothetical protein hi0826) (db:swissprot) YCIB_HAEIN P43810 HAEMOPHILUS INFLUENZAE 727 -11538333 166526 intracellular septation protein a homolog hi0826 (db:pir2.dat) A64159 A64159 Haemophilus influenzae 727 -11538333 7500921823 hi0826 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to sp:p21366 gb:x13583 pid:43213 pid:902381) (le:843) (re:1400) (di:direct) U32765 U32765 g1573840 Haemophilus influenzae Rd 71421 -11538333 6500734475 sp:p21366:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0826 HI0826 Haemophilus influenzae 727 -11538333

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895293	16301	38457	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895294	16302	38458	747	248

Description

5000695140 gb:u18997_137:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0831 HI0831 Haemophilus influenzae 727 -11538334 166527 hypothetical protein hi0831 (db:pir2.dat) B64159 B64159 Haemophilus influenzae 727 -11538334 7500960673 hi0831 monofunctional biosynthetic peptidoglycan (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to sp:p46022 pid:606147 gb:u00096) (le:4460) (re:5044) (di:direct) U32765 U32765 g1573845 Haemophilus influenzae Rd 71421 -11538334 6500734476 gb:u18997_137:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0831 HI0831 Haemophilus influenzae 727 -11538334

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895309	16303	38459	894	297

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895310	16304	38460	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895315	16305	38461	810	269

Description

5000695141 sp:p33920:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0839 HI0839 Haemophilus influenzae 727 -11538335 111634 hi0839 (de:hypothetical protein hi0839) (db:swissprot) YEJK_HAEIN P44896 HAEMOPHILUS INFLUENZAE 727 -11538335 166530 hypothetical protein hi0839 (db:pir2.dat) D64159 D64159 Haemophilus influenzae 727 -11538335 7500923066 hi0839 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to sp:p33920 pid:405914 gb:u00096) (le:11155) (re:12180) (di:complement) U32765 U32765 g1573853 Haemophilus influenzae Rd 71421 -11538335 6500734477 sp:p33920:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0839 HI0839 Haemophilus influenzae 727 -11538335

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895325	16306	38462	474	157

Description

5000695142 sp:p33921:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0840 HI0840 Haemophilus influenzae 727 -11538336 111636 hi0840 (de:hypothetical protein hi0840) (db:swissprot) YEJL_HAEIN P44897 HAEMOPHILUS INFLUENZAE 727 -11538336 166531 hypothetical protein hi0840 (cl:hypothetical protein hi0840) (db:pir2.dat) E64159 E64159 Haemophilus influenzae 727 -11538336 7500923068 hi0840 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to sp:p33921 pid:405915 gb:u00096) (le:89) (re:307) (di:direct) U32766 U32766 g1573855 Haemophilus influenzae Rd 71421 -11538336 6500734478 sp:p33921:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0840 HI0840 Haemophilus influenzae 727 -11538336

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895339	16307	38463	702	233

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895349	16308	38464	300	99

Description

5000695143 sp:p33922:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0841 HI0841 Haemophilus influenzae 727 -11538337 111638 hi0841 (de:hypothetical protein hi0842) (db:swissprot) YEJM_HAEIN P44898 HAEMOPHILUS INFLUENZAE 727 -11538337 166532 hypothetical protein hi0841 (cl:hypothetical protein hi0841) (db:pir2.dat) F64159 F64159 Haemophilus influenzae 727 -11538337 7500923070 hi0841 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to sp:p33922 pid:453987 gb:u00096) (le:309) (re:2066) (di:direct) U32766 U32766 g1573856 Haemophilus influenzae Rd 71421 -11538337 6500734479 sp:p33922:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0841 HI0841 Haemophilus influenzae 727 -11538337

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895350	16309	38465	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895361	16310	38466	576	192

Description

5000695144 gb:m94205_1:hypothetical protein:orf1 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0845 HI0845 Haemophilus influenzae 727 -11538338 113318 hi0845 (de:hypothetical protein hi0845 (orf1)) (db:swissprot) YIHD_HAEIN P44900 HAEMOPHILUS INFLUENZAE 727 -11538338 167098 conserved hypothetical protein hi0845 (db:pir2.dat) A46411 G64159 Haemophilus influenzae 727 -11538338 241258 (fn:unknown) (sr:haemophilus influenzae (strain rd) dna) (db:genpept-bct1) (de:haemophilus influenzae disulfide oxidoreductase (por) gene,complete cds.) (nt:the product of this gene is undetectable on) (le:344) (re:610) (di:direct) HEADSFO M94205 g148886 Haemophilus influenzae 727 -11538338 7500937481 hi0845 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32126 pid:304964 gb:u00096) (le:4059) (re:4325) (di:direct) U32766 U32766 g1573859 Haemophilus influenzae Rd 71421 -11538338 6500734480 gb:m94205_1:hypothetical protein:orf1 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0845 HI0845 Haemophilus influenzae 727 -11538338

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895391	16311	38467	213	70

Description

5000695145 gb:m94205_1:hypothetical protein:orf3 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0847 HI0847 Haemophilus influenzae 727 -11538339 113267 hi0847 (de:hypothetical protein hi0847 (orf3)) (db:swissprot) YIFE_HAEIN P31811 HAEMOPHILUS INFLUENZAE 727 -11538339 166535 hypothetical protein hi0847 (db:pir2.dat) H64159 H64159 Haemophilus influenzae 727 -11538339 7500937424 hi0847 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p27827 pid:148172 gb:u00096) (le:5015) (re:5350) (di:direct) U32766 U32766 g1573861 Haemophilus influenzae Rd 71421 -11538339 6500734481 gb:m94205_1:hypothetical protein:orf3 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0847 HI0847 Haemophilus influenzae 727 -11538339

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895401	16312	38468	300	99

Description

5000695146 sp:p37633:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0849 HI0849 Haemophilus influenzae 727 -11538340 7500976263 hi0849 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to sp:p37633 pid:912465 gb:u00096) (le:6774) (re:7340) (di:direct) U32766 U32766 g1573863 Haemophilus influenzae Rd 71421 -11538340 6500734482 sp:p37633:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0849 HI0849 Haemophilus influenzae 727 -11538340 112876 yhiq_haein (de:hypothetical protein hi0849.) P44901 P44901 Haemophilus influenzae 727 -11538340

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895411	16313	38469	2703	900

Description

GTC ORF with score 239 to: (or:Homo sapiens) (sr:human) (db:genpept-pri1) (de:human plectin (plec1) gene, exons 3-32, and complete cds.) (nt:also known as hemidesmosomal protein hd1;) (le:u63609:7:1:453:714:1771) (re:199:62:620:806:1937) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895431	16314	38470	816	272

Description

5000695147 gp:l41667_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0850 HI0850 Haemophilus influenzae 727 -11538341 109297 hi0850 (de:hypothetical protein hi0850) (db:swissprot) Y850_HAEIN P44060 HAEMOPHILUS INFLUENZAE 727 -11538341 166537 hypothetical protein hi0850 (db:pir2.dat) F64014 F64014 Haemophilus influenzae 727 -11538341 7500895559 hi0850 sigma-e factor regulatory protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to sp:p46187 pid:987645 pid:1045631) (le:7334) (re:7768) (di:direct) U32766 U32766 g1573864 Haemophilus influenzae Rd 71421 -11538341 6500734483 gp:l41667_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0850 HI0850 Haemophilus influenzae 727 -11538341

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895432	16315	38471	324	107

Description

6500734484 mobb:hi0851 hypothetical protein:gb:l19201_1:molybdopterin-guanine dinucleotide biosynthesis protein b (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0851 HI0851 Haemophilus influenzae 727 -11538342 83962 mobb:hi0851 (de:molybdopterin-guanine dinucleotide biosynthesis protein b) (db:swissprot) MOBB_HAEIN P44902 HAEMOPHILUS INFLUENZAE 727 -11538342 166538 hypothetical protein hi0851 (db:pir2.dat) A64160 A64160 Haemophilus influenzae 727 -11538342 7500885746 hi0851 molybdopterin-guanine dinucleotide biosynthesis (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32125 pid:304962 gb:u00096) (le:8170) (re:8706) (di:direct) U32766 U32766 g1573865 Haemophilus influenzae Rd 71421 -11538342 5000695148 (de:(hi0851) (pn:molybdopterin-guanine dinucleotide biosynthesis protein b:hypothetical protein:gb:l19201_1) (gn:mobb) (gtcfc:13.7:14.1) (ec:) (mobb_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0851 HI0851 Haemophilus influenzae 727 10026169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895433	16316	38472	255	84

Description

5000695149 gb:l10328_120:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0852 HI0852 Haemophilus influenzae 727 -11538343 113251 hi0852 (de:hypothetical protein hi0852) (db:swissprot) YIEO_HAEIN P44903 HAEMOPHILUS INFLUENZAE 727 -11538343 166539 hypothetical protein hi0852 (cl:multidrug-efflux transporter) (db:pir2.dat) B64160 B64160 Haemophilus influenzae 727 -11538343 7500937404 hi0852 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 81 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p31474 pid:290604 gb:u00096) (le:8703) (re:10094) (di:direct) U32766 U32766 g1573866 Haemophilus influenzae Rd 71421 -11538343 6500734485 gb:l10328_120:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0852 HI0852 Haemophilus influenzae 727 -11538343

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895434	16317	38473	207	68

Description

5000695150 gb:u18997_40:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0855 HI0855 Haemophilus influenzae 727 -11538344 112618 hi0855 (de:hypothetical protein hi0855) (db:swissprot) YHAN_HAEIN P44904 HAEMOPHILUS INFLUENZAE 727 -11538344 166541 hypothetical protein hi0855 (db:pir2.dat) C64160 C64160 Haemophilus influenzae 727 -11538344 7500936752 hi0855 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to sp:p42627 pid:606050 gb:u00096) (le:2824) (re:3171) (di:complement) U32767 U32767 g1573870 Haemophilus influenzae Rd 71421 -11538344 6500734486 gb:u18997_40:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0855 HI0855 Haemophilus influenzae 727 -11538344

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895435	16318	38474	309	102

Description

5000695151 gb:m12965_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0858 HI0858 Haemophilus influenzae 727 -11538345 112317 hi0858 (de:hypothetical protein hi0858) (db:swissprot) YGFA_HAEIN P44905 HAEMOPHILUS INFLUENZAE 727 -11538345 157264 hypothetical protein hi0858 (cl:conserved hypothetical protein hi0858) (db:pir2.dat) D64160 D64160 Haemophilus influenzae 727 -11538345 7500924147 hi0858 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to gb:m12965 sp:p09160 pid:147874) (le:6747) (re:7310) (di:direct) U32767 U32767 g1573873 Haemophilus influenzae Rd 71421 -11538345 6500734487 gb:m12965_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0858 HI0858 Haemophilus influenzae 727 -11538345

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895470	16319	38475	372	123

Description

5000695152 gb:u14003_92:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0860 HI0860 Haemophilus influenzae 727 -11538346 113719 hi0860 (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase hi0860,) (db:swissprot) YJFH_HAEIN P44906 HAEMOPHILUS INFLUENZAE 727 -11538346 166543 hypothetical protein hi0860 (cl:conserved hypothetical protein hi0860) (db:pir2.dat) E64160 E64160 Haemophilus influenzae 727 -11538346 7500937985 hi0860 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p39290 pid:537021 gb:u00096) (le:10045) (re:10785) (di:complement) U32767 U32767 g1573875 Haemophilus influenzae Rd 71421 -11538346 6500734488 gb:u14003_92:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0860 HI0860 Haemophilus influenzae 727 -11538346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895474	16320	38476	258	85

Description

5000695153 sp:p37619:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0862 HI0862 Haemophilus influenzae 727 -11538347 112832 hi0862 (de:hypothetical protein hi0862) (db:swissprot) YHHQ_HAEIN P44908 HAEMOPHILUS INFLUENZAE 727 -11538347 166544 hypothetical protein hi0862 (db:pir2.dat) F64160 F64160 Haemophilus influenzae 727 -11538347 7500936955 hi0862 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 83 of 163 of the complete genome.) (nt:similar to sp:p37619 pid:466607 gb:u00096) (le:126) (re:833) (di:complement) U32768 U32768 g1573879 Haemophilus influenzae Rd 71421 -11538347 6500734489 sp:p37619:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0862 HI0862 Haemophilus influenzae 727 -11538347

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895475	16321	38477	255	84

Description

5000695154 hypothetical protein:gb:l19201_15:hypothetical 68 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0864 HI0864 Haemophilus influenzae 727 -11538348 113326 typa:hi0864 (de:gtp-binding protein typa/bipa homolog) (db:swissprot) TYPA_HAEIN P44910 HAEMOPHILUS INFLUENZAE 727 -11538348 166545 gtp-binding protein hi0864 (cl:translation elongation factor tu homology) (db:pir2.dat) G64160 G64160 Haemophilus influenzae 727 -11538348 7500893597 hi0864 gtp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 83 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32132 pid:304976 gb:u00096) (le:1746) (re:3596) (di:complement) U32768 U32768 g1573881 Haemophilus influenzae Rd 71421 -11538348 6500734490 hypothetical protein:gb:l19201_15:hypothetical 68 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0864 HI0864 Haemophilus influenzae 727 -11538348

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895478	16322	38478	360	119

Description

5000695155 gb:m94855_1:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0867 HI0867 Haemophilus influenzae 727 -11538349 4000708216 hi0867 (de:hypothetical protein hi0867) (db:swissprot) Y867_HAEIN Q57484 HAEMOPHILUS INFLUENZAE 727 -11538349 166964 hypothetical protein hi0867 (db:pir2.dat) H64160 H64160 Haemophilus influenzae 727 -11538349 7500895571 hi0867 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 83 of 163 of the complete genome.) (nt:similar to sp:p37781 pid:454902 percent ident:) (le:6583) (re:7797) (di:direct) U32768 U32768 g1573884 Haemophilus influenzae Rd 71421 -11538349 6500734491 gb:m94855_1:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0867 HI0867 Haemophilus influenzae 727 -11538349

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895484	16323	38479	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895487	16324	38480	492	163

Description

5000695156 sp:p36679:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0890 HI0890 Haemophilus influenzae 727 -11538350 109595 hi0890 (de:hypothetical protein hi0890) (db:swissprot) YACE_HAEIN P44920 HAEMOPHILUS INFLUENZAE 727 -11538350 166554 hypothetical protein hi0890 (cl:conserved hypothetical protein ydr196c) (db:pir2.dat) A64161 A64161 Haemophilus influenzae 727 -11538350 7500896032 hi0890 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to sp:p36679 gb:u00096 pid:1786292 percent) (le:1416) (re:2048) (di:direct) U32771 U32771 g1573909 Haemophilus influenzae Rd 71421 -11538350 6500734492 sp:p36679:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0890 HI0890 Haemophilus influenzae 727 -11538350

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895488	16325	38481	855	284

Description

5000695157 sp:p36681:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0891 HI0891 Haemophilus influenzae 727 -11538351 109602 hi0891 (de:hypothetical protein hi0891) (db:swissprot) YACG_HAEIN P44921 HAEMOPHILUS INFLUENZAE 727 -11538351 7500896037 hi0891 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to sp:p36681 gb:u00096 pid:1786290 percent) (le:2089) (re:2247) (di:direct) U32771 U32771 g1573910 Haemophilus influenzae Rd 71421 -11538351 6500734493 sp:p36681:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0891 HI0891 Haemophilus influenzae 727 -11538351

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895493	16326	38482	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895496	16327	38483	1461	486

Description

5000695158 sp:p30134:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0906 HI0906 Haemophilus influenzae 727 -11538352 111905 hi0906 (de:hypothetical protein hi0906) (db:swissprot) YFHC_HAEIN P44931 HAEMOPHILUS INFLUENZAE 727 -11538352 166558 hypothetical protein hi0906 (cl:hypothetical protein yaaj) (db:pir2.dat) C64161 C64161 Haemophilus influenzae 727 -11538352 7500923481 hi0906 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to sp:p30134 pid:296183 pid:987637) (le:4952) (re:5473) (di:direct) U32772 U32772 g1573925 Haemophilus influenzae Rd 71421 -11538352 6500734494 sp:p30134:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0906 HI0906 Haemophilus influenzae 727 -11538352

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895500	16328	38484	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895503	16329	38485	213	70

Description

5000695159 gp:l14679_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0912 HI0912 Haemophilus influenzae 727 -11538353 109320 hi0912 (de:hypothetical protein hi0912) (db:swissprot) Y912_HAEIN P44074 HAEMOPHILUS INFLUENZAE 727 -11538353 166561 hypothetical protein hi0912 (cl:bioc homology) (db:pir2.dat) B64016 B64016 Haemophilus influenzae 727 -11538353 7500895658 hi0912 h. influenzae predicted coding region hi0912 (db:genpept-bct1) (de:haemophilus influenzae rd section 88 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:81) (re:845) (di:direct) U32773 U32773 g1573933 Haemophilus influenzae Rd 71421 -11538353 6500734495 gp:l14679_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0912 HI0912 Haemophilus influenzae 727 -11538353

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895509	16330	38486	345	114

Description

5000695160 sp:p37764:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0918 HI0918 Haemophilus influenzae 727 -11538354 109696 hi0918 (de:hypothetical protein hi0918) (db:swissprot) YAEL_HAEIN P44936 HAEMOPHILUS INFLUENZAE 727 -11538354 166562 hypothetical protein hi0918 (db:pir2.dat) D64161 D64161 Haemophilus influenzae 727 -11538354 7500896094 hi0918 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 88 of 163 of the complete genome.) (nt:similar to sp:p37764 pid:1208948 gb:u00096) (le:7055) (re:8386) (di:complement) U32773 U32773 g1573939 Haemophilus influenzae Rd 71421 -11538354 6500734496 sp:p37764:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0918 HI0918 Haemophilus influenzae 727 -11538354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895514	16331	38487	1518	506

Description

5000695161 sp:p38119:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0920 HI0920 Haemophilus influenzae 727 -11538355 109321 hi0920 (de:hypothetical protein hi0920) (db:swissprot) YAES_HAEIN P44938 HAEMOPHILUS INFLUENZAE 727 -11538355 166563 conserved hypothetical protein hi0920 (cl:conserved hypothetical protein ybr002c) (db:pir2.dat) E64161 E64161 Haemophilus influenzae 727 -11538355 7500896101 hi0920 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 88 of 163 of the complete genome.) (nt:similar to pid:1208946 gb:u00096 sp:q47675) (le:9280) (re:9999) (di:complement) U32773 U32773 g1573941 Haemophilus influenzae Rd 71421 -11538355 6500734497 sp:p38119:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0920 HI0920 Haemophilus influenzae 727 -11538355

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895521	16332	38488	1218	405

Description

5000695162 gb:m77129_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0929 HI0929 Haemophilus influenzae 727 -11538356 112388 hi0929 (de:hypothetical protein hi0929) (db:swissprot) YGIC_HAEIN P44940 HAEMOPHILUS INFLUENZAE 727 -11538356 166566 hypothetical protein hi0929 (cl:conserved hypothetical protein hi0929) (db:pir2.dat) F64161 F64161 Haemophilus influenzae 727 -11538356 7500924253 hi0929 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to gb:m77129 sp:p24196 pid:146678) (le:146) (re:1327) (di:complement) U32775 U32775 g1573952 Haemophilus influenzae Rd 71421 -11538356 6500734498 gb:m77129_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0929 HI0929 Haemophilus influenzae 727 -11538356

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895526	16333	38489	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895538	16334	38490	303	100

Description

5000695163 sp:p37631:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0933 HI0933 Haemophilus influenzae 727 -11538357 112872 hi0933 (de:hypothetical protein hi0933) (db:swissprot) YHIN_HAEIN P44941 HAEMOPHILUS INFLUENZAE 727 -11538357 166569 hypothetical protein hi0933 (db:pir2.dat) G64161 G64161 Haemophilus influenzae 727 -11538357 7500936984 hi0933 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to sp:p37631 pid:912464 gb:u00096) (le:3855) (re:5060) (di:complement) U32775 U32775 g1573954 Haemophilus influenzae Rd 71421 -11538357 6500734499 sp:p37631:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0933 HI0933 Haemophilus influenzae 727 -11538357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895544	16335	38491	201	66

Description

5000695164 sp:p25538:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0943 HI0943 Haemophilus influenzae 727 -11538358 110173 hi0943 (de:hypothetical protein hi0943) (db:swissprot) YBAD_HAEIN P44946 HAEMOPHILUS INFLUENZAE 727 -11538358 166576 ybad protein homolog hi0943 (cl:conserved hypothetical protein hi0943) (db:pir2.dat) B64162 B64162 Haemophilus influenzae 727 -11538358 7500896532 hi0943 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to sp:p25538 gb:x64395 pid:42148 gb:u00096) (le:15415) (re:15864) (di:direct) U32775 U32775 g1573963 Haemophilus influenzae Rd 71421 -11538358 6500734500 sp:p25538:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0943 HI0943 Haemophilus influenzae 727 -11538358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895559	16336	38492	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895584	16337	38493	726	241

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895588	16338	38494	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895595	16339	38495	1074	357

Description

5000695165 sp:p18355:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0948 HI0948 Haemophilus influenzae 727 -11538359 166577 hypothetical protein hi0948 (db:pir2.dat) C64162 C64162 Haemophilus influenzae 727 -11538359 7500960675 hi0948 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to sp:p18355 percent ident: 43.42;) (le:3068) (re:3301) (di:complement) U32776 U32776 g1573973 Haemophilus influenzae Rd 71421 -11538359 6500734501 sp:p18355:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0948 HI0948 Haemophilus influenzae 727 -11538359

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895619	16340	38496	1236	411

Description

5000695166 gb:u18997_278:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0956 HI0956 Haemophilus influenzae 727 -11538360 112767 hi0956 (de:hypothetical protein hi0956) (db:swissprot) YHEU_HAEIN P44954 HAEMOPHILUS INFLUENZAE 727 -11538360 166578 hypothetical protein hi0956 (cl:hypothetical protein hi0956) (db:pir2.dat) E64162 E64162 Haemophilus influenzae 727 -11538360 7500936887 hi0956 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to sp:p45536 pid:606288 gb:u00096) (le:9008) (re:9178) (di:direct) U32776 U32776 g1573981 Haemophilus influenzae Rd 71421 -11538360 6500734502 gb:u18997_278:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0956 HI0956 Haemophilus influenzae 727 -11538360

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895649	16341	38497	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895662	16342	38498	333	110

Description

5000695167 gb:d10483_18:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0963 HI0963 Haemophilus influenzae 727 -11538361 166583 hypothetical protein hi0963 (cl:conserved hypothetical protein hi0963) (db:pir2.dat) H64162 H64162 Haemophilus influenzae 727 -11538361 7500955729 hi0963 riboflavin kinase / fmn adenylyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p08391 gb:m10428 pid:147762) (le:6114) (re:7052) (di:complement) U32777 U32777 g1573988 Haemophilus influenzae Rd 71421 -11538361 6500734503 gb:d10483_18:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0963 HI0963 Haemophilus influenzae 727 -11538361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895664	16343	38499	993	330

Description

5000695169 gb:l21902_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0976 HI0976 Haemophilus influenzae 727 -11538362 5500686454 hi0976 (de:hypothetical protein hi0976) (db:swissprot) Y976_HAEIN Q57147 HAEMOPHILUS INFLUENZAE 727 -11538362 166588 hypothetical protein hi0976 (db:pir2.dat) B64163 B64163 Haemophilus influenzae 727 -11538362 7500895777 hi0976 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:similar to gb:al009126 percent ident: 25.21;) (le:6563) (re:6949) (di:direct) U32778 U32778 g1574004 Haemophilus influenzae Rd 71421 -11538362 6500734504 gb:l21902_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0976 HI0976 Haemophilus influenzae 727 -11538362

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895667	16344	38500	477	158

Description

5000695170 gp:u18657_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0983 HI0983 Haemophilus influenzae 727 -11538363 109340 hi0983 (de:hypothetical protein hi0983) (db:swissprot) Y983_HAEIN P43907 HAEMOPHILUS INFLUENZAE 727 -11538363 7500895791 hi0983 h. influenzae predicted coding region hi0983 (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1863) (re:2444) (di:complement) U32779 U32779 g1574012 Haemophilus influenzae Rd 71421 -11538363 6500734505 gp:u18657_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0983 HI0983 Haemophilus influenzae 727 -11538363

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895668	16345	38501	1044	347

Description

5000695171 gp:u18657_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0984 HI0984 Haemophilus influenzae 727 -11538364 109485 hi0984 (de:hypothetical protein hi0984) (db:swissprot) YAAA_HAEIN P43908 HAEMOPHILUS INFLUENZAE 727 -11538364 166592 hypothetical protein hi0984 dpra+ 3 region (db:pir2.dat) E64163 E64163 Haemophilus influenzae 727 -11538364 241597 (db:genpept-bct1) (de:haemophilus influenzae leua (leua) gene, partial cds, dpra (dpra+),orf272 and orf193 genes, complete cds, and pfka (pfka) gene,partial cds.) (nt:orf272) (le:1916) (re:2734) (di:direct) HIU18657 U18657 g609333 Haemophilus influenzae 727 -11538364 7500895959 hi0984 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p11288 pid:216438) (le:2437) (re:3255) (di:complement) U32779 U32779 g1574013 Haemophilus influenzae Rd 71421 -11538364 6500734506 gp:u18657_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0984 HI0984 Haemophilus influenzae 727 -11538364

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895684	16346	38502	1179	392

Description

5000695172 hypothetical protein:sp:p22834:hypothetical 9 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1000 HI1000 Haemophilus influenzae 727 -11538365 113206 hi1000 (de:hypothetical 9.5 kd protein in rnpa 3'region) (db:swissprot) YIDD_HAEIN P44972 HAEMOPHILUS INFLUENZAE 727 -11538365 166596 hypothetical protein hi1000 (cl:conserved hypothetical protein hi1000) (db:pir2.dat) G64163 G64163 Haemophilus influenzae 727 -11538365 7500937363 hi1000 hemolysin:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to pid:1005414 percent ident: 63.64;) (le:598) (re:858) (di:direct) U32781 U32781 g1574031 Haemophilus influenzae Rd 71421 -11538365 6500734507 hypothetical protein:sp:p22834:hypothetical 9 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1000 HI1000 Haemophilus influenzae 727 -11538365

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895699	16347	38503	351	116

Description

5000695173 hypothetical protein:gb:l10328_69:60 kd inner-membrane protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1001 HI1001 Haemophilus influenzae 727 -11538366 57613 hi1001 (de:60 kd inner-membrane protein) (db:swissprot) 60IM_HAEIN P44973 HAEMOPHILUS INFLUENZAE 727 -11538366 166597 probable 60k inner membrane protein (cl:probable 60k inner membrane protein:stage iii sporulation protein homology) (db:pir2.dat) H64163 H64163 Haemophilus influenzae 727 -11538366 7500876133 hi1001 inner membrane protein:60 kda yidc (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p25714 pid:290553 gb:u00096) (le:858) (re:2483) (di:direct) U32781 U32781 g1574032 Haemophilus influenzae Rd 71421 -11538366 6500734508 hypothetical protein:gb:l10328_69:60 kd inner-membrane protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1001 HI1001 Haemophilus influenzae 727 -11538366

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895701	16348	38504	498	166

Description

5000695174 gb:u14003_187:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1005 HI1005 Haemophilus influenzae 727 -11538367 113776 hi1005 (de:hypothetical protein hi1005) (db:swissprot) YA05_HAEIN P44974 HAEMOPHILUS INFLUENZAE 727 -11538367 166600 hypothetical protein hi1005 (db:pir2.dat) I64163 I64163 Haemophilus influenzae 727 -11538367 7500895820 hi1005 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 96 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p75785 pid:1787035 percent) (le:6144) (re:7703) (di:direct) U32781 U32781 g1574035 Haemophilus influenzae Rd 71421 -11538367 6500734509 gb:u14003_187:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1005 HI1005 Haemophilus influenzae 727 -11538367

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895704	16349	38505	1134	378

Description

5000695175 gb:d90212_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1010 HI1010 Haemophilus influenzae 727 -11538368 109364 hi1010 (de:hypothetical protein hi1010) (db:swissprot) YGBJ_HAEIN P44979 HAEMOPHILUS INFLUENZAE 727 -11538368 166602 hypothetical protein hi1010 (cl:3-hydroxyisobutyrate dehydrogenase:3-hydroxyisobutyrate dehydrogenase homology) (db:pir2.dat) B64164 B64164 Haemophilus influenzae 727 -11538368 7500924028 hi1010 3-hydroxyisobutyrate dehydrogenase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to pid:882629 gb:u00096 pid:1789092 percent) (le:110) (re:1015) (di:direct) U32782 U32782 g1574042 Haemophilus influenzae Rd 71421 -11538368 6500734510 gb:d90212_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1010 HI1010 Haemophilus influenzae 727 -11538368

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895706	16350	38506	345	114

Description

5000695178 sp:p37678:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1024 HI1024 Haemophilus influenzae 727 -11538369 113734 sgbh:hi1024 (ec:4.1.2.-) (de:3-hexulose 6-phosphate formaldehyde lyase)) (db:swissprot) SGBH_HAEIN P44988 HAEMOPHILUS INFLUENZAE 727 -11538369 166609 hypothetical protein hi1024 (cl:hypothetical protein hi1024) (db:pir2.dat) F64164 F64164 Haemophilus influenzae 727 -11538369 7500891594 hi1024 hexulose-6-phosphate synthase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 98 of 163 of the complete genome.) (nt:similar to sp:p37678 pid:466719 gb:u00096) (le:3339) (re:4016) (di:complement) U32783 U32783 g1574056 Haemophilus influenzae Rd 71421 -11538369 6500734511 sp:p37678:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1024 HI1024 Haemophilus influenzae 727 -11538369

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895707	16351	38507	441	146

Description

5000695179 sp:p37679:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1026 HI1026 Haemophilus influenzae 727 -11538370 113141 sgbu:hi1026 (ec:5.-.-.-) (de:putative hexulose-6-phosphate isomerase, (humpi)) (db:swissprot) SGBU_HAEIN P44990 HAEMOPHILUS INFLUENZAE 727 -11538370 166610 hypothetical protein hi1026 (cl:hypothetical protein hi1026) (db:pir2.dat) G64164 G64164 Haemophilus influenzae 727 -11538370 7500891596 hi1026 hexulose-6-phosphate isomerase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 98 of 163 of the complete genome.) (nt:similar to sp:p37679 pid:466720 gb:u00096) (le:4755) (re:5615) (di:complement) U32783 U32783 g1574058 Haemophilus influenzae Rd 71421 -11538370 6500734512 sp:p37679:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1026 HI1026 Haemophilus influenzae 727 -11538370

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895710	16352	38508	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895715	16353	38509	888	295

Description

5000695180 hypothetical protein:sp:p37676:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1028 HI1028 Haemophilus influenzae 727 -11538371 113138 hi1028 (de:hypothetical protein hi1028 precursor) (db:swissprot) YIAO_HAEIN P44992 HAEMOPHILUS INFLUENZAE 727 -11538371 166612 hypothetical protein hi1028 (cl:conserved hypothetical protein hi1028) (db:pir2.dat) I64164 I64164 Haemophilus influenzae 727 -11538371 7500937301 hi1028 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 98 of 163 of the complete genome.) (nt:similar to sp:p37676 pid:466717 gb:u00096) (le:7145) (re:8131) (di:complement) U32783 U32783 g1574060 Haemophilus influenzae Rd 71421 -11538371 6500734513 hypothetical protein:sp:p37676:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1028 HI1028 Haemophilus influenzae 727 -11538371

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895724	16354	38510	2166	721

Description

5000695181 sp:p37675:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1029 HI1029 Haemophilus influenzae 727 -11538372 113136 hi1029 (de:hypothetical protein hi1029) (db:swissprot) YIAN_HAEIN P44993 HAEMOPHILUS INFLUENZAE 727 -11538372 166613 conserved hypothetical protein hi1029 (cl:conserved hypothetical protein hi1029) (db:pir2.dat) A64165 A64165 Haemophilus influenzae 727 -11538372 7500937299 hi1029 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 98 of 163 of the complete genome.) (nt:similar to sp:p37675 pid:466716 gb:u00096) (le:8162) (re:9439) (di:complement) U32783 U32783 g1574061 Haemophilus influenzae Rd 71421 -11538372 6500734514 sp:p37675:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1029 HI1029 Haemophilus influenzae 727 -11538372

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895740	16355	38511	543	180

Description

5000695182 sp:p37674:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1030 HI1030 Haemophilus influenzae 727 -11538373 113134 hi1030 (de:hypothetical protein hi1030) (db:swissprot) YIAM_HAEIN P44994 HAEMOPHILUS INFLUENZAE 727 -11538373 166614 hypothetical protein hi1030 (db:pir2.dat) B64165 B64165 Haemophilus influenzae 727 -11538373 7500937297 hi1030 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 98 of 163 of the complete genome.) (nt:similar to sp:p37674 pid:466715 gb:u00096) (le:9436) (re:9921) (di:complement) U32783 U32783 g1574062 Haemophilus influenzae Rd 71421 -11538373 6500734515 sp:p37674:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1030 HI1030 Haemophilus influenzae 727 -11538373

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895741	16356	38512	1191	396

Description

5000695183 sp:p37672:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1031 HI1031 Haemophilus influenzae 727 -11538374 113130 hi1031 (de:hypothetical protein hi1031) (db:swissprot) YIAK_HAEIN P44995 HAEMOPHILUS INFLUENZAE 727 -11538374 166615 hypothetical protein hi1031 (db:pir2.dat) C64165 C64165 Haemophilus influenzae 727 -11538374 7500937294 hi1031 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 98 of 163 of the complete genome.) (nt:similar to sp:p37672 pid:466713 gb:u00096) (le:9993) (re:10991) (di:complement) U32783 U32783 g1574063 Haemophilus influenzae Rd 71421 -11538374 6500734516 sp:p37672:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1031 HI1031 Haemophilus influenzae 727 -11538374

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895750	16357	38513	192	63

Description

5000695184 hypothetical protein:sp:p37671:hypothetical transcriptional regulator hi1032 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1032 HI1032 Haemophilus influenzae 727 -11538375 113128 hi1032 (de:hypothetical transcriptional regulator hi1032) (db:swissprot) YIAJ_HAEIN P44996 HAEMOPHILUS INFLUENZAE 727 -11538375 166616 hypothetical protein hi1032 (cl:acetate operon repressor) (db:pir2.dat) D64165 D64165 Haemophilus influenzae 727 -11538375 7500937292 hi1032 transcriptional regulator:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to sp:p37671 pid:466712 gb:u00096) (le:118) (re:924) (di:direct) U32784 U32784 g1574065 Haemophilus influenzae Rd 71421 -11538375 6500734517 hypothetical protein:sp:p37671:hypothetical transcriptional regulator hi1032 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1032 HI1032 Haemophilus influenzae 727 -11538375

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895762	16358	38514	651	216

Description

5000695185 gp:d50472_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1036 HI1036 Haemophilus influenzae 727 -11538376 166618 hypothetical protein hi1036 (cl:hypothetical protein hi1036) (db:pir2.dat) G64018 G64018 Haemophilus influenzae 727 -11538376 7500960678 hi1036 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to pid:801880 sp:p52059 pid:801882 percent) (le:3760) (re:4314) (di:direct) U32784 U32784 g1574069 Haemophilus influenzae Rd 71421 -11538376 6500734518 gp:d50472_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1036 HI1036 Haemophilus influenzae 727 -11538376

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895763	16359	38515	1356	451

Description

5000695186 gp:u19362_6:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1037 HI1037 Haemophilus influenzae 727 -11538377 109395 hi1037 (de:hypothetical protein hi1037) (db:swissprot) YAFJ_HAEIN P44098 HAEMOPHILUS INFLUENZAE 727 -11538377 166619 hypothetical protein hi1037 (cl:hypothetical protein hi1037) (db:pir2.dat) H64018 H64018 Haemophilus influenzae 727 -11538377 7500896127 hi1037 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to pid:984579 gb:u00096 sp:q47147) (le:4495) (re:5379) (di:complement) U32784 U32784 g1574070 Haemophilus influenzae Rd 71421 -11538377 6500734519 gp:u19362_6:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1037 HI1037 Haemophilus influenzae 727 -11538377

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895781	16360	38516	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895783	16361	38517	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895784	16362	38518	495	164

Description

5000695187 sp:p33939:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1043 HI1043 Haemophilus influenzae 727 -11538378 109404 hi1043 (de:hypothetical protein hi1043) (db:swissprot) YA43_HAEIN P44101 HAEMOPHILUS INFLUENZAE 727 -11538378 166622 hypothetical protein hi1043 (cl:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) B64019 B64019 Haemophilus influenzae 727 -11538378 7500895861 hi1043 ferredoxin-type protein napf (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the completegenome.) (nt:similar to sp:p33939 pid:453990 gb:u00096) (le:82) (re:582) (di:complement) U32785 U32785 g1574077 Haemophilus influenzae Rd 71421 -11538378 6500734520 sp:p33939:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1043 HI1043 Haemophilus influenzae 727 -11538378

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895806	16363	38519	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895809	16364	38520	786	262

Description

5000695188 gb:m66060_5:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1053 HI1053 Haemophilus influenzae 727 -11538379 4000708220 hi1053 (de:hypothetical protein hi1053) (db:swissprot) YA53_HAEIN Q57498 HAEMOPHILUS INFLUENZAE 727 -11538379 166625 conserved hypothetical protein hi1053 (cl:haemophilus influenzae conserved hypothetical protein hi1053) (db:pir2.dat) E64165 E64165 Haemophilus influenzae 727 -11538379 7500895879 hi1053 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to gb:m66060 sp:p27749 pid:141897 percent) (le:1077) (re:1418) (di:direct) U32786 U32786 g1574607 Haemophilus influenzae Rd 71421 -11538379 6500734521 gb:m66060_5:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1053 HI1053 Haemophilus influenzae 727 -11538379

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895818	16365	38521	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895819	16366	38522	336	111

Description

5000695189 gb:u14003_187:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1064 HI1064 Haemophilus influenzae 727 -11538380 5500686462 hi1064 (de:hypothetical protein hi1064) (db:swissprot) YA64_HAEIN P71367 HAEMOPHILUS INFLUENZAE 727 -11538380 166630 hypothetical protein hi1064 (db:pir2.dat) F64165 F64165 Haemophilus influenzae 727 -11538380 7500895895 hi1064 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75785 pid:1787035 percent) (le:10090) (re:11547) (di:complement) U32786 U32786 g1574615 Haemophilus influenzae Rd 71421 -11538380 6500734522 gb:u14003_187:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1064 HI1064 Haemophilus influenzae 727 -11538380

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895835	16367	38523	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895848	16368	38524	1089	362

Description

5000695190 gp:d42105_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1070 HI1070 Haemophilus influenzae 727 -11538381 7500883525 hrpa:hi1070 (de:atp-dependent helicase hrpa homolog) (db:swissprot) HRPA_HAEIN P45018 HAEMOPHILUS INFLUENZAE 727 -11538381 7500883526 hi1070 atp-dependent helicase hrpa (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to sp:p43329 pid:806328 gb:u00096) (le:4288) (re:8202) (di:complement) U32787 U32787 g1574628 Haemophilus influenzae Rd 71421 -11538381 6500734523 gp:d42105_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1070 HI1070 Haemophilus influenzae 727 -11538381

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895850	16369	38525	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895855	16370	38526	2598	865

Description

5000695191 sp:p32065:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1073 HI1073 Haemophilus influenzae 727 -11538382 112295 hi1073 (de:hypothetical protein hi1073) (db:swissprot) YGDD_HAEIN P45019 HAEMOPHILUS INFLUENZAE 727 -11538382 166634 hypothetical protein hi1073 (db:pir2.dat) H64165 H64165 Haemophilus influenzae 727 -11538382 7500924081 hi1073 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to sp:p32065 gb:u01030 gb:x73413 pid:312767) (le:8199) (re:8573) (di:complement) U32787 U32787 g1574624 Haemophilus influenzae Rd 71421 -11538382 6500734524 sp:p32065:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1073 HI1073 Haemophilus influenzae 727 -11538382

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895874	16371	38527	522	173

Description

5000695192 gb:u18997_118:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1082 HI1082 Haemophilus influenzae 727 -11538383 116098 hi1082 (de:hypothetical protein hi1082) (db:swissprot) YRBA_HAEIN P45026 HAEMOPHILUS INFLUENZAE 727 -11538383 166636 hypothetical protein hi1082 (cl:bola protein) (db:pir2.dat) I64165 I64165 Haemophilus influenzae 727 -11538383 7500952610 hi1082 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to sp:p43781 pid:606128 gb:u00096) (le:6832) (re:7089) (di:complement) U32788 U32788 g1574636 Haemophilus influenzae Rd 71421 -11538383 6500734525 gb:u18997_118:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1082 HI1082 Haemophilus influenzae 727 -11538383

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895881	16372	38528	1368	455

Description

5000695193 gb:m34995_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1083 HI1083 Haemophilus influenzae 727 -11538384 5500686464 hi1083 (de:hypothetical protein hi1083) (db:swissprot) YA83_HAEIN Q57407 HAEMOPHILUS INFLUENZAE 727 -11538384 166637 hypothetical protein hi1083 (db:pir2.dat) A64166 A64166 Haemophilus influenzae 727 -11538384 7500895930 hi1083 anti-sigma factor b antagonist:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to gb:m34995 sp:p17903 gb:l35574 pid:143458) (le:7110) (re:7427) (di:complement) U32788 U32788 g1574637 Haemophilus influenzae Rd 71421 -11538384 6500734526 gb:m34995_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1083 HI1083 Haemophilus influenzae 727 -11538384

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895882	16373	38529	606	202

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895890	16374	38530	579	192

Description

5000695194 hypothetical protein:gb:u18997_120:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1084 HI1084 Haemophilus influenzae 727 -11538385 116101 hi1084 (de:hypothetical protein hi1084 precursor) (db:swissprot) YRBC_HAEIN P45028 HAEMOPHILUS INFLUENZAE 727 -11538385 166638 hypothetical protein hi1084 (cl:hypothetical protein hi1084) (db:pir2.dat) B64166 B64166 Haemophilus influenzae 727 -11538385 7500952613 hi1084 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to sp:p45390 pid:606130 gb:u00096) (le:7438) (re:8082) (di:complement) U32788 U32788 g1574638 Haemophilus influenzae Rd 71421 -11538385 6500734527 hypothetical protein:gb:u18997_120:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1084 HI1084 Haemophilus influenzae 727 -11538385

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895894	16375	38531	1221	406

Description

5000695195 gb:u18997_121:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1085 HI1085 Haemophilus influenzae 727 -11538386 116103 hi1085 (de:hypothetical protein hi1085) (db:swissprot) YRBD_HAEIN P45029 HAEMOPHILUS INFLUENZAE 727 -11538386 166639 hypothetical protein hi1085 (db:pir2.dat) C64166 C64166 Haemophilus influenzae 727 -11538386 7500952615 hi1085 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to sp:p45391 pid:606131 gb:u00096) (le:8112) (re:8615) (di:complement) U32788 U32788 g1574639 Haemophilus influenzae Rd 71421 -11538386 6500734528 gb:u18997_121:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1085 HI1085 Haemophilus influenzae 727 -11538386

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895896	16376	38532	1995	665

Description

5000695196 gb:u18997_122:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1086 HI1086 Haemophilus influenzae 727 -11538387 116105 hi1086 (de:hypothetical protein hi1086) (db:swissprot) YRBE_HAEIN P45030 HAEMOPHILUS INFLUENZAE 727 -11538387 166640 hypothetical protein hi1086 (cl:conserved hypothetical protein hi1086) (db:pir2.dat) D64166 D64166 Haemophilus influenzae 727 -11538387 7500952617 hi1086 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to sp:p45392 pid:606132 gb:u00096) (le:8626) (re:9411) (di:complement) U32788 U32788 g1574640 Haemophilus influenzae Rd 71421 -11538387 6500734529 gb:u18997_122:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1086 HI1086 Haemophilus influenzae 727 -11538387

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895914	16377	38533	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895927	16378	38534	732	244

Description

6500734530 ccma:hi1089 hypothetical protein:sp:p33931:heme exporter protein a:cytochrome c-type biogenesis atp-binding protein ccma (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1089 HI1089 Haemophilus influenzae 727 -11538388 63442 ccma:hi1089 (de:protein ccma)) (db:swissprot) CCMA_HAEIN P45032 HAEMOPHILUS INFLUENZAE 727 -11538388 166641 cytochrome c biogenesis protein cycv homolog:hypothetical protein hi1089 (cl:cytochrome c biogenesis protein cycv:atp-binding cassette homology) (db:pir2.dat) E64166 E64166 Haemophilus influenzae 727 -11538388 7500878356 hi1089 heme exporter atp-binding protein a ccma (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to sp:p33931 pid:405926 gb:u00096) (le:1141) (re:1779) (di:direct) U32789 U32789 g1574644 Haemophilus influenzae Rd 71421 -11538388 5000695197 (de:(hi1089) (pn:heme exporter protein a:cytochrome c-type biogenesis atp- binding protein ccma:hypothetical protein:p33931) (gn:ccma) (gtcfc:13.7:14.1) (ec:) (ccma_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influ) HI1089 HI1089 Haemophilus influenzae 727 10006111

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895937	16379	38535	2523	840

Description

6500734531 ccmb:hi1090 hypothetical protein:sp:p33930:heme exporter protein b:cytochrome c-type biogenesis protein ccmb (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1090 HI1090 Haemophilus influenzae 727 -11538389 63447 ccmb:hi1090 (de:heme exporter protein b (cytochrome c-type biogenesis protein ccmb)) (db:swissprot) CCMB_HAEIN P45033 HAEMOPHILUS INFLUENZAE 727 -11538389 166642 heme export protein b (cl:cytochrome c biogenesis protein cycw) (db:pir2.dat) F64166 F64166 Haemophilus influenzae 727 -11538389 7500878358 hi1090 heme exporter protein b ccmb (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to sp:p33930 pid:405925 gb:u00096) (le:1784) (re:2449) (di:direct) U32789 U32789 g1574645 Haemophilus influenzae Rd 71421 -11538389 5000695198 (de:(hi1090) (pn:heme exporter protein b:cytochrome c-type biogenesis protein ccmb:hypothetical protein:p33930) (gn:ccmb) (gtcfc:13.7:14.1) (ec:) (ccmb_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1090 HI1090 Haemophilus influenzae 727 10006116

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895945	16380	38536	471	157

Description

6500734532 ccmc:hi1091 hypothetical protein:sp:p33929:heme exporter protein c:cytochrome c-type biogenesis protein ccmc (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1091 HI1091 Haemophilus influenzae 727 -11538390 63452 ccmc:hi1091 (de:heme exporter protein c (cytochrome c-type biogenesis protein ccmc)) (db:swissprot) CCMC_HAEIN P45034 HAEMOPHILUS INFLUENZAE 727 -11538390 166643 heme export protein c (cl:helc protein) (db:pir2.dat) G64166 G64166 Haemophilus influenzae 727 -11538390 7500878360 hi1091 heme exporter protein c ccmc (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to sp:p33929 pid:405924 gb:u00096) (le:2507) (re:3247) (di:direct) U32789 U32789 g1574646 Haemophilus influenzae Rd 71421 -11538390 5000695199 (de:(hi1091) (pn:heme exporter protein c:cytochrome c-type biogenesis protein ccmc:hypothetical protein:p33929) (gn:ccmc) (gtcfc:13.7:14.1) (ec:) (ccmc_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1091 HI1091 Haemophilus influenzae 727 10006121

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895969	16381	38537	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895972	16382	38538	1260	419

Description

6500734533 ccmd:hi1092 hypothetical protein:sp:p36770:heme exporter protein d:cytochrome c-type biogenesis protein ccmd (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1092 HI1092 Haemophilus influenzae 727 -11538391 63459 ccmd:hi1092 (de:heme exporter protein d (cytochrome c-type biogenesis protein ccmd)) (db:swissprot) CCMD_HAEIN P45035 HAEMOPHILUS INFLUENZAE 727 -11538391 166644 heme export protein d homolog hi1092 (cl:heme export protein d) (db:pir2.dat) H64166 H64166 Haemophilus influenzae 727 -11538391 7500878362 hi1092 heme exporter protein d ccmd (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to sp:p36770 pid:453988 gb:u00096) (le:3289) (re:3492) (di:direct) U32789 U32789 g1574647 Haemophilus influenzae Rd 71421 -11538391 5000695200 (de:(hi1092) (pn:heme exporter protein d:cytochrome c-type biogenesis protein ccmd:hypothetical protein:p36770) (gn:ccmd) (gtcfc:13.7:14.1) (ec:) (ccmd_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1092 HI1092 Haemophilus influenzae 727 10006128

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895974	16383	38539	1020	339

Description

GTC ORF with score 258 to: (sr:human) (db:genpept) (de:homo sapiens s164 gene, partial cds; ps1 and hypothetical proteingenes, complete cds; and s171 gene, partial cds.) (nt:unknown; intron-exon boundaries defined by ests) (le:<1465:5979:14890:17363) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895975	16384	38540	360	119

Description

6500734534 ccme:hi1093 hypothetical protein:sp:p33928:cytochrome c-type biogenesis protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1093 HI1093 Haemophilus influenzae 727 -11538392 63465 ccme:hi1093 (de:cytochrome c-type biogenesis protein ccme) (db:swissprot) CCME_HAEIN P45036 HAEMOPHILUS INFLUENZAE 727 -11538392 166645 hypothetical protein hi1093 (db:pir2.dat) I64166 I64166 Haemophilus influenzae 727 -11538392 7500878364 hi1093 cytochrome c-type biogenesis protein ccme (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to sp:p33928 pid:405922 gb:u00096) (le:3489) (re:4010) (di:direct) U32789 U32789 g1574648 Haemophilus influenzae Rd 71421 -11538392 5000695201 (de:(hi1093) (pn:cytochrome c-type biogenesis protein :hypothetical protein:p33928) (gn:ccme) (gtcfc:13.7:14.1) (ec:) (ccme_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1093 HI1093 Haemophilus influenzae 727 10006134

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895976	16385	38541	1116	371

Description

6500734535 ccmf:hi1094 hypothetical protein:sp:p33927:cytochrome c-type biogenesis protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1094 HI1094 Haemophilus influenzae 727 -11538393 63469 ccmf:hi1094 (de:cytochrome c-type biogenesis protein ccmf) (db:swissprot) CCMF_HAEIN P45037 HAEMOPHILUS INFLUENZAE 727 -11538393 136989 cyck protein homolog hi1094 (cl:nrfe protein) (db:pir2.dat) A64167 A64167 Haemophilus influenzae 727 -11538393 7500878366 hi1094 cytochrome c-type biogenesis protein ccmf (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to sp:p33927 pid:405921 gb:u00096) (le:4007) (re:5953) (di:direct) U32789 U32789 g1574649 Haemophilus influenzae Rd 71421 -11538393 5000695202 (de:(hi1094) (pn:cytochrome c-type biogenesis protein :hypothetical protein:p33927) (gn:ccmf) (gtcfc:13.7:14.1) (ec:) (ccmf_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1094 HI1094 Haemophilus influenzae 727 10006138

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895980	16386	38542	234	77

Description

6500734536 dsbe-1:hi1095 hypothetical protein:sp:p33926:thiol:disulfide interchange protein dsbe homolog 1 precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1095 HI1095 Haemophilus influenzae 727 -11538394 69321 dsbe-1:hi1095 (de:thiol:disulfide interchange protein dsbe homolog 1 precursor) (db:swissprot) DSE1_HAEIN P45038 HAEMOPHILUS INFLUENZAE 727 -11538394 166646 dsbe thiol:disulfide interchange protein dsbe precursor (cl:cytochrome c biogenesis protein cycx) (db:pir2.dat) B64167 B64167 Haemophilus influenzae 727 -11538394 7500880676 hi1095 th:disulfide interchange protein dsbe (db:genpept-bct1) (de:haemophilus influenzae rd section 104 of 163 of the completegenome.) (nt:similar to sp:p33926 pid:405920 gb:u00096) (le:6092) (re:6637) (di:direct) U32789 U32789 g1574650 Haemophilus influenzae Rd 71421 -11538394 5000695203 (de:(hi1095) (pn:thiol:disulfide interchange protein dsbe homolog 1 precursor:hypothetical protein:p33926) (gn:dsbe-1) (gtcfc:13.7:14.1) (ec:) (dse1_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1095 HI1095 Haemophilus influenzae 727 10011904

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501895995	16387	38543	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896006	16388	38544	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896026	16389	38545	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896055	16390	38546	486	161

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896063	16391	38547	897	298

Description

5000695204 hypothetical protein:sp:p24253:hypothetical gtp-binding protein hi1118 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1118 HI1118 Haemophilus influenzae 727 -11538395 113316 hi1118 (de:hypothetical gtp-binding protein hi1118) (db:swissprot) YIHA_HAEIN P46453 HAEMOPHILUS INFLUENZAE 727 -11538395 7500937479 hi1118 conserved hypothetical gtp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the completegenome.) (nt:similar to gb:j01663 sp:p24253 pid:147313) (le:88) (re:705) (di:complement) U32792 U32792 g1574673 Haemophilus influenzae Rd 71421 -11538395 6500734537 hypothetical protein:sp:p24253:hypothetical gtp-binding protein hi1118 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1118 HI1118 Haemophilus influenzae 727 -11538395

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896072	16392	38548	297	98

Description

5000695205 sp:p22186:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1129 HI1129 Haemophilus influenzae 727 -11538396 109531 hi1129 (de:hypothetical protein hi1129) (db:swissprot) YABB_HAEIN P45056 HAEMOPHILUS INFLUENZAE 727 -11538396 166654 yabb protein homolog hi1129 (cl:hypothetical protein mg221) (db:pir2.dat) E64167 E64167 Haemophilus influenzae 727 -11538396 7500895993 hi1129 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 108 of 163 of the completegenome.) (nt:similar to sp:p22186 gb:x52063 pid:40849 pid:42319) (le:131) (re:586) (di:direct) U32793 U32793 g1574684 Haemophilus influenzae Rd 71421 -11538396 6500734538 sp:p22186:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1129 HI1129 Haemophilus influenzae 727 -11538396

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896079	16393	38549	600	199

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896091	16394	38550	531	176

Description

5000695206 gb:d10483_63:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1130 HI1130 Haemophilus influenzae 727 -11538397 109534 hi1130 (de:hypothetical protein hi1130) (db:swissprot) YABC_HAEIN P45057 HAEMOPHILUS INFLUENZAE 727 -11538397 157252 yabc protein homolog hi1130 (cl:escherichia coli yabc protein) (db:pir2.dat) F64167 F64167 Haemophilus influenzae 727 -11538397 7500895995 hi1130 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 108 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p18595 gb:x52063 pid:216497) (le:617) (re:1582) (di:direct) U32793 U32793 g1574685 Haemophilus influenzae Rd 71421 -11538397 6500734539 gb:d10483_63:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1130 HI1130 Haemophilus influenzae 727 -11538397

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896122	16395	38551	1056	351

Description

5000695207 sp:p33995:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1146 HI1146 Haemophilus influenzae 727 -11538398 166655 hypothetical protein hi1146 (cl:bacillus subtilis conserved hypothetical protein yvcj) (db:pir2.dat) G64167 G64167 Haemophilus influenzae 727 -11538398 7500960681 hi1146 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to sp:p33995 gb:z27094 pid:414888) (le:8212) (re:9081) (di:complement) U32794 U32794 g1574702 Haemophilus influenzae Rd 71421 -11538398 6500734540 sp:p33995:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1146 HI1146 Haemophilus influenzae 727 -11538398

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896126	16396	38552	1332	443

Description

GTC ORF with score 116 to: (fn:transcriptional regulation) (db:genpept-vrl) (de:human herpesvirus 6 replication origin-binding protein (hdrfo),partial cds, helicase-primase component (hdrf1), virion protein(hdlf1), putative helicase (hdrf2), putative ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896137	16397	38553	456	151

Description

6500734541 ptsn:hi1147 nitrogen regulatory iia protein:nitrogen regulatory iia protein homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1147 HI1147 Haemophilus influenzae 727 -11538399 92327 ptsn:hi1147 (de:nitrogen regulatory iia protein homolog) (db:swissprot) PTSN_HAEIN P45072 HAEMOPHILUS INFLUENZAE 727 -11538399 166656 hypothetical protein hi1147 (db:pir2.dat) H64167 H64167 Haemophilus influenzae 727 -11538399 7500889007 hi1147 nitrogen regulatory iia protein ptsn (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to gb:d12938 sp:p31222 gb:z27094 pid:285783) (le:9087) (re:9581) (di:complement) U32794 U32794 g1574703 Haemophilus influenzae Rd 71421 -11538399 5000695208 (de:(hi1147) (pn:nitrogen regulatory iia protein homolog:nitrogen regulatory iia protein:ptsn) (gn:ptsn) (gtcfc:13.7:14.1) (ec:) (ptsn_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1147 HI1147 Haemophilus influenzae 727 10034359

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896143	16398	38554	615	204

Description

5000695209 hypothetical protein:gb:d12938_1:probable abc transporter atp-binding protein hi1148 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1148 HI1148 Haemophilus influenzae 727 -11538400 112632 hi1148 (de:probable abc transporter atp-binding protein hi1148) (db:swissprot) YHBG_HAEIN P45073 HAEMOPHILUS INFLUENZAE 727 -11538400 166657 hypothetical protein hi1148 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) I64167 I64167 Haemophilus influenzae 727 -11538400 7500936771 hi1148 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to gb:d12938 sp:p31220 pid:285780) (le:9584) (re:10309) (di:complement) U32794 U32794 g1574704 Haemophilus influenzae Rd 71421 -11538400 6500734542 hypothetical protein:gb:d12938_1:probable abc transporter atp-binding protein hi1148 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1148 HI1148 Haemophilus influenzae 727 -11538400

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896158	16399	38555	213	70

Description

5000695210 hypothetical protein:gb:u12684_1:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1149 HI1149 Haemophilus influenzae 727 -11538401 7500976275 hi1149 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to gb:u12684 sp:p38685 pid:551336) (le:10313) (re:10792) (di:complement) U32794 U32794 g1574705 Haemophilus influenzae Rd 71421 -11538401 6500734543 hypothetical protein:gb:u12684_1:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1149 HI1149 Haemophilus influenzae 727 -11538401

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896159	16400	38556	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896165	16401	38557	1134	377

Description

5000695211 gp:u18997_128:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1150 HI1150 Haemophilus influenzae 727 -11538402 116115 hi1150 (de:hypothetical protein hi1150) (db:swissprot) YRBK_HAEIN P45075 HAEMOPHILUS INFLUENZAE 727 -11538402 166659 hypothetical protein hi1150 (db:pir2.dat) B64168 B64168 Haemophilus influenzae 727 -11538402 7500952628 hi1150 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to sp:p45397 pid:606138 gb:u00096) (le:10812) (re:11441) (di:complement) U32794 U32794 g1574706 Haemophilus influenzae Rd 71421 -11538402 6500734544 gp:u18997_128:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1150 HI1150 Haemophilus influenzae 727 -11538402

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896166	16402	38558	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896170	16403	38559	888	295

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896171	16404	38560	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896181	16405	38561	1164	387

Description

5000695212 sp:p26650:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1151 HI1151 Haemophilus influenzae 727 -11538403 113748 hi1151 (de:hypothetical protein hi1151) (db:swissprot) YJGA_HAEIN P45076 HAEMOPHILUS INFLUENZAE 727 -11538403 166660 hypothetical protein hi1151 (db:pir2.dat) C64168 C64168 Haemophilus influenzae 727 -11538403 7500938012 hi1151 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to sp:p26650 gb:m95096 pid:148266) (le:11477) (re:12013) (di:complement) U32794 U32794 g1574707 Haemophilus influenzae Rd 71421 -11538403 6500734545 sp:p26650:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1151 HI1151 Haemophilus influenzae 727 -11538403

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896191	16406	38562	204	67

Description

5000695213 sp:p37010:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1165 HI1165 Haemophilus influenzae 727 -11538404 111352 hi1165 (de:hypothetical protein hi1165) (db:swissprot) YDHD_HAEIN P45085 HAEMOPHILUS INFLUENZAE 727 -11538404 166663 hypothetical protein hi1165 (cl:conserved hypothetical protein hi1165) (db:pir2.dat) F64168 F64168 Haemophilus influenzae 727 -11538404 7500922320 hi1165 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 111 of 163 of the completegenome.) (nt:similar to pid:2407233 percent ident: 78.50;) (le:7108) (re:7470) (di:direct) U32796 U32796 g1574092 Haemophilus influenzae Rd 71421 -11538404 6500734546 sp:p37010:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1165 HI1165 Haemophilus influenzae 727 -11538404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896217	16407	38563	795	264

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896219	16408	38564	1344	447

Description

GTC ORF with score 141 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896228	16409	38565	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896229	16410	38566	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896230	16411	38567	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896232	16412	38568	390	129

Description

6500734547 sprt:hi1173 hypothetical protein:sp:p39902:protein homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1173 HI1173 Haemophilus influenzae 727 -11538405 99324 sprt:hi1173 (de:sprt protein homolog) (db:swissprot) SPRT_HAEIN P44119 HAEMOPHILUS INFLUENZAE 727 -11538405 166666 hypothetical protein hi1173 (cl:hypothetical protein hi1173) (db:pir2.dat) B64021 B64021 Haemophilus influenzae 727 -11538405 7500892000 hi1173 sprt protein sprt (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to sp:p39902 pid:1208420 pid:882473) (le:4264) (re:4734) (di:direct) U32797 U32797 g1574100 Haemophilus influenzae Rd 71421 -11538405 5000695214 (de:(hi1173) (pn:protein homolog:hypothetical protein:p39902) (gn:sprt) (gtcfc:13.7:14.1) (ec:) (sprt_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1173 HI1173 Haemophilus influenzae 727 10041183

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896239	16413	38569	318	105

Description

GTC ORF with score 100 to: (db:genpept-inv) (de:crithidia fasciculata universal minicircle sequence binding protein(umsbp1 and umsbp2) genes, nuclear genes encoding kinetoplastproteins, complete cds.) (nt:umsbp; cchc-type zinc finger protein) (le:1032)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896240	16414	38570	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896241	16415	38571	201	66

Description

5000695215 gmha:isn:hi1181 hypothetical protein:gb:u18997_79:phosphoheptose isomerase (gtcfc:14.1) (ec:5.-.-.-) (keggfc:14.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1181 HI1181 Haemophilus influenzae 727 -11538406 74226 lpca:gmha:isn:hi1181 (ec:5.-.-.-) (de:phosphoheptose isomerase,) (db:swissprot) LPCA_HAEIN P45093 HAEMOPHILUS INFLUENZAE 727 -11538406 166668 phosphoheptose isomerase (cl:phosphoheptose isomerase) (ec:5.-.-.-) (db:pir2.dat) G64168 G64168 Haemophilus influenzae 727 -11538406 7500885110 hi1181 phosphoheptose isomerase gmha (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1552792 pid:1786416) (le:8862) (re:9446) (di:complement) U32797 U32797 g1574106 Haemophilus influenzae Rd 71421 -11538406 6500734548 gmha:isn hypothetical protein:gb:u18997_79:phosphoheptose isomerase (gtcfc:14.1) (ec:5.-.-.-) (keggfc:14.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1181 HI1181 Haemophilus influenzae 727 -11538406

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896271	16416	38572	597	198

Description

5000695216 sp:p32066:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1195 HI1195 Haemophilus influenzae 727 -11538407 166674 hypothetical protein hi1195 (db:pir2.dat) H64168 H64168 Haemophilus influenzae 727 -11538407 7500960684 hi1195 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to sp:p32066 gb:x73413 pid:312768) (le:1018) (re:2250) (di:direct) U32799 U32799 g1574124 Haemophilus influenzae Rd 71421 -11538407 6500734549 sp:p32066:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1195 HI1195 Haemophilus influenzae 727 -11538407

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896282	16417	38573	1128	375

Description

5000695217 gb:u18111_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1198 HI1198 Haemophilus influenzae 727 -11538408 110825 hi1198 (de:hypothetical protein hi1198) (db:swissprot) YCIO_HAEIN P45103 HAEMOPHILUS INFLUENZAE 727 -11538408 166675 probable translation factor hi1198 (cl:hypothetical protein hi1198) (db:pir2.dat) I64168 I64168 Haemophilus influenzae 727 -11538408 7500921831 hi1198 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to sp:p45847 pid:602960 gb:u00096) (le:4457) (re:5080) (di:direct) U32799 U32799 g1574127 Haemophilus influenzae Rd 71421 -11538408 6500734550 gb:u18111_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1198 HI1198 Haemophilus influenzae 727 -11538408

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896310	16418	38574	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896314	16419	38575	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896327	16420	38576	813	271

Description

5000695218 gb:u18111_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1199 HI1199 Haemophilus influenzae 727 -11538409 110820 hi1199 (de:hypothetical protein hi1199) (db:swissprot) YCIL_HAEIN P45104 HAEMOPHILUS INFLUENZAE 727 -11538409 166676 hypothetical protein hi1199 (db:pir2.dat) A64169 A64169 Haemophilus influenzae 727 -11538409 7500921829 hi1199 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to pid:602963 gb:u00096 pid:1787524 percent) (le:5128) (re:6201) (di:direct) U32799 U32799 g1574128 Haemophilus influenzae Rd 71421 -11538409 6500734551 gb:u18111_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1199 HI1199 Haemophilus influenzae 727 -11538409

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896328	16421	38577	528	175

Description

5000695219 sp:p37066:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1234 HI1234 Haemophilus influenzae 727 -11538410 110629 mgsa:hi1234 (ec:4.2.99.11) (de:methylglyoxal synthase,) (db:swissprot) MGSA_HAEIN P45120 HAEMOPHILUS INFLUENZAE 727 -11538410 166684 mgsa methylglyoxal synthase (cl:escherichia coli yccg protein) (ec:4.2.99.11) (db:pir2.dat) D64169 D64169 Haemophilus influenzae 727 -11538410 7500885605 hi1234 methylglyoxal synthase mgsa (db:genpept-bct1) (de:haemophilus influenzae rd section 118 of 163 of the completegenome.) (nt:similar to sp:p37066 gb:u00096 pid:1787197) (le:4813) (re:5271) (di:direct) U32803 U32803 g1574165 Haemophilus influenzae Rd 71421 -11538410 6500734552 sp:p37066:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1234 HI1234 Haemophilus influenzae 727 -11538410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896339	16422	38578	603	200

Description

5000695220 hypothetical protein:gpx80762_3:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1236 HI1236 Haemophilus influenzae 727 -11538411 110503 hi1236 (de:hypothetical protein hi1236) (db:swissprot) YC36_HAEIN P44132 HAEMOPHILUS INFLUENZAE 727 -11538411 166686 hypothetical protein hi1236 (db:pir2.dat) F64022 F64022 Haemophilus influenzae 727 -11538411 7500921464 hi1236 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 118 of 163 of the completegenome.) (nt:similar to pid:868023 gb:u00096 pid:1787900 percent) (le:5765) (re:6868) (di:complement) U32803 U32803 g1574166 Haemophilus influenzae Rd 71421 -11538411 6500734553 hypothetical protein:gpx80762_3:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1236 HI1236 Haemophilus influenzae 727 -11538411

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896345	16423	38579	402	133

Description

GTC ORF with score 104 to: (or:Homo sapiens) (sr:homo sapiens spinal cord cdna to mrna, clone:hoprp1) (db:genpept-pri2) (de:human mrna for mobp (myelin-associated oligodendrocytic basicprotein), complete cds, clone hoprp1.) (le:9) (re:557) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896346	16424	38580	663	220

Description

5000695221 hypothetical protein:gb:l10328_12:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1240 HI1240 Haemophilus influenzae 727 -11538412 113188 hi1240 (de:hypothetical protein hi1240 precursor) (db:swissprot) YICG_HAEIN P45122 HAEMOPHILUS INFLUENZAE 727 -11538412 166687 conserved hypothetical protein hi1240 (cl:hypothetical protein b1832) (db:pir2.dat) E64169 E64169 Haemophilus influenzae 727 -11538412 7500937339 hi1240 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the completegenome.) (nt:similar to gb:l10328 sp:p31432 pid:290496 gb:u00096) (le:1344) (re:2006) (di:complement) U32804 U32804 g1574172 Haemophilus influenzae Rd 71421 -11538412 6500734554 hypothetical protein:gb:l10328_12:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1240 HI1240 Haemophilus influenzae 727 -11538412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896351	16425	38581	405	134

Description

5000695222 sp:p33918:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1243 HI1243 Haemophilus influenzae 727 -11538413 111626 rsua:hi1243 (ec:4.2.1.70) (de:hydrolyase)) (db:swissprot) RSUA_HAEIN P45124 HAEMOPHILUS INFLUENZAE 727 -11538413 166689 hypothetical protein hi1243 (cl:conserved hypothetical protein hi1243) (db:pir2.dat) F64169 F64169 Haemophilus influenzae 727 -11538413 7500891164 hi1243 16s pseudouridylate 516 synthase rsua (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the completegenome.) (nt:similar to sp:p33918 pid:405907 gb:u00096) (le:4134) (re:4832) (di:complement) U32804 U32804 g1574175 Haemophilus influenzae Rd 71421 -11538413 6500734555 sp:p33918:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1243 HI1243 Haemophilus influenzae 727 -11538413

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896359	16426	38582	1491	496

Description

5000695223 hypothetical protein:gb:u14003_302:abc transporter atp-binding protein hi1252 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1252 HI1252 Haemophilus influenzae 727 -11538414 113852 hi1252 (de:abc transporter atp-binding protein hi1252) (db:swissprot) YJJK_HAEIN P45127 HAEMOPHILUS INFLUENZAE 727 -11538414 166695 hypothetical protein hi1252 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) G64169 G64169 Haemophilus influenzae 727 -11538414 7500938119 hi1252 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 120 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p37797 pid:537231 gb:u00096) (le:3143) (re:4813) (di:direct) U32805 U32805 g1574184 Haemophilus influenzae Rd 71421 -11538414 6500734556 hypothetical protein:gb:u14003_302:abc transporter atp-binding protein hi1252 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1252 HI1252 Haemophilus influenzae 727 -11538414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896360	16427	38583	396	131

Description

6500734557 sana:hi1262 hypothetical protein:sp:p33017:protein homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1262 HI1262 Haemophilus influenzae 727 -11538415 97894 sana:hi1262 (de:sana protein homolog) (db:swissprot) SANA_HAEIN P45130 HAEMOPHILUS INFLUENZAE 727 -11538415 166701 hypothetical protein hi1262 (cl:conserved hypothetical protein hi1262) (db:pir2.dat) H64169 H64169 Haemophilus influenzae 727 -11538415 7500891299 hi1262 sana protein sana (db:genpept-bct1) (de:haemophilus influenzae rd section 121 of 163 of the completegenome.) (nt:similar to sp:p33017 pid:405877 pid:1161522) (le:2611) (re:3345) (di:complement) U32806 U32806 g1574720 Haemophilus influenzae Rd 71421 -11538415 5000695224 (de:(hi1262) (pn:protein homolog:hypothetical protein:p33017) (gn:sana) (gtcfc:13.7:14.1) (ec:) (sana_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1262 HI1262 Haemophilus influenzae 727 10039773

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896374	16428	38584	879	292

Description

5000695225 sp:p19769:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1280 HI1280 Haemophilus influenzae 727 -11538416 166709 hypothetical protein hi1280 (db:pir2.dat) G64024 G64024 Haemophilus influenzae 727 -11538416 110550 hi1280 (de:hypothetical protein hi1280) (db:swissprot) YC80_HAEIN P44151 HAEMOPHILUS INFLUENZAE 727 -11538416 6500734558 sp:p19769:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1280 HI1280 Haemophilus influenzae 727 -11538416

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896389	16429	38585	504	167

Description

5000695226 sp:p03843:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1282 HI1282 Haemophilus influenzae 727 -11538417 112628 hi1282 (de:hypothetical protein hi1282) (db:swissprot) YHBC_HAEIN P45138 HAEMOPHILUS INFLUENZAE 727 -11538417 157283 hypothetical protein hi1282 (cl:nus operon 15k protein) (db:pir2.dat) I64169 I64169 Haemophilus influenzae 727 -11538417 7500936768 hi1282 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 123 of 163 of the completegenome.) (nt:similar to sp:p03843 pid:42143 pid:606110 gb:u00096) (le:1193) (re:1618) (di:direct) U32808 U32808 g1574740 Haemophilus influenzae Rd 71421 -11538417 6500734559 sp:p03843:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1282 HI1282 Haemophilus influenzae 727 -11538417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896397	16430	38586	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896399	16431	38587	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896400	16432	38588	453	150

Description

6500734560 rbfa:hi1288 hypothetical protein:sp:p09170:ribosome-binding factor a (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1288 HI1288 Haemophilus influenzae 727 -11538418 93166 rbfa:hi1288 (de:ribosome-binding factor a) (db:swissprot) RBFA_HAEIN P45141 HAEMOPHILUS INFLUENZAE 727 -11538418 157253 ribosome-binding factor hi1288 (cl:escherichia coli protein p15b) (db:pir2.dat) A64170 A64170 Haemophilus influenzae 727 -11538418 7500889412 hi1288 ribosome binding factor a rbfa (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to sp:p09170 gb:x13270 pid:42218 pid:42222) (le:288) (re:674) (di:direct) U32809 U32809 g1574747 Haemophilus influenzae Rd 71421 -11538418 5000695227 (de:(hi1288) (pn:ribosome-binding factor a:hypothetical protein:p09170) (gn:rbfa) (gtcfc:13.7:14.1) (ec:) (rbfa_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1288 HI1288 Haemophilus influenzae 727 10035173

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896401	16433	38589	444	147

Description

6500734561 trub:hi1289 trna pseudouridine 55 synthase:psi55 synthase:p35 protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1289 HI1289 Haemophilus influenzae 727 -11538419 102501 trub:hi1289 (ec:4.2.1.70) (de:hydrolyase)) (db:swissprot) TRUB_HAEIN P45142 HAEMOPHILUS INFLUENZAE 727 -11538419 157255 hypothetical protein hi1289 (cl:escherichia coli protein p35) (db:pir2.dat) B64170 B64170 Haemophilus influenzae 727 -11538419 7500893524 hi1289 trna pseudouridine 55 synthase trub (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to sp:p09171 gb:x13270 pid:42219 pid:42223) (le:674) (re:1612) (di:direct) U32809 U32809 g1574748 Haemophilus influenzae Rd 71421 -11538419 5000695228 (de:(hi1289) (pn:psi55 synthase:p35 protein:trna pseudouridine 55 synthase:trub) (gn:trub) (gtcfc:13.7:14.1) (ec:) (trub_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1289 HI1289 Haemophilus influenzae 727 10044320

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896408	16434	38590	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896412	16435	38591	615	204

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896445	16436	38592	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896468	16437	38593	1959	652

Description

GTC ORF with score 132 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0143.) (nt:unnamed protein product) (le:<1) (re:951) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896469	16438	38594	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896475	16439	38595	270	89

Description

5000695229 sp:p33372:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1297 HI1297 Haemophilus influenzae 727 -11538420 115250 hi1297 (de:hypothetical protein hi1297) (db:swissprot) YOHJ_HAEIN P45145 HAEMOPHILUS INFLUENZAE 727 -11538420 166715 hypothetical protein hi1297 (cl:conserved hypothetical protein hi1297) (db:pir2.dat) C64170 C64170 Haemophilus influenzae 727 -11538420 7500952105 hi1297 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to sp:p33372 pid:405872 gb:u00096) (le:6755) (re:7177) (di:direct) U32809 U32809 g1574755 Haemophilus influenzae Rd 71421 -11538420 6500734562 sp:p33372:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1297 HI1297 Haemophilus influenzae 727 -11538420

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896495	16440	38596	1944	648

Description

5000695230 sp:p33373:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1298 HI1298 Haemophilus influenzae 727 -11538421 115252 hi1298 (de:hypothetical protein hi1298) (db:swissprot) YOHK_HAEIN P45146 HAEMOPHILUS INFLUENZAE 727 -11538421 166716 hypothetical protein hi1298 (cl:yohk protein) (db:pir2.dat) D64170 D64170 Haemophilus influenzae 727 -11538421 7500952107 hi1298 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to sp:p33373 pid:405873 gb:u00096) (le:7196) (re:7891) (di:direct) U32809 U32809 g1574756 Haemophilus influenzae Rd 71421 -11538421 6500734563 sp:p33373:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1298 HI1298 Haemophilus influenzae 727 -11538421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896496	16441	38597	345	114

Description

5000695231 gb:u14003_302:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1300 HI1300 Haemophilus influenzae 727 -11538422 5500686139 uup-a:hi1300 (de:abc transporter atp-binding protein uup-1) (db:swissprot) UUP1_HAEIN Q57242 HAEMOPHILUS INFLUENZAE 727 -11538422 166717 uup-a abc-type transport protein uup-1 (cl:atp-binding cassette homology) (db:pir2.dat) E64170 E64170 Haemophilus influenzae 727 -11538422 7500893879 hi1300 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to sp:p43673 gb:u00096 pid:1787182) (le:9462) (re:11405) (di:direct) U32809 U32809 g1574757 Haemophilus influenzae Rd 71421 -11538422 6500734564 gb:u14003_302:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1300 HI1300 Haemophilus influenzae 727 -11538422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896506	16442	38598	384	127

Description

5000695232 gb:d26562_23:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1301 HI1301 Haemophilus influenzae 727 -11538423 109646 hi1301 (de:hypothetical protein hi1301) (db:swissprot) YADF_HAEIN P45148 HAEMOPHILUS INFLUENZAE 727 -11538423 166718 conserved hypothetical protein hi1301 (db:pir2.dat) F64170 F64170 Haemophilus influenzae 727 -11538423 7500896068 hi1301 carbonic anhydrase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to pid:1513236 percent ident: 57.55;) (le:11433) (re:12122) (di:complement) U32809 U32809 g1574758 Haemophilus influenzae Rd 71421 -11538423 6500734565 gb:d26562_23:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1301 HI1301 Haemophilus influenzae 727 -11538423

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896522	16443	38599	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896531	16444	38600	1401	466

Description

5000695233 gb:m14031_5:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1314 HI1314 Haemophilus influenzae 727 -11538424 5500686504 hi1314 (de:hypothetical lipoprotein hi1314 precursor) (db:swissprot) YD14_HAEIN Q57223 HAEMOPHILUS INFLUENZAE 727 -11538424 166722 hypothetical protein hi1314 (cl:conserved hypothetical protein hi1314) (db:pir2.dat) H64170 H64170 Haemophilus influenzae 727 -11538424 7500922059 hi1314 lipoprotein nlpc (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to gb:m14031 sp:p23898 pid:145446 gb:u00096) (le:10541) (re:11026) (di:direct) U32810 U32810 g1574772 Haemophilus influenzae Rd 71421 -11538424 6500734566 gb:m14031_5:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1314 HI1314 Haemophilus influenzae 727 -11538424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896533	16445	38601	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896537	16446	38602	414	137

Description

5000695234 gb:l10328_44:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1315 HI1315 Haemophilus influenzae 727 -11538425 5500686505 hi1315 (de:hypothetical protein hi1315) (db:swissprot) YD15_HAEIN P71375 HAEMOPHILUS INFLUENZAE 727 -11538425 166723 hypothetical protein hi1315 (db:pir2.dat) I64170 I64170 Haemophilus influenzae 727 -11538425 7500922060 hi1315 h. influenzae predicted coding region hi1315 (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:113) (re:430) (di:direct) U32811 U32811 g1574775 Haemophilus influenzae Rd 71421 -11538425 6500734567 gb:l10328_44:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1315 HI1315 Haemophilus influenzae 727 -11538425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896554	16447	38603	264	87

Description

5000695235 gp:u13148_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1317 HI1317 Haemophilus influenzae 727 -11538426 111089 hi1317 (de:hypothetical protein hi1317) (db:swissprot) YD17_HAEIN P44160 HAEMOPHILUS INFLUENZAE 727 -11538426 166725 hypothetical protein hi1317 (db:pir2.dat) G64025 G64025 Haemophilus influenzae 727 -11538426 7500922062 hi1317 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 126 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p39173 pid:1736408) (le:1485) (re:2300) (di:direct) U32811 U32811 g1574777 Haemophilus influenzae Rd 71421 -11538426 6500734568 gp:u13148_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1317 HI1317 Haemophilus influenzae 727 -11538426

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896555	16448	38604	339	112

Description

5000695236 hi1463:mrsa-a:hi1337:mrsa-b:hi1337 hypothetical protein:gb:l12968_1:mrsa protein homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1337 HI1337 Haemophilus influenzae 727 -11538427 84247 mrsa-a:hi1337:mrsa-b:hi1463 (de:mrsa protein homolog) (db:swissprot) MRSA_HAEIN P45164 HAEMOPHILUS INFLUENZAE 727 -11538427 166781 hypothetical protein hi1463:hypothetical protein hi1337 (cl:probable phosphorylating protein urec) (db:pir2.dat) C64172 C64172 Haemophilus influenzae 727 -11538427 7500885895 hi1337 mrsa protein mrsa (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to gb:l12968 sp:p31120 gb:u01376 pid:290443) (le:951) (re:2288) (di:direct) U32813 U32813 g1574798 Haemophilus influenzae Rd 71421 -11538427 7500885896 hi1463 mrsa protein mrsa (db:genpept-bct1) (de:haemophilus influenzae rd section 139 of 163 of the completegenome.) (nt:similar to gb:l12968 sp:p31120 gb:u01376 pid:290443) (le:5134) (re:6471) (di:complement) U32824 U32824 g1574303 Haemophilus influenzae Rd 71421 -11538427 6500734569 hi1463:mrsa-a:hi1337:mrsa-b hypothetical protein:gb:l12968_1:mrsa protein homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1337 HI1337 Haemophilus influenzae 727 -11538427

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896556	16449	38605	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896557	16450	38606	285	94

Description

5000695237 hypothetical protein:gb:u14003_302:hypothetical abc transporter atp-binding protein hi1342 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1342 HI1342 Haemophilus influenzae 727 -11538428 111129 uup-b:hi1342 (de:abc transporter atp-binding protein uup-2) (db:swissprot) UUP2_HAEIN P45167 HAEMOPHILUS INFLUENZAE 727 -11538428 166732 uup-b abc-type transport protein uup-2 (cl:atp-binding cassette homology) (db:pir2.dat) B64171 B64171 Haemophilus influenzae 727 -11538428 7500893880 hi1342 abc transporter:atp-binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 128 of 163 of the completegenome.) (nt:similar to sp:p43673 gb:u00096 pid:1787182) (le:6089) (re:7468) (di:direct) U32813 U32813 g1574802 Haemophilus influenzae Rd 71421 -11538428 6500734570 hypothetical protein:gb:u14003_302:hypothetical abc transporter atp-binding protein hi1342 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1342 HI1342 Haemophilus influenzae 727 -11538428

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896558	16451	38607	336	111

Description

GTC ORF with score 134 to: (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae transcription initiation factor tfiifsmall subunit (tfg3) gene, complete cds.) (nt:30 kda subunit of taf complex; tfg3p; tfiif) (le:128:242) (re:136:967) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896559	16452	38608	375	124

Description

5000695238 hypothetical protein:gp:u20964_2:hypothetical transcriptional regulator hi1364:orf2 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1364 HI1364 Haemophilus influenzae 727 -11538429 112704 hi1364 (de:hypothetical transcriptional regulator hi1364 (orf2)) (db:swissprot) YHCS_HAEIN P43011 HAEMOPHILUS INFLUENZAE 727 -11538429 166736 hypothetical protein hi1364 (cl:conserved hypothetical protein hi1364) (db:pir2.dat) D64171 D64171 Haemophilus influenzae 727 -11538429 7500936826 hi1364 transcriptional regulator:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 131 of 163 of the completegenome.) (nt:similar to sp:p37641 pid:466658 gb:u00096) (le:3252) (re:4118) (di:complement) U32816 U32816 g1574196 Haemophilus influenzae Rd 71421 -11538429 6500734571 hypothetical protein:gp:u20964_2:hypothetical transcriptional regulator hi1364:orf2 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1364 HI1364 Haemophilus influenzae 727 -11538429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896587	16453	38609	723	240

Description

5000695239 gp:u20964_4:hypothetical protein:orf3 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1366 HI1366 Haemophilus influenzae 727 -11538430 111159 acpd:hi1366 (de:acyl carrier protein phosphodiesterase (acp phosphodiesterase)) (db:swissprot) ACPD_HAEIN P43013 HAEMOPHILUS INFLUENZAE 727 -11538430 166737 acyl-carrier-protein phosphodiesterase, hi1366:conserved hypothetical protein hi1366) (cl:acyl carrier protein phosphodiesterase) (ec:3.1.4.14) (db:pir2.dat) G64026 G64026 Haemophilus influenzae 727 -11538430 7500876351 orf3 (db:genpept-bct2) (de:haemophilus influenzae dna topoisomerase i (topa) gene, completecds, putative pyridine nucleotide transhydrogenase beta subunit(pntb) gene, partial cds, orf2 and orf3 genes, complete cds andputative threonyl-trna synthetase (thrs)... HIU20964 U20964 g687791 Haemophilus influenzae 727 -11538430 241617 hi1366 acyl carrier protein phosphodiesterase acpd (db:genpept-bct1) (de:haemophilus influenzae rd section 131 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1742298 pid:1742303) (le:6896) (re:7480) (di:complement) U32816 U32816 g1574198 Haemophilus influenzae Rd 71421 -11538430 6500734572 gp:u20964_4:hypothetical protein:orf3 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1366 HI1366 Haemophilus influenzae 727 -11538430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896598	16454	38610	720	239

Description

6500734573 hypothetical protein:sp:p31828:hypothetical zinc protease hi1368 (gtcfc:14.1) (ec:3.4.99.-) (keggfc:14.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1368 HI1368 Haemophilus influenzae 727 -11538431 111269 pqql:hi1368 (ec:3.4.99.-) (de:probable zinc protease pqql,) (db:swissprot) PQQL_HAEIN P45181 HAEMOPHILUS INFLUENZAE 727 -11538431 166738 hypothetical protein hi1368 (db:pir2.dat) E64171 E64171 Haemophilus influenzae 727 -11538431 7500888386 hi1368 zinc protease:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 131 of 163 of the completegenome.) (nt:similar to sp:p31828 gb:x71917 pid:535004 gb:u00096) (le:9815) (re:12595) (di:complement) U32816 U32816 g1574200 Haemophilus influenzae Rd 71421 -11538431 5000695240 (de:(hi1368) (pn:hypothetical zinc protease hi1368:hypothetical protein:p31828) (gtcfc:13.7:14.1) (ec:3.4.99.-) (yddc_haein) (keggfc:11.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1368 HI1368 Haemophilus influenzae 727 10052999

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896624	16455	38611	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896632	16456	38612	435	144

Description

5000695241 sp:p31827:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1369 HI1369 Haemophilus influenzae 727 -11538432 111267 hi1369 (de:hypothetical protein hi1369) (db:swissprot) YDDB_HAEIN P45182 HAEMOPHILUS INFLUENZAE 727 -11538432 166739 hypothetical protein hi1369 (db:pir2.dat) F64171 F64171 Haemophilus influenzae 727 -11538432 7500922211 hi1369 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 132 of 163 of the completegenome.) (nt:similar to sp:p31827 gb:x71917 pid:311346 gb:u00096) (le:82) (re:2601) (di:complement) U32817 U32817 g1574202 Haemophilus influenzae Rd 71421 -11538432 6500734574 sp:p31827:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1369 HI1369 Haemophilus influenzae 727 -11538432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896635	16457	38613	255	84

Description

5000695242 sp:p21417:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1412 HI1412 Haemophilus influenzae 727 -11538433 111400 hi1412 (de:hypothetical protein hi1412) (db:swissprot) YE12_HAEIN P45197 HAEMOPHILUS INFLUENZAE 727 -11538433 166756 hypothetical protein hi1412 (db:pir2.dat) G64171 G64171 Haemophilus influenzae 727 -11538433 7500922610 hi1412 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:similar to sp:p21417 pid:1196685 percent ident:) (le:628) (re:1149) (di:complement) U32821 U32821 g1574250 Haemophilus influenzae Rd 71421 -11538433 6500734575 sp:p21417:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1412 HI1412 Haemophilus influenzae 727 -11538433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896637	16458	38614	621	206

Description

5000695243 sp:p03807:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1426 HI1426 Haemophilus influenzae 727 -11538434 166767 hypothetical protein hi1426 (cl:ydaa protein) (db:pir2.dat) G64029 G64029 Haemophilus influenzae 727 -11538434 7500960687 hi1426 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 136 of 163 of the completegenome.) (nt:similar to sp:p03807 pid:146962 gb:u00096) (le:8454) (re:9476) (di:direct) U32821 U32821 g1574260 Haemophilus influenzae Rd 71421 -11538434 6500734576 sp:p03807:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1426 HI1426 Haemophilus influenzae 727 -11538434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896639	16459	38615	1137	378

Description

5000695244 sp:p37174:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1434 HI1434 Haemophilus influenzae 727 -11538435 110178 hi1434 (de:hypothetical protein hi1434) (db:swissprot) YBAK_HAEIN P45202 HAEMOPHILUS INFLUENZAE 727 -11538435 166769 hypothetical protein hi1434 (cl:conserved hypothetical protein hi1434) (db:pir2.dat) H64171 H64171 Haemophilus influenzae 727 -11538435 7500896537 hi1434 transcriptional regulator:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to gb:l23802 sp:p36922 pid:388109 percent) (le:5904) (re:6380) (di:direct) U32822 U32822 g1574272 Haemophilus influenzae Rd 71421 -11538435 6500734577 sp:p37174:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1434 HI1434 Haemophilus influenzae 727 -11538435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896652	16460	38616	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896655	16461	38617	462	153

Description

5000695245 pir:s45107:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1435 HI1435 Haemophilus influenzae 727 -11538436 166770 hypothetical protein hi1435 (db:pir2.dat) I64029 I64029 Haemophilus influenzae 727 -11538436 7500960688 hi1435 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to pid:882688 gb:u00096 sp:q46918) (le:7228) (re:7776) (di:complement) U32822 U32822 g1574274 Haemophilus influenzae Rd 71421 -11538436 6500734578 pir:s45107:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1435 HI1435 Haemophilus influenzae 727 -11538436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896656	16462	38618	618	205

Description

5000695246 gb:x79474_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1436 HI1436 Haemophilus influenzae 727 -11538437 7500952374 hi1436 (de:hypothetical protein hi1436) (db:swissprot) YQCC_HAEIN Q57152 HAEMOPHILUS INFLUENZAE 727 -11538437 166771 hypothetical protein hi1436 (cl:hypothetical protein hi1436) (db:pir2.dat) I64171 I64171 Haemophilus influenzae 727 -11538437 7500952376 hi1436 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to pid:882688 gb:u00096 pid:882687 percent) (le:7770) (re:8090) (di:complement) U32822 U32822 g1574275 Haemophilus influenzae Rd 71421 -11538437 6500734579 gb:x79474_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1436 HI1436 Haemophilus influenzae 727 -11538437

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896659	16463	38619	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896676	16464	38620	687	228

Description

5000695247 hypothetical protein:gp:u00018_4:hypothetical cytochrome c-type biogenesis protein hi1454 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1454 HI1454 Haemophilus influenzae 727 -11538438 111430 hi1454 (de:hypothetical cytochrome c-type biogenesis protein hi1454) (db:swissprot) YE54_HAEIN P44202 HAEMOPHILUS INFLUENZAE 727 -11538438 166778 hypothetical protein hi1454 (db:pir2.dat) E64030 E64030 Haemophilus influenzae 727 -11538438 7500922706 hi1454 cytochrome c-type biogenesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to sp:p45706 pid:870925 pid:1405449) (le:8085) (re:8726) (di:complement) U32823 U32823 g1574292 Haemophilus influenzae Rd 71421 -11538438 6500734580 hypothetical protein:gp:u00018_4:hypothetical cytochrome c-type biogenesis protein hi1454 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1454 HI1454 Haemophilus influenzae 727 -11538438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896684	16465	38621	561	186

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896685	16466	38622	948	315

Description

GTC ORF with score 120 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome 1 bac f5o8 sequence, completesequence.) (nt:strong similarity to pfam pf|00069 eukaryotic) (le:21143:21479:21726) (re:21388:21640:21873) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896687	16467	38623	504	167

Description

5000695248 sp:q06424:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1497 HI1497 Haemophilus influenzae 727 -11538439 111454 hi1497 (de:hypothetical protein hi1497) (db:swissprot) YE97_HAEIN P44221 HAEMOPHILUS INFLUENZAE 727 -11538439 166798 hypothetical protein hi1497 (db:pir2.dat) F64032 F64032 Haemophilus influenzae 727 -11538439 7500922793 hi1497 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 141 of 163 of the completegenome.) (nt:similar to sp:q06424 pid:288658 percent ident:) (le:6173) (re:6400) (di:direct) U32826 U32826 g1574327 Haemophilus influenzae Rd 71421 -11538439 6500734581 sp:q06424:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1497 HI1497 Haemophilus influenzae 727 -11538439

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896689	16468	38624	384	127

Description

5000695249 gb:m68961_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1542 HI1542 Haemophilus influenzae 727 -11538440 111366 hi1542 (de:hypothetical protein hi1542) (db:swissprot) YDJA_HAEIN P45244 HAEMOPHILUS INFLUENZAE 727 -11538440 166825 hypothetical protein hi1542 (db:pir2.dat) D64172 D64172 Haemophilus influenzae 727 -11538440 7500922376 hi1542 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to pid:2253239 percent ident: 50.27;) (le:9211) (re:9765) (di:direct) U32829 U32829 g1574384 Haemophilus influenzae Rd 71421 -11538440 6500734582 gb:m68961_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1542 HI1542 Haemophilus influenzae 727 -11538440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896691	16469	38625	510	169

Description

5000695250 sp:p20101:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1558 HI1558 Haemophilus influenzae 727 -11538441 110778 hi1558 (de:hypothetical protein hi1558) (db:swissprot) YCHA_HAEIN P45252 HAEMOPHILUS INFLUENZAE 727 -11538441 166831 hypothetical protein hi1558 (db:pir2.dat) E64172 E64172 Haemophilus influenzae 727 -11538441 7500921811 hi1558 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to sp:p20101 gb:x05552 pid:41872) (le:13048) (re:13851) (di:complement) U32830 U32830 g1574402 Haemophilus influenzae Rd 71421 -11538441 6500734583 sp:p20101:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1558 HI1558 Haemophilus influenzae 727 -11538441

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896697	16470	38626	525	174

Description

5000695251 gb:x75627_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1590 HI1590 Haemophilus influenzae 727 -11538442 110571 hi1590 (de:hypothetical protein hi1590) (db:swissprot) YCAJ_HAEIN P45262 HAEMOPHILUS INFLUENZAE 727 -11538442 166843 hypothetical protein hi1590 (cl:haemophilus influenzae conserved hypothetical protein hi1590) (db:pir2.dat) F64172 F64172 Haemophilus influenzae 727 -11538442 7500921547 hi1590 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:similar to sp:p45526 gb:u00096 pid:1787119 percent) (le:2281) (re:3621) (di:complement) U32833 U32833 g1574435 Haemophilus influenzae Rd 71421 -11538442 6500734584 gb:x75627_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1590 HI1590 Haemophilus influenzae 727 -11538442

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896701	16471	38627	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896728	16472	38628	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896738	16473	38629	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896746	16474	38630	2106	701

Description

5000695252 lola:lpla:hi1591 hypothetical protein:gb:x75627_3:outer membrane lipoproteins carrier protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1591 HI1591 Haemophilus influenzae 727 -11538443 82307 lola:lpla:hi1591 (de:outer membrane lipoproteins carrier protein precursor) (db:swissprot) LOLA_HAEIN P45263 HAEMOPHILUS INFLUENZAE 727 -11538443 166844 outer membrane lipoprotein carrier protein homolog hi1591 (db:pir2.dat) G64172 G64172 Haemophilus influenzae 727 -11538443 7500885094 hi1591 outer membrane lipoproteins carrier protein (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:similar to sp:p39178 pid:974728 gb:u00096) (le:3682) (re:4299) (di:complement) U32833 U32833 g1574436 Haemophilus influenzae Rd 71421 -11538443 6500734585 lola:lpla hypothetical protein:gb:x75627_3:outer membrane lipoproteins carrier protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1591 HI1591 Haemophilus influenzae 727 -11538443

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896748	16475	38631	570	189

Description

5000695253 sp:p30871:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1598 HI1598 Haemophilus influenzae 727 -11538444 112392 hi1598 (de:hypothetical protein hi1598) (db:swissprot) YGIF_HAEIN P45267 HAEMOPHILUS INFLUENZAE 727 -11538444 166848 hypothetical protein hi1598 (db:pir2.dat) H64172 H64172 Haemophilus influenzae 727 -11538444 7500924256 hi1598 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 148 of 163 of the completegenome.) (nt:similar to sp:p30871 gb:z21844 pid:49399 gb:u00096) (le:9159) (re:10217) (di:complement) U32833 U32833 g1574441 Haemophilus influenzae Rd 71421 -11538444 6500734586 sp:p30871:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1598 HI1598 Haemophilus influenzae 727 -11538444

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896765	16476	38632	579	192

Description

GTC ORF with score 300 to: (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:belongs to the insect-type alcohol dehydrogenase /) (le:4769) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896767	16477	38633	519	172

Description

5000695254 hypothetical protein:sp:p39202:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1605 HI1605 Haemophilus influenzae 727 -11538445 112400 hi1605 (de:hypothetical protein hi1605 precursor) (db:swissprot) YGIM_HAEIN P44272 HAEMOPHILUS INFLUENZAE 727 -11538445 166854 hypothetical protein hi1605 (cl:hypothetical protein hi1605) (db:pir2.dat) C64038 C64038 Haemophilus influenzae 727 -11538445 7500924261 hi1605 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:similar to sp:p39202 pid:1203798 gb:u00096) (le:4897) (re:5508) (di:direct) U32834 U32834 g1574447 Haemophilus influenzae Rd 71421 -11538445 6500734587 hypothetical protein:sp:p39202:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1605 HI1605 Haemophilus influenzae 727 -11538445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896770	16478	38634	510	169

Description

5000695255 gb:m77237_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1608 HI1608 Haemophilus influenzae 727 -11538446 110780 hi1608 (de:hypothetical protein hi1608) (db:swissprot) YCHB_HAEIN P45271 HAEMOPHILUS INFLUENZAE 727 -11538446 7500921813 hi1608 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:similar to gb:d10264 gb:m77237 sp:p24209 pid:147382) (le:7469) (re:8410) (di:direct) U32834 U32834 g1574450 Haemophilus influenzae Rd 71421 -11538446 6500734588 gb:m77237_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1608 HI1608 Haemophilus influenzae 727 -11538446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896799	16479	38635	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896807	16480	38636	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896814	16481	38637	1980	659

Description

5000695256 sp:p37340:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1612 HI1612 Haemophilus influenzae 727 -11538447 111354 hi1612 (de:hypothetical protein hi1612) (db:swissprot) YDHE_HAEIN P45272 HAEMOPHILUS INFLUENZAE 727 -11538447 166857 hypothetical protein hi1612 (cl:conserved hypothetical protein hi1612) (db:pir2.dat) B64173 B64173 Haemophilus influenzae 727 -11538447 7500922321 hi1612 conserved hypothetical transmembrane protein (db:genpept-bct1) (de:haemophilus influenzae rd section 149 of 163 of the completegenome.) (nt:similar to sp:p37340 gb:u00096 pid:1549276) (le:11554) (re:12948) (di:complement) U32834 U32834 g1574453 Haemophilus influenzae Rd 71421 -11538447 6500734589 sp:p37340:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1612 HI1612 Haemophilus influenzae 727 -11538447

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896816	16482	38638	585	194

Description

5000695257 gb:d26185_111:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1627 HI1627 Haemophilus influenzae 727 -11538448 166864 hypothetical protein hi1627 (db:pir2.dat) C64173 C64173 Haemophilus influenzae 727 -11538448 7500960695 hi1627 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:similar to pid:2407234 percent ident: 56.64;) (le:86) (re:436) (di:direct) U32836 U32836 g1574474 Haemophilus influenzae Rd 71421 -11538448 6500734590 gb:d26185_111:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1627 HI1627 Haemophilus influenzae 727 -11538448

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896827	16483	38639	480	160

Description

5000695258 gb:u18997_162:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1628 HI1628 Haemophilus influenzae 727 -11538449 112667 hi1628 (de:hypothetical protein hi1628) (db:swissprot) YHCB_HAEIN P45279 HAEMOPHILUS INFLUENZAE 727 -11538449 166865 hypothetical protein hi1628 (cl:hypothetical protein hi1628) (db:pir2.dat) D64173 D64173 Haemophilus influenzae 727 -11538449 7500936804 hi1628 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:similar to sp:p39436 pid:606172 gb:u00096) (le:467) (re:871) (di:direct) U32836 U32836 g1574475 Haemophilus influenzae Rd 71421 -11538449 6500734591 gb:u18997_162:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1628 HI1628 Haemophilus influenzae 727 -11538449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896832	16484	38640	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896843	16485	38641	339	112

Description

5000695259 sp:p33019:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1643 HI1643 Haemophilus influenzae 727 -11538450 111606 hi1643 (de:hypothetical protein hi1643) (db:swissprot) YEIH_HAEIN P45290 HAEMOPHILUS INFLUENZAE 727 -11538450 166868 hypothetical protein hi1643 (db:pir2.dat) E64173 E64173 Haemophilus influenzae 727 -11538450 7500923048 hi1643 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p33019 pid:405879 gb:u00096) (le:5478) (re:6494) (di:direct) U32837 U32837 g1574491 Haemophilus influenzae Rd 71421 -11538450 6500734592 sp:p33019:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1643 HI1643 Haemophilus influenzae 727 -11538450

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896844	16486	38642	660	219

Description

5000695260 gb:d26185_75:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1647 HI1647 Haemophilus influenzae 727 -11538451 112161 hi1647 (de:hypothetical protein hi1647) (db:swissprot) YG47_HAEIN P45293 HAEMOPHILUS INFLUENZAE 727 -11538451 166869 hypothetical protein hi1647 (db:pir2.dat) F64173 F64173 Haemophilus influenzae 727 -11538451 7500923831 hi1647 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to pid:2408046 percent ident: 70.18;) (le:9692) (re:10567) (di:direct) U32837 U32837 g1574495 Haemophilus influenzae Rd 71421 -11538451 6500734593 gb:d26185_75:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1647 HI1647 Haemophilus influenzae 727 -11538451

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896851	16487	38643	1497	499

Description

5000695261 gb:d26185_76:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1648 HI1648 Haemophilus influenzae 727 -11538452 112163 hi1648 (de:hypothetical protein hi1648) (db:swissprot) YG48_HAEIN P45294 HAEMOPHILUS INFLUENZAE 727 -11538452 166870 hypothetical protein hi1648 (cl:conserved hypothetical protein hi1648) (db:pir2.dat) G64173 G64173 Haemophilus influenzae 727 -11538452 7500923835 hi1648 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to gb:d26185 sp:p37528 pid:467402) (le:10619) (re:11146) (di:direct) U32837 U32837 g1574496 Haemophilus influenzae Rd 71421 -11538452 6500734594 gb:d26185_76:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1648 HI1648 Haemophilus influenzae 727 -11538452

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896896	16488	38644	1305	434

Description

6500734595 nlpc:hi1652 hypothetical protein:gb:m14031_5:probable lipoprotein homolog precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1652 HI1652 Haemophilus influenzae 727 -11538453 86105 nlpc:hi1652 (de:probable lipoprotein nlpc homolog precursor) (db:swissprot) NLPC_HAEIN P45296 HAEMOPHILUS INFLUENZAE 727 -11538453 166873 hypothetical protein hi1652 (cl:conserved hypothetical protein hi1314) (db:pir2.dat) H64173 H64173 Haemophilus influenzae 727 -11538453 7500886496 hi1652 lipoprotein spr (db:genpept-bct1) (de:haemophilus influenzae rd section 153 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77685 pid:1498150) (le:3513) (re:4064) (di:complement) U32838 U32838 g1574501 Haemophilus influenzae Rd 71421 -11538453 5000695262 (de:(hi1652) (pn:probable lipoprotein homolog precursor:hypothetical protein:gb:m14031_5) (gn:nlpc) (gtcfc:13.7:14.1) (ec:) (nlpc_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1652 HI1652 Haemophilus influenzae 727 10028272

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896897	16489	38645	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896931	16490	38646	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896932	16491	38647	486	161

Description

5000695263 gb:u18997_173:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1653 HI1653 Haemophilus influenzae 727 -11538454 166874 hypothetical protein hi1653 (db:pir2.dat) I64173 I64173 Haemophilus influenzae 727 -11538454 6500734596 gb:u18997_173:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1653 HI1653 Haemophilus influenzae 727 -11538454

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896933	16492	38648	537	178

Description

5000695264 gb:d26185_99:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1654 HI1654 Haemophilus influenzae 727 -11538455 116078 hi1654 (de:hypothetical protein hi1654) (db:swissprot) YRAL_HAEIN P45298 HAEMOPHILUS INFLUENZAE 727 -11538455 166875 hypothetical protein hi1654 (cl:conserved hypothetical protein mg056) (db:pir2.dat) A64174 A64174 Haemophilus influenzae 727 -11538455 7500952598 hi1654 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 153 of 163 of the completegenome.) (nt:similar to sp:p45528 pid:606086 gb:u00096) (le:5726) (re:6577) (di:complement) U32838 U32838 g1574503 Haemophilus influenzae Rd 71421 -11538455 6500734597 gb:d26185_99:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1654 HI1654 Haemophilus influenzae 727 -11538455

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896935	16493	38649	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896942	16494	38650	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501896950	16495	38651	306	101

Description

5000695265 gb:u18997_77:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1655 HI1655 Haemophilus influenzae 727 -11538456 116080 hi1655 (de:hypothetical protein hi1655) (db:swissprot) YRAM_HAEIN P45299 HAEMOPHILUS INFLUENZAE 727 -11538456 166876 hypothetical protein hi1655 (db:pir2.dat) B64174 B64174 Haemophilus influenzae 727 -11538456 7500952601 hi1655 antigen (db:genpept-bct1) (de:haemophilus influenzae rd section 153 of 163 of the completegenome.) (nt:similar to pid:1353671 percent ident: 40.04;) (le:6649) (re:8376) (di:direct) U32838 U32838 g1574504 Haemophilus influenzae Rd 71421 -11538456 6500734598 gb:u18997_77:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1655 HI1655 Haemophilus influenzae 727 -11538456

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897005	16496	38652	606	201

Description

5000695266 gb:u18997_78:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1656 HI1656 Haemophilus influenzae 727 -11538457 116082 hi1656 (de:hypothetical protein hi1656) (db:swissprot) YRAN_HAEIN P45300 HAEMOPHILUS INFLUENZAE 727 -11538457 166877 hypothetical protein hi1656 (cl:hypothetical protein hi1656) (db:pir2.dat) C64174 C64174 Haemophilus influenzae 727 -11538457 7500952603 hi1656 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 153 of 163 of the completegenome.) (nt:similar to sp:p45465 pid:606088 gb:u00096) (le:8376) (re:8735) (di:direct) U32838 U32838 g1574505 Haemophilus influenzae Rd 71421 -11538457 6500734599 gb:u18997_78:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1656 HI1656 Haemophilus influenzae 727 -11538457

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897011	16497	38653	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897013	16498	38654	264	87

Description

5000695267 gb:u18997_79:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1657 HI1657 Haemophilus influenzae 727 -11538458 116084 hi1657 (de:hypothetical protein hi1657) (db:swissprot) YRAO_HAEIN P52606 HAEMOPHILUS INFLUENZAE 727 -11538458 7500952605 hi1657 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 153 of 163 of the completegenome.) (nt:similar to sp:p45466 pid:606089 gb:u00096) (le:8748) (re:9332) (di:direct) U32838 U32838 g1574506 Haemophilus influenzae Rd 71421 -11538458 6500734600 gb:u18997_79:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1657 HI1657 Haemophilus influenzae 727 -11538458

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897014	16499	38655	324	107

Description

5000695268 gb:u00011_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1663 HI1663 Haemophilus influenzae 727 -11538459 118684 hi1663 (de:hypothetical protein hi1663) (db:swissprot) YCBL_HAEIN Q57544 HAEMOPHILUS INFLUENZAE 727 -11538459 166878 probable hydrolase:hi1663 (cl:glyoxalase) (ec:3.-.-.-) (db:pir2.dat) D64174 D64174 Haemophilus influenzae 727 -11538459 7500921579 hi1663 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 154 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p75849 pid:1787158 percent) (le:8195) (re:8833) (di:complement) U32839 U32839 g1574513 Haemophilus influenzae Rd 71421 -11538459 6500734601 gb:u00011_3:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1663 HI1663 Haemophilus influenzae 727 -11538459

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897019	16500	38656	516	171

Description

5000695269 gb:u14003_289:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1664 HI1664 Haemophilus influenzae 727 -11538460 166879 hypothetical protein hi1664 (db:pir2.dat) E64174 E64174 Haemophilus influenzae 727 -11538460 7500960696 hi1664 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 154 of 163 of the completegenome.) (nt:similar to gb:u00089 sp:p78005 pid:1673805 percent) (le:8843) (re:9622) (di:complement) U32839 U32839 g1574514 Haemophilus influenzae Rd 71421 -11538460 6500734602 gb:u14003_289:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1664 HI1664 Haemophilus influenzae 727 -11538460

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897022	16501	38657	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897023	16502	38658	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897024	16503	38659	1116	371

Description

GTC ORF with score 520 to: (fn:nucleates actin polymerization in a calcium) (sr:slime mold) (db:genpept-inv) (de:physarum polycephalum actin-binding protein fragmin p mrna,complete cds.) (nt:calcium-dependent f-actin severing and capping) (le:1) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897038	16504	38660	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897052	16505	38661	387	129

Description

5000695270 gp:x81561_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1671 HI1671 Haemophilus influenzae 727 -11538461 112235 hi1671 (de:hypothetical protein hi1671) (db:swissprot) YEBS_HAEIN P44287 HAEMOPHILUS INFLUENZAE 727 -11538461 166884 hypothetical protein hi1671 (cl:hypothetical protein hi1671) (db:pir2.dat) I64039 I64039 Haemophilus influenzae 727 -11538461 7500923963 hi1671 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1736474 pid:1736480) (le:2997) (re:4247) (di:direct) U32840 U32840 g1574521 Haemophilus influenzae Rd 71421 -11538461 6500734603 gp:x81561_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1671 HI1671 Haemophilus influenzae 727 -11538461

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897061	16506	38662	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897063	16507	38663	564	187

Description

5000695271 gp:x81561_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1672 HI1672 Haemophilus influenzae 727 -11538462 112236 hi1672 (de:hypothetical protein hi1672) (db:swissprot) YG72_HAEIN P44288 HAEMOPHILUS INFLUENZAE 727 -11538462 166885 hypothetical protein hi1672 (cl:hypothetical protein b1834) (db:pir2.dat) A64040 A64040 Haemophilus influenzae 727 -11538462 7500923964 hi1672 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1736475 pid:1736481) (le:4231) (re:6876) (di:direct) U32840 U32840 g1574522 Haemophilus influenzae Rd 71421 -11538462 6500734604 gp:x81561_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1672 HI1672 Haemophilus influenzae 727 -11538462

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897068	16508	38664	1461	486

Description

5000695272 gb:u14003_121:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1677 HI1677 Haemophilus influenzae 727 -11538463 116400 hi1677 (de:hypothetical protein hi1677) (db:swissprot) YTFE_HAEIN P45312 HAEMOPHILUS INFLUENZAE 727 -11538463 166886 hypothetical protein hi1677 (db:pir2.dat) F64174 F64174 Haemophilus influenzae 727 -11538463 7500952756 hi1677 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 155 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p39313 pid:537050 gb:u00096) (le:9663) (re:10334) (di:direct) U32840 U32840 g1574527 Haemophilus influenzae Rd 71421 -11538463 6500734605 gb:u14003_121:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1677 HI1677 Haemophilus influenzae 727 -11538463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897078	16509	38665	822	273

Description

5000695273 gb:u18997_126:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1679 HI1679 Haemophilus influenzae 727 -11538464 116112 hi1679 (de:hypothetical protein hi1679) (db:swissprot) YRBI_HAEIN P45314 HAEMOPHILUS INFLUENZAE 727 -11538464 166887 hypothetical protein hi1679 (cl:hypothetical protein hi1679) (db:pir2.dat) G64174 G64174 Haemophilus influenzae 727 -11538464 7500952626 hi1679 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to sp:p45398 pid:606137 gb:u00096) (le:1547) (re:2089) (di:direct) U32841 U32841 g1574531 Haemophilus influenzae Rd 71421 -11538464 6500734606 gb:u18997_126:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1679 HI1679 Haemophilus influenzae 727 -11538464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897084	16510	38666	1296	431

Description

5000695274 hypothetical protein:sp:p29740:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1681 HI1681 Haemophilus influenzae 727 -11538465 112238 hi1681 (de:hypothetical protein hi1681 precursor) (db:swissprot) YG81_HAEIN P44290 HAEMOPHILUS INFLUENZAE 727 -11538465 166889 hypothetical protein hi1681 (db:pir2.dat) C64040 C64040 Haemophilus influenzae 727 -11538465 7500923977 hi1681 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1787198 percent ident:) (le:4411) (re:5076) (di:complement) U32841 U32841 g1574533 Haemophilus influenzae Rd 71421 -11538465 6500734607 hypothetical protein:sp:p29740:hypothetical protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1681 HI1681 Haemophilus influenzae 727 -11538465

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897085	16511	38667	216	71

Description

5000695275 gb:d13625_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1684 HI1684 Haemophilus influenzae 727 -11538466 166890 hypothetical protein hi1684 (cl:conserved hypothetical protein hi1684:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) H64174 H64174 Haemophilus influenzae 727 -11538466 7500960697 hi1684 iron-sulfur cluster binding protein (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1742687 pid:1742695) (le:7283) (re:7864) (di:direct) U32841 U32841 g1574536 Haemophilus influenzae Rd 71421 -11538466 6500734608 gb:d13625_1:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1684 HI1684 Haemophilus influenzae 727 -11538466

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897086	16512	38668	597	198

Description

5000695276 gb:d13625_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1688 HI1688 Haemophilus influenzae 727 -11538467 4000708203 hi1688 (de:hypothetical protein hi1688) (db:swissprot) YDGQ_HAEIN Q57020 HAEMOPHILUS INFLUENZAE 727 -11538467 166892 conserved hypothetical protein hi1688 (cl:conserved hypothetical protein hi1688) (db:pir2.dat) I64174 I64174 Haemophilus influenzae 727 -11538467 7500922313 hi1688 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77179 pid:1787919 percent) (le:12030) (re:12737) (di:direct) U32841 U32841 g1574540 Haemophilus influenzae Rd 71421 -11538467 6500734609 gb:d13625_2:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1688 HI1688 Haemophilus influenzae 727 -11538467

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897101	16513	38669	3684	1228

Description

6500734610 moda:hi1693 lsg locus hypothetical protein:gb:m94855_8:molybdate-binding periplasmic protein precursor (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1693 HI1693 Haemophilus influenzae 727 -11538468 83980 moda:hi1693 (de:molybdate-binding periplasmic protein precursor) (db:swissprot) MODA_HAEIN P45323 HAEMOPHILUS INFLUENZAE 727 -11538468 166965 moda molybdate-binding periplasmic protein:protein hi1693 (cl:molybdate-binding periplasmic protein) (db:pir2.dat) A64175 A64175 Haemophilus influenzae 727 -11538468 7500885749 hi1693 molybdenum abc transporter:periplasmic-binding (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to gb:l34009 sp:p37329 pid:504498) (le:4118) (re:4882) (di:complement) U32842 U32842 g1574546 Haemophilus influenzae Rd 71421 -11538468 5000695277 (de:(hi1693) (pn:molybdate-binding periplasmic protein precursor:lsg locus hypothetical protein:gb:m94855_8) (gn:moda) (gtcfc:13.7:14.1) (ec:) (moda_haein) (keggfc:11.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1693 HI1693 Haemophilus influenzae 727 10026186

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897131	16514	38670	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897135	16515	38671	882	293

Description

5000695278 lsg locus hypothetical protein:gb:m94855_7:molybdenum transport protein mode homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1694 HI1694 Haemophilus influenzae 727 -11538469 83993 mode:hi1694 (de:molybdenum transport protein mode homolog) (db:swissprot) MODE_HAEIN P45324 HAEMOPHILUS INFLUENZAE 727 -11538469 166966 repressor mode homolog hi1694 (cl:repressor protein mode) (db:pir2.dat) B64175 B64175 Haemophilus influenzae 727 -11538469 7500885754 hi1694 molybdenum transport protein mode (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to pid:1002825 sp:p46930 gb:u00096) (le:5020) (re:5787) (di:direct) U32842 U32842 g1574547 Haemophilus influenzae Rd 71421 -11538469 6500734611 lsg locus hypothetical protein:gb:m94855_7:molybdenum transport protein mode homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1694 HI1694 Haemophilus influenzae 727 -11538469

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897155	16516	38672	306	101

Description

GTC ORF with score 117 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897174	16517	38673	351	116

Description

GTC ORF with score 103 to: (sr:lyme disease spirochete) (db:genpept-bct2) (de:borrelia burgdorferi (section 29 of 70) of the complete genome.) (nt:similar to gp:1753229 percent identity: 100.00;) (le:4313) (re:4762) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897185	16518	38674	1050	349

Description

5000695279 gb:m94855_6:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1695 HI1695 Haemophilus influenzae 727 -11538470 166967 hypothetical protein hi1695 lsg locus (db:pir2.dat) C64175 C64175 Haemophilus influenzae 727 -11538470 7500960698 hi1695 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to pid:600434 sp:q46635 percent ident:) (le:5896) (re:6699) (di:complement) U32842 U32842 g1574548 Haemophilus influenzae Rd 71421 -11538470 6500734612 gb:m94855_6:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1695 HI1695 Haemophilus influenzae 727 -11538470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897188	16519	38675	471	156

Description

5000695280 gb:m94855_5:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1696 HI1696 Haemophilus influenzae 727 -11538471 166968 hypothetical protein hi1696 lsg locus (db:pir2.dat) D64175 D64175 Haemophilus influenzae 727 -11538471 7500960699 hi1696 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to pid:1944156 percent ident: 80.82;) (le:6701) (re:7585) (di:complement) U32842 U32842 g1574549 Haemophilus influenzae Rd 71421 -11538471 6500734613 gb:m94855_5:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1696 HI1696 Haemophilus influenzae 727 -11538471

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897189	16520	38676	267	88

Description

5000695281 gb:m94855_4:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1697 HI1697 Haemophilus influenzae 727 -11538472 7500976300 hi1697 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to gb:u05670 percent ident: 28.57;) (le:7597) (re:8370) (di:complement) U32842 U32842 g1574550 Haemophilus influenzae Rd 71421 -11538472 6500734614 gb:m94855_4:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1697 HI1697 Haemophilus influenzae 727 -11538472

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897207	16521	38677	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897208	16522	38678	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897226	16523	38679	438	145

Description

5000695282 gb:m94855_3:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1698 HI1698 Haemophilus influenzae 727 -11538473 166970 hypothetical protein hi1698 lsg locus (db:pir2.dat) F64175 F64175 Haemophilus influenzae 727 -11538473 7500960700 hi1698 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to pid:633695 percent ident: 38.48;) (le:8382) (re:9443) (di:complement) U32842 U32842 g1574551 Haemophilus influenzae Rd 71421 -11538473 6500734615 gb:m94855_3:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1698 HI1698 Haemophilus influenzae 727 -11538473

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897230	16524	38680	567	188

Description

5000695283 gb:m94855_2:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1699 HI1699 Haemophilus influenzae 727 -11538474 166971 hypothetical protein hi1699 lsg locus (db:pir2.dat) G64175 G64175 Haemophilus influenzae 727 -11538474 7500960701 hi1699 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to pid:1546004 percent ident: 29.35;) (le:9445) (re:10359) (di:complement) U32842 U32842 g1574553 Haemophilus influenzae Rd 71421 -11538474 6500734616 gb:m94855_2:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1699 HI1699 Haemophilus influenzae 727 -11538474

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897231	16525	38681	591	196

Description

5000695284 gb:m94855_1:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1700 HI1700 Haemophilus influenzae 727 -11538475 166972 hypothetical protein hi1700 lsg locus (db:pir2.dat) H64175 H64175 Haemophilus influenzae 727 -11538475 7500960702 hi1700 lipopolysaccharide biosynthesis protein (db:genpept-bct1) (de:haemophilus influenzae rd section 157 of 163 of the completegenome.) (nt:similar to gb:ae000666 percent ident: 23.40;) (le:10356) (re:11570) (di:complement) U32842 U32842 g1574552 Haemophilus influenzae Rd 71421 -11538475 6500734617 gb:m94855_1:lsg locus hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1700 HI1700 Haemophilus influenzae 727 -11538475

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897234	16526	38682	546	181

Description

5000695285 gb:u14003_175:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1703 HI1703 Haemophilus influenzae 727 -11538476 113768 hi1703 (de:hypothetical protein hi1703) (db:swissprot) YJGQ_HAEIN P45332 HAEMOPHILUS INFLUENZAE 727 -11538476 166894 hypothetical protein hi1703 (db:pir2.dat) I64175 I64175 Haemophilus influenzae 727 -11538476 7500938029 hi1703 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 158 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p39341 pid:537104 gb:u00096) (le:3521) (re:4597) (di:complement) U32843 U32843 g1574557 Haemophilus influenzae Rd 71421 -11538476 6500734618 gb:u14003_175:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1703 HI1703 Haemophilus influenzae 727 -11538476

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897244	16527	38683	399	132

Description

5000695286 gb:u14003_174:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1704 HI1704 Haemophilus influenzae 727 -11538477 113766 hi1704 (de:hypothetical protein hi1704) (db:swissprot) YJGP_HAEIN P45333 HAEMOPHILUS INFLUENZAE 727 -11538477 166895 hypothetical protein hi1704 (db:pir2.dat) A64176 A64176 Haemophilus influenzae 727 -11538477 7500938027 hi1704 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 158 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p39340 pid:537103 gb:u00096) (le:4581) (re:5699) (di:complement) U32843 U32843 g1574558 Haemophilus influenzae Rd 71421 -11538477 6500734619 gb:u14003_174:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1704 HI1704 Haemophilus influenzae 727 -11538477

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897247	16528	38684	306	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897267	16529	38685	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897270	16530	38686	426	141

Description

5000695287 gb:u14003_76:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1714 HI1714 Haemophilus influenzae 727 -11538478 113700 hi1714 (de:hypothetical protein hi1714) (db:swissprot) YJEQ_HAEIN P45339 HAEMOPHILUS INFLUENZAE 727 -11538478 166898 hypothetical protein hi1714 (cl:conserved hypothetical protein hi1714) (db:pir2.dat) B64176 B64176 Haemophilus influenzae 727 -11538478 7500937970 hi1714 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p39286 pid:537005 gb:u00096) (le:3720) (re:4760) (di:complement) U32844 U32844 g1574569 Haemophilus influenzae Rd 71421 -11538478 6500734620 gb:u14003_76:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1714 HI1714 Haemophilus influenzae 727 -11538478

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897275	16531	38687	411	136

Description

5000695288 hypothetical protein:gb:u14003_77:protein hi1715 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1715 HI1715 Haemophilus influenzae 727 -11538479 113702 orn:hi1715 (ec:3.1.-.-) (de:oligoribonuclease,) (db:swissprot) ORN_HAEIN P45340 HAEMOPHILUS INFLUENZAE 727 -11538479 166899 hypothetical protein hi1715 (db:pir2.dat) C64176 C64176 Haemophilus influenzae 727 -11538479 7500887364 hi1715 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p39287 pid:537006 gb:u00096) (le:4831) (re:5379) (di:direct) U32844 U32844 g1574570 Haemophilus influenzae Rd 71421 -11538479 6500734621 hypothetical protein:gb:u14003_77:protein hi1715 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1715 HI1715 Haemophilus influenzae 727 -11538479

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897278	16532	38688	1311	436

Description

GTC ORF with score 136 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 196 of 400 of the completegenome.) (nt:f313; 100 pct identical to yeic_ecoli sw: p30235) (le:1003) (re:1944) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897279	16533	38689	501	166

Description

5000695289 gb:u09558_1:hypothetical protein:insertion element is1223 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1720 HI1720 Haemophilus influenzae 727 -11538480 7000687883 hi1720 (de:hypothetical protein hi1720) (db:swissprot) YH20_HAEIN Q57066 HAEMOPHILUS INFLUENZAE 727 -11538480 166902 hypothetical protein hi1720 (db:pir2.dat) D64176 D64176 Haemophilus influenzae 727 -11538480 7500936695 hi1720 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to gb:u09558 pid:495495 percent ident:) (le:61) (re:627) (di:direct) U32845 U32845 g1574576 Haemophilus influenzae Rd 71421 -11538480 6500734622 gb:u09558_1:hypothetical protein:insertion element is1223 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1720 HI1720 Haemophilus influenzae 727 -11538480

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897283	16534	38690	243	80

Description

GTC ORF with score 103 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t24c12.) (nt:coded for by c. elegans cdna yk41a1.3; coded for by) (le:10021:10474:10788) (re:10249:10732:10902) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897284	16535	38691	183	60

Description

5000695290 sp:p19769:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1721 HI1721 Haemophilus influenzae 727 -11538481 5500686601 hi1721 (de:hypothetical transposase-like protein hi1721) (db:swissprot) YH21_HAEIN O05086 HAEMOPHILUS INFLUENZAE 727 -11538481 166903 hypothetical protein hi1721 (db:pir2.dat) E64176 E64176 Haemophilus influenzae 727 -11538481 7500936698 hi1721 transposase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to sp:p19769 gb:x07037 pid:581111) (le:795) (re:1445) (di:direct) U32845 U32845 g1574577 Haemophilus influenzae Rd 71421 -11538481 6500734623 sp:p19769:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1721 HI1721 Haemophilus influenzae 727 -11538481

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897285	16536	38692	291	96

Description

GTC ORF with score 151 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t24c12.) (nt:coded for by c. elegans cdna yk41a1.3; coded for by) (le:10021:10474:10788) (re:10249:10732:10902) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897291	16537	38693	243	80

Description

5000695291 gb:d26562_45:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1723 HI1723 Haemophilus influenzae 727 -11538482 109660 hi1723 (de:hypothetical protein hi1723) (db:swissprot) YADR_HAEIN P45344 HAEMOPHILUS INFLUENZAE 727 -11538482 166904 hypothetical protein hi1723 (cl:conserved hypothetical protein hi0376) (db:pir2.dat) F64176 F64176 Haemophilus influenzae 727 -11538482 7500896075 hi1723 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to gb:d26562 sp:p37026 pid:473815 gb:u00096) (le:2450) (re:2794) (di:direct) U32845 U32845 g1574579 Haemophilus influenzae Rd 71421 -11538482 6500734624 gb:d26562_45:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1723 HI1723 Haemophilus influenzae 727 -11538482

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897293	16538	38694	393	130

Description

6500734625 accc:hp0370 biotin carboxylase (gtcfc:1.10:1.8:3.1:3.2:8.1) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0370 HP0370 Helicobacter pylori 210 -11538483 7000689228 biotin carboxylase (cl:biotin carboxylase:biotin carboxylase homology) (db:pir2.dat) B64566 B64566 Helicobacter pylori 210 -11538483 7500954521 hp0370 biotin carboxylase accc (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:similar to egad:17503 percent identity: 52.13;) (le:8630) (re:10006) (di:complement) HPAE000553 AE000553 g2313468 Helicobacter pylori 210 -11538483 7502852321 hp0370 biotin carboxylase accc (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:similar to egad:17503 percent identity: 52.13;) (le:8630) (re:10006) (di:complement) HPAE000553 AE000553 g2313468 Helicobacter pylori 26695 85962 -11538483

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897302	16539	38695	600	199

Description

6500734626 acca:hp0557 acetyl-coenzyme a carboxylase (gtcfc:1.10:1.8:3.1:3.2:8.1) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0557 HP0557 Helicobacter pylori 210 -11538484 7500876287 acca:hp0557 (sr:,campylobacter pylori) (ec:6.4.1.2) (de:(ec 6.4.1.2)) (db:swissprot) ACCA_HELPY O25283 HELICOBACTER PYLORI 210 -11538484 7000689229 acca acetyl-coa carboxylase::carboxyltransferase alpha chain (cl:acetyl-coa carboxylase, carboxyltransferase alpha chain) (ec:6.4.1.2) (db:pir2.dat) E64589 E64589 Helicobacter pylori 210 -11538484 7500876289 hp0557 acetyl-coenzyme a carboxylase acca (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:similar to egad:21130 percent identity: 50.33;) (le:973) (re:1911) (di:complement) HPAE000570 AE000570 g2313675 Helicobacter pylori 210 -11538484 7502852322 hp0557 acetyl-coenzyme a carboxylase acca (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:similar to egad:21130 percent identity: 50.33;) (le:973) (re:1911) (di:complement) HPAE000570 AE000570 g2313675 Helicobacter pylori 26695 85962 -11538484

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897304	16540	38696	702	233

Description

6500734627 fada:hp0690 acetyl coenzyme a acetyltransferase thiolase:acetyl coenzyme a acetyltransferase:thiolase (gtcfc:1.10:1.11:1.8:3.1:3.2:3.3:5.14:5.9:8.1) (ec:2.3.1.9) (keggfc:1.8:1.10:1.11:3.1:3.2:3.3:5.9:5.14) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0690 HP0690 Helicobacter pylori 210 -11538485 7000689068 acetyl coenzyme a acetyltransferase (cl:acetyl-coa acetyltransferase) (db:pir2.dat) B64606 B64606 Helicobacter pylori 210 -11538485 7500953989 hp0690 acetyl coenzyme a acetyltransferase thiolase (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:similar to egad:27938 percent identity: 52.04;) (le:3319) (re:4494) (di:direct) HPAE000582 AE000582 g2313814 Helicobacter pylori 210 -11538485 7502852323 hp0690 acetyl coenzyme a acetyltransferase thiolase (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:similar to egad:27938 percent identity: 52.04;) (le:3319) (re:4494) (di:direct) HPAE000582 AE000582 g2313814 Helicobacter pylori 26695 85962 -11538485

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897320	16541	38697	876	291

Description

6500734628 accd:hp0950 acetyl-coa carboxylase beta subunit (gtcfc:1.10:1.8:3.1:3.2:8.1) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0950 HP0950 Helicobacter pylori 210 -11538486 7000689607 acetyl-coa carboxylase beta subunit (cl:acetyl-coa carboxylase, carboxyltransferase beta chain) (db:pir2.dat) F64638 F64638 Helicobacter pylori 210 -11538486 7500954528 hp0950 acetyl-coa carboxylase beta subunit accd (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:28260 percent identity: 49.42;) (le:4431) (re:5300) (di:complement) HPAE000604 AE000604 g2314089 Helicobacter pylori 210 -11538486 7502852324 hp0950 acetyl-coa carboxylase beta subunit accd (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:28260 percent identity: 49.42;) (le:4431) (re:5300) (di:complement) HPAE000604 AE000604 g2314089 Helicobacter pylori 26695 85962 -11538486

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897321	16542	38698	513	170

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897331	16543	38699	402	133

Description

6500734629 acoe:hp1045 acetyl-coa synthetase (gtcfc:1.10:1.8:2.5:3.1:3.2:8.1) (ec:6.2.1.1) (keggfc:1.8:1.10:2.4) (tigrfc:7.1) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:energy metabolism-reductive ca... HP1045 HP1045 Helicobacter pylori 210 -11538487 7000689221 acetyl-coa synthetase (cl:acetate--coa ligase:acetate--coa ligase homology) (db:pir2.dat) E64650 E64650 Helicobacter pylori 210 -11538487 7500954491 hp1045 acetyl-coa synthetase acoe (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to egad:20343 percent identity: 52.32;) (le:6257) (re:8245) (di:direct) HPAE000612 AE000612 g2314192 Helicobacter pylori 210 -11538487 7502852325 hp1045 acetyl-coa synthetase acoe (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to egad:20343 percent identity: 52.32;) (le:6257) (re:8245) (di:direct) HPAE000612 AE000612 g2314192 Helicobacter pylori 26695 85962 -11538487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897343	16544	38700	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897346	16545	38701	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897364	16546	38702	492	163

Description

6500734630 eno:hp0154 enolase:2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase (gtcfc:1.1) (ec:4.2.1.11) (keggfc:1.1) (tigrfc:6.9) (db:gtc-helicobacter pylori) HP0154 HP0154 Helicobacter pylori 210 -11538488 70201 eno:hp0154 (sr:,campylobacter pylori) (ec:4.2.1.11) (de:glycerate hydro-lyase)) (db:swissprot) ENO_HELPY P48285 HELICOBACTER PYLORI 210 -11538488 7000685161 phosphopyruvate hydratase::enolase (cl:enolase) (ec:4.2.1.11) (db:pir2.dat) S58684 B64539 Helicobacter pylori 210 -11538488 7500881038 hp0154 enolase eno (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to egad:19397 percent identity: 56.90;) (le:7764) (re:9044) (di:direct) HPAE000536 AE000536 g2313236 Helicobacter pylori 210 -11538488 7502852326 hp0154 enolase eno (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to egad:19397 percent identity: 56.90;) (le:7764) (re:9044) (di:direct) HPAE000536 AE000536 g2313236 Helicobacter pylori 26695 85962 -11538488

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897365	16547	38703	507	168

Description

6500734631 tsr:hp0176 fructose-bisphosphate aldolase (gtcfc:1.1:1.3:1.5:2.4) (ec:4.1.2.13) (keggfc:1.1:1.3:1.5:2.3) (tigrfc:6.9) (db:gtc-helicobacter pylori) HP0176 HP0176 Helicobacter pylori 210 -11538489 5500684858 fbaa:fba:hp0176 (sr:,campylobacter pylori) (ec:4.1.2.13) (de:fructose-bisphosphate aldolase,) (db:swissprot) ALF_HELPY P56109 HELICOBACTER PYLORI 210 -11538489 7000684556 fructose-bisphosphate aldolase (cl:fructose-bisphosphate aldolase ii) (db:pir2.dat) H64541 H64541 Helicobacter pylori 210 -11538489 7500876747 hp0176 fructose-bisphosphate aldolase tsr (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:similar to egad:19200 percent identity: 45.96;) (le:1162) (re:2085) (di:direct) HPAE000538 AE000538 g2313265 Helicobacter pylori 210 -11538489 7502852327 hp0176 fructose-bisphosphate aldolase tsr (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:similar to egad:19200 percent identity: 45.96;) (le:1162) (re:2085) (di:direct) HPAE000538 AE000538 g2313265 Helicobacter pylori 26695 85962 -11538489

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897382	16548	38704	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897401	16549	38705	1725	575

Description

6500734632 tpi:hp0194 triosephosphate isomerase (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (keggfc:1.1:1.5:2.3:8.1) (tigrfc:6.9) (db:gtc-helicobacter pylori) HP0194 HP0194 Helicobacter pylori 210 -11538490 5500686074 tpia:tpi:hp0194 (sr:,campylobacter pylori) (ec:5.3.1.1) (de:triosephosphate isomerase, (tim)) (db:swissprot) TPIS_HELPY P56076 HELICOBACTER PYLORI 210 -11538490 7000686820 triosephosphate isomerase (db:pir2.dat) B64544 B64544 Helicobacter pylori 210 -11538490 7500893312 hp0194 triosephosphate isomerase tpi (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:similar to egad:40397 percent identity: 34.47;) (le:8010) (re:8714) (di:direct) HPAE000539 AE000539 g2313281 Helicobacter pylori 210 -11538490 7502852328 hp0194 triosephosphate isomerase tpi (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:similar to egad:40397 percent identity: 34.47;) (le:8010) (re:8714) (di:direct) HPAE000539 AE000539 g2313281 Helicobacter pylori 26695 85962 -11538490

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897419	16550	38706	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897421	16551	38707	618	205

Description

6500734633 gap:hp0921 glyceraldehyde-3-phosphate dehydrogenase (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (tigrfc:6.9) (db:gtc-helicobacter pylori) HP0921 HP0921 Helicobacter pylori 210 -11538491 5500685249 gapa:gap:hp0921 (sr:,campylobacter pylori) (ec:1.2.1.12) (de:glyceraldehyde 3-phosphate dehydrogenase, (gapdh)) (db:swissprot) G3P_HELPY P55971 HELICOBACTER PYLORI 210 -11538491 7000685336 glyceraldehyde-3-phosphate dehydrogenase (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir2.dat) A64635 A64635 Helicobacter pylori 210 -11538491 7500881971 hp0921 glyceraldehyde-3-phosphate dehydrogenase gap (db:genpept-bct1) (de:helicobacter pylori section 79 of 134 of the complete genome.) (nt:similar to egad:13795 percent identity: 46.48;) (le:9597) (re:10595) (di:direct) HPAE000601 AE000601 g2314056 Helicobacter pylori 210 -11538491 7502852329 hp0921 glyceraldehyde-3-phosphate dehydrogenase gap (db:genpept) (de:helicobacter pylori 26695 section 79 of 134 of the complete genome.) (nt:similar to egad:13795 percent identity: 46.48;) (le:9597) (re:10595) (di:direct) HPAE000601 AE000601 g2314056 Helicobacter pylori 26695 85962 -11538491

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897424	16552	38708	1419	472

Description

6500734634 pgm:hp0974 phosphoglycerate mutase (gtcfc:1.1) (ec:5.4.2.1) (keggfc:1.1) (tigrfc:6.9) (db:gtc-helicobacter pylori) HP0974 HP0974 Helicobacter pylori 210 -11538492 7000686154 pgm:hp0974 (sr:,campylobacter pylori) (ec:5.4.2.1) (de:(ec 5.4.2.1) (phosphoglyceromutase) (bpg-independent pgam)) (db:swissprot) PMGI_HELPY P56196 HELICOBACTER PYLORI 210 -11538492 7000686155 probable phosphoglycerate mutase::2:3-bisphosphoglycerate-independent:phosphoglycerate phosphomutase:phosphoglyceromutase (cl:phosphoglycerate mutase, 2, 3-bisphosphoglycerate-independent) (ec:5.4.2.1) (db:pir2.dat) F64641 F64641 Helicobacter pylori 210 -11538492 7500888192 hp0974 phosphoglycerate mutase pgm (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:similar to egad:31178 percent identity: 44.62;) (le:1160) (re:2635) (di:direct) HPAE000606 AE000606 g2314116 Helicobacter pylori 210 -11538492 7502852330 hp0974 phosphoglycerate mutase pgm (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:similar to egad:31178 percent identity: 44.62;) (le:1160) (re:2635) (di:direct) HPAE000606 AE000606 g2314116 Helicobacter pylori 26695 85962 -11538492

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897426	16553	38709	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897427	16554	38710	771	256

Description

6500734635 glucokinase glk:glucokinase:glk (gtcfc:1.1:1.3:1.5:1.6:7.2) (ec:2.7.1.2) (keggfc:1.1:1.3:1.5:1.6:7.1) (tigrfc:6.9) (db:gtc-helicobacter pylori) HP1103 HP1103 Helicobacter pylori 210 -11538493 7000689960 glucokinase (cl:glucokinase) (db:pir2.dat) G64657 G64657 Helicobacter pylori 210 -11538493 7500958748 hp1103 glucokinase glk (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to egad:30337 percent identity: 41.51;) (le:10640) (re:11650) (di:direct) HPAE000616 AE000616 g2314252 Helicobacter pylori 210 -11538493 7502852331 hp1103 glucokinase glk (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to egad:30337 percent identity: 41.51;) (le:10640) (re:11650) (di:direct) HPAE000616 AE000616 g2314252 Helicobacter pylori 26695 85962 -11538493

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897428	16555	38711	204	67

Description

6500734636 pgi:hp1166 glucose-6-phosphate isomerase (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (keggfc:1.1:1.3:7.1) (tigrfc:6.9) (db:gtc-helicobacter pylori) HP1166 HP1166 Helicobacter pylori 210 -11538494 7500882019 pgi:hp1166 (sr:,campylobacter pylori) (ec:5.3.1.9) (de:isomerase) (pgi) (phosphohexose isomerase) (phi)) (db:swissprot) G6PI_HELPY O25781 HELICOBACTER PYLORI 210 -11538494 7000689196 glucose-6-phosphate isomerase (cl:glucose-6-phosphate isomerase) (ec:5.3.1.9) (db:pir2.dat) F64665 F64665 Helicobacter pylori 210 -11538494 7500882021 hp1166 glucose-6-phosphate isomerase pgi (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:similar to egad:7650 percent identity: 53.32;) (le:4266) (re:5903) (di:direct) HPAE000622 AE000622 g2314323 Helicobacter pylori 210 -11538494 7502852332 hp1166 glucose-6-phosphate isomerase pgi (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:similar to egad:7650 percent identity: 53.32;) (le:4266) (re:5903) (di:direct) HPAE000622 AE000622 g2314323 Helicobacter pylori 26695 85962 -11538494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897434	16556	38712	282	93

Description

6500734637 phosphoglycerate kinase (gtcfc:1.1:2.4) (ec:2.7.2.3) (keggfc:1.1:2.3) (tigrfc:6.8) (db:gtc-helicobacter pylori) HP1345 HP1345 Helicobacter pylori 210 -11538495 5500685726 pgk:hp1345 (sr:,campylobacter pylori) (ec:2.7.2.3) (de:phosphoglycerate kinase,) (db:swissprot) PGK_HELPY P56154 HELICOBACTER PYLORI 210 -11538495 7000686125 probable phosphoglycerate kinase (cl:phosphoglycerate kinase) (ec:2.7.2.3) (db:pir2.dat) A64688 A64688 Helicobacter pylori 210 -11538495 7500887933 hp1345 phosphoglycerate kinase (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:25924 percent identity: 47.31;) (le:11169) (re:12377) (di:complement) HPAE000635 AE000635 g2314511 Helicobacter pylori 210 -11538495 7502852333 hp1345 phosphoglycerate kinase (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:25924 percent identity: 47.31;) (le:11169) (re:12377) (di:complement) HPAE000635 AE000635 g2314511 Helicobacter pylori 26695 85962 -11538495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897436	16557	38713	900	299

Description

6500734638 gap:hp1346 glyceraldehyde-3-phosphate dehydrogenase (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (tigrfc:6.9) (db:gtc-helicobacter pylori) HP1346 HP1346 Helicobacter pylori 210 -11538496 7000689970 glyceraldehyde-3-phosphate dehydrogenase (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir2.dat) B64688 B64688 Helicobacter pylori 210 -11538496 7500958755 hp1346 glyceraldehyde-3-phosphate dehydrogenase gap (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:13804 percent identity: 46.69;) (le:12393) (re:13385) (di:complement) HPAE000635 AE000635 g2314512 Helicobacter pylori 210 -11538496 7502852334 hp1346 glyceraldehyde-3-phosphate dehydrogenase gap (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:13804 percent identity: 46.69;) (le:12393) (re:13385) (di:complement) HPAE000635 AE000635 g2314512 Helicobacter pylori 26695 85962 -11538496

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897459	16558	38714	282	93

Description

6500734639 fructose-1:6-bisphosphatase (gtcfc:1.1:1.3:1.5:2.4) (ec:3.1.3.11) (keggfc:1.1:1.3:1.5:2.3) (tigrfc:6.8) (db:gtc-helicobacter pylori) HP1385 HP1385 Helicobacter pylori 210 -11538497 7502852335 fbp:hp1385 (sr:,campylobacter pylori) (ec:3.1.3.11) (de:1-phosphohydrolase) (fbpase)) (db:swissprot) F16P_HELPY O25936 HELICOBACTER PYLORI 210 -11538497 7000689953 fructose-1:6-bisphosphatase (db:pir2.dat) A64693 A64693 Helicobacter pylori 210 -11538497 7500958741 hp1385 fructose-1:6-bisphosphatase (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:similar to sp:q05079 percent identity: 36.44;) (le:6376) (re:7248) (di:complement) HPAE000638 AE000638 g2314552 Helicobacter pylori 210 -11538497 7502852336 hp1385 fructose-1:6-bisphosphatase (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:similar to sp:q05079 percent identity: 36.44;) (le:6376) (re:7248) (di:complement) HPAE000638 AE000638 g2314552 Helicobacter pylori 26695 85962 -11538497

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897460	16559	38715	414	137

Description

6500734640 ppsa:hp0121 phosphoenolpyruvate synthase (gtcfc:1.1:1.8:2.5) (ec:2.7.9.2) (keggfc:1.8:2.4) (tigrfc:6.8) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-glycolysis--gluconeogenesis:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:energy metabolism-reductive carboxylate cy... HP0121 HP0121 Helicobacter pylori 210 -11538498 5500685749 ppsa:hp0121 (sr:,campylobacter pylori) (ec:2.7.9.2) (de:(pep synthase)) (db:swissprot) PPSA_HELPY P56070 HELICOBACTER PYLORI 210 -11538498 7000686168 phosphoenolpyruvate synthase (db:pir2.dat) A64535 A64535 Helicobacter pylori 210 -11538498 7500888378 hp0121 phosphoenolpyruvate synthase ppsa (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:similar to egad:21248 percent identity: 52.41;) (le:1466) (re:3904) (di:complement) HPAE000534 AE000534 g2313206 Helicobacter pylori 210 -11538498 7502852337 hp0121 phosphoenolpyruvate synthase ppsa (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:similar to egad:21248 percent identity: 52.41;) (le:1466) (re:3904) (di:complement) HPAE000534 AE000534 g2313206 Helicobacter pylori 26695 85962 -11538498

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897461	16560	38716	1440	479

Description

6500734641 cute:hp0180 apolipoprotein n-acyltransferase (gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1:11.1) (ec:2.3.1.-) (keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0180 HP0180 Helicobacter pylori 210 -11538499 7000689641 apolipoprotein n-acyltransferase (db:pir2.dat) D64542 D64542 Helicobacter pylori 210 -11538499 7500958458 hp0180 apolipoprotein n-acyltransferase cute (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:similar to egad:28933 percent identity: 28.03;) (le:4843) (re:6120) (di:complement) HPAE000538 AE000538 g2313269 Helicobacter pylori 210 -11538499 7502852338 hp0180 apolipoprotein n-acyltransferase cute (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:similar to egad:28933 percent identity: 28.03;) (le:4843) (re:6120) (di:complement) HPAE000538 AE000538 g2313269 Helicobacter pylori 26695 85962 -11538499

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897474	16561	38717	513	170

Description

6500734642 frdb:hp0191 fumarate reductase:iron-sulfur subunit (gtcfc:1.11:1.2:2.1:2.5:2.8) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.3) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-oxidative phosphoryla... HP0191 HP0191 Helicobacter pylori 210 -11538500 5500685231 frdb:hp0191 (sr:,campylobacter pylori) (ec:1.3.99.1) (de:fumarate reductase iron-sulfur protein,) (db:swissprot) FRDB_HELPY O06914 HELICOBACTER PYLORI 210 -11538500 7000685318 fumarate reductase:iron-sulfur subunit (cl:fumarate reductase iron-sulfur protein:ferredoxin 2(4fe-4s) homology:ferredoxin (2fe-2s) homology) (db:pir2.dat) G64543 G64543 Helicobacter pylori 210 -11538500 7500881742 hp0191 fumarate reductase:iron-sulfur subunit frdb (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:similar to egad:6731 percent identity: 70.76;) (le:4144) (re:4881) (di:complement) HPAE000539 AE000539 g2313278 Helicobacter pylori 210 -11538500 7502852339 hp0191 fumarate reductase:iron-sulfur subunit frdb (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:similar to egad:6731 percent identity: 70.76;) (le:4144) (re:4881) (di:complement) HPAE000539 AE000539 g2313278 Helicobacter pylori 26695 85962 -11538500

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897476	16562	38718	414	137

Description

6500734643 frda:hp0192 fumarate reductase:flavoprotein subunit (gtcfc:2.8:9.5) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.3) (db:gtc-helicobacter pylori) (keggfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-butanoate metabolism:energy metabolism-oxidative phosphorylation:energy ... HP0192 HP0192 Helicobacter pylori 210 -11538501 5500685230 frda:hp0192 (sr:,campylobacter pylori) (ec:1.3.99.1) (de:fumarate reductase flavoprotein subunit,) (db:swissprot) FRDA_HELPY O06913 HELICOBACTER PYLORI 210 -11538501 7000685317 fumarate reductase:flavoprotein subunit (cl:fumarate reductase flavoprotein:3-oxosteroid 1-dehydrogenase homology:fumarate reductase flavoprotein homology) (db:pir2.dat) H64543 H64543 Helicobacter pylori 210 -11538501 7500881740 hp0192 fumarate reductase:flavoprotein subunit frda (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:similar to egad:7943 percent identity: 69.41;) (le:4874) (re:7018) (di:complement) HPAE000539 AE000539 g2313279 Helicobacter pylori 210 -11538501 7502852340 hp0192 fumarate reductase:flavoprotein subunit frda (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:similar to egad:7943 percent identity: 69.41;) (le:4874) (re:7018) (di:complement) HPAE000539 AE000539 g2313279 Helicobacter pylori 26695 85962 -11538501

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897488	16563	38719	606	201

Description

6500734644 lpxd:hp0196 udp-3-0-hydroxymyristoyl glucosamine n-acyltransferase:udp-3-0-:3-hydroxymyristoyl glucosaminen-acyltransferase (gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1:11.3) (ec:2.3.1.-) (keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0196 HP0196 Helicobacter pylori 210 -11538502 7000690777 udp-3-o-3-hydroxymyristoyl glucosamine n-acyltransferase,) (cl:udp-3-o-(3-hydroxymyristoyl) glucosamine n-acyltransferase) (ec:2.3.1.-) (db:pir2.dat) D64544 D64544 Helicobacter pylori 210 -11538502 7500959541 hp0196 udp-3-0-3-hydroxymyristoyl glucosamine (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:similar to egad:23061 percent identity: 39.46;) (le:9561) (re:10571) (di:direct) HPAE000539 AE000539 g2313283 Helicobacter pylori 210 -11538502 7502852341 hp0196 udp-3-0-3-hydroxymyristoyl glucosamine (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:similar to egad:23061 percent identity: 39.46;) (le:9561) (re:10571) (di:direct) HPAE000539 AE000539 g2313283 Helicobacter pylori 26695 85962 -11538502

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897493	16564	38720	939	312

Description

GTC ORF with score 189 to: (fn:essential for slug migration) (db:genpept-inv) (de:dictyostelium discoideum miga (miga) gene, complete cds.) (nt:n-terminus of this protein is similar to other btb) (le:884:2998) (re:2899:3423) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897498	16565	38721	657	219

Description

6500734645 fabz:hp1376 3r-hydroxymyristoyl-acyl carrier protein dehydratase:3r-hydroxymyristoyl-:acyl carrier proteindehydratase (gtcfc:1.11:1.5:3.1:3.2:3.5:5.12:5.13:5.15:6.5:8.1) (ec:4.2.1.-) (keggfc:1.5:1.11:3.5:5.12:5.13:5.15:6.5) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP1376 HP1376 Helicobacter pylori 210 -11538503 7000689585 3r -hydroxymyristoyl-acyl carrier protein dehydratase,) (cl:(3r)-hydroxymyristoyl-(acyl carrier protein) dehydratase) (ec:4.2.1.-) (db:pir2.dat) H64691 H64691 Helicobacter pylori 210 -11538503 7500958406 hp1376 3r -hydroxymyristoyl-acyl carrier protein (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:8948 percent identity: 47.41;) (le:12629) (re:13108) (di:complement) HPAE000637 AE000637 g2314546 Helicobacter pylori 210 -11538503 7502852342 hp1376 3r -hydroxymyristoyl-acyl carrier protein (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:8948 percent identity: 47.41;) (le:12629) (re:13108) (di:complement) HPAE000637 AE000637 g2314546 Helicobacter pylori 26695 85962 -11538503

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897504	16566	38722	750	249

Description

6500734646 glta:hp0026 citrate synthase glta:citrate synthase (gtcfc:1.2:1.9) (ec:4.1.3.7) (keggfc:1.2:1.9) (tigrfc:6.12) (db:gtc-helicobacter pylori) HP0026 HP0026 Helicobacter pylori 210 -11538504 5500684997 glta:hp0026 (sr:,campylobacter pylori) (ec:4.1.3.7) (de:citrate synthase,) (db:swissprot) CISY_HELPY P56062 HELICOBACTER PYLORI 210 -11538504 7000684823 citrate synthase (cl:citrate (si)-synthase) (db:pir2.dat) B64523 B64523 Helicobacter pylori 210 -11538504 7500878760 hp0026 citrate synthase glta (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to egad:10463 percent identity: 47.78;) (le:2949) (re:4229) (di:complement) HPAE000525 AE000525 g2313103 Helicobacter pylori 210 -11538504 7502852343 hp0026 citrate synthase glta (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to egad:10463 percent identity: 47.78;) (le:2949) (re:4229) (di:complement) HPAE000525 AE000525 g2313103 Helicobacter pylori 26695 85962 -11538504

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897514	16567	38723	378	125

Description

6500734647 icd:hp0027 isocitrate dehydrogenase (gtcfc:1.2:2.5:6.16) (ec:1.1.1.42) (keggfc:1.2:2.4:6.9) (tigrfc:6.12) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation):metabolism of other amino acids-glu... HP0027 HP0027 Helicobacter pylori 210 -11538505 5500685413 icd:hp0027 (sr:,campylobacter pylori) (ec:1.1.1.42) (de:decarboxylase) (idh) (nadp+-specific icdh) (idp)) (db:swissprot) IDH_HELPY P56063 HELICOBACTER PYLORI 210 -11538505 7000685608 icd isocitrate dehydrogenase nadp+::oxalosuccinate decarboxylase (cl:isocitrate dehydrogenase (nadp)) (ec:1.1.1.42) (db:pir2.dat) C64523 C64523 Helicobacter pylori 210 -11538505 7500883826 hp0027 isocitrate dehydrogenase icd (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to egad:14655 percent identity: 70.73;) (le:4428) (re:5705) (di:direct) HPAE000525 AE000525 g2313104 Helicobacter pylori 210 -11538505 7502852344 hp0027 isocitrate dehydrogenase icd (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to egad:14655 percent identity: 70.73;) (le:4428) (re:5705) (di:direct) HPAE000525 AE000525 g2313104 Helicobacter pylori 26695 85962 -11538505

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897530	16568	38724	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897559	16569	38725	855	284

Description

6500734648 fumc:hp1325 fumarase fumc:fumarase (gtcfc:1.2:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (tigrfc:6.12) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation)) (keggfc:carbohydrate metabolism-citrate cycl... HP1325 HP1325 Helicobacter pylori 210 -11538506 7000689188 fumarate hydratase (cl:fumarate hydratase) (ec:4.2.1.2) (db:pir2.dat) E64685 E64685 Helicobacter pylori 210 -11538506 7500954411 hp1325 fumarase fumc (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:similar to egad:8789 percent identity: 63.68;) (le:2949) (re:4340) (di:complement) HPAE000634 AE000634 g2314492 Helicobacter pylori 210 -11538506 7502852345 hp1325 fumarase fumc (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:similar to egad:8789 percent identity: 63.68;) (le:2949) (re:4340) (di:complement) HPAE000634 AE000634 g2314492 Helicobacter pylori 26695 85962 -11538506

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897560	16570	38726	261	86

Description

6500734649 glcd:hp0509 glycolate oxidase subunit (gtcfc:1.2) (keggfc:14.2) (tigrfc:6.12) (db:gtc-helicobacter pylori) HP0509 HP0509 Helicobacter pylori 210 -11538507 7000689974 glycolate oxidase subunit (cl:glycolate oxidase chain glcd) (db:pir2.dat) E64583 E64583 Helicobacter pylori 210 -11538507 7500958758 hp0509 glycolate oxidase subunit glcd (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:similar to gp:1763300 percent identity: 98.01;) (le:4980) (re:6359) (di:direct) HPAE000565 AE000565 g2313619 Helicobacter pylori 210 -11538507 7502852346 hp0509 glycolate oxidase subunit glcd (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:similar to gp:1763300 percent identity: 98.01;) (le:4980) (re:6359) (di:direct) HPAE000565 AE000565 g2313619 Helicobacter pylori 26695 85962 -11538507

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897576	16571	38727	2691	896

Description

6500734650 acnb:hp0779 aconitase b acnb:aconitase b (gtcfc:1.2) (keggfc:14.2) (tigrfc:6.12) (db:gtc-helicobacter pylori) HP0779 HP0779 Helicobacter pylori 210 -11538508 7500876328 acnb:hp0779 (sr:,campylobacter pylori) (ec:4.2.1.3) (de:(aconitase 2)) (db:swissprot) ACO2_HELPY P56418 HELICOBACTER PYLORI 210 -11538508 7000689608 acnb aconitate hydratase:2:aconitase b (ec:4.2.1.3) (db:pir2.dat) C64617 C64617 Helicobacter pylori 210 -11538508 7500876330 hp0779 aconitase b acnb (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:similar to egad:19491 percent identity: 64.01;) (le:895) (re:3456) (di:direct) HPAE000590 AE000590 g2313908 Helicobacter pylori 210 -11538508 7502852347 hp0779 aconitase b acnb (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:similar to egad:19491 percent identity: 64.01;) (le:895) (re:3456) (di:direct) HPAE000590 AE000590 g2313908 Helicobacter pylori 26695 85962 -11538508

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897578	16572	38728	582	193

Description

6500734651 prsa:hp0742 phosphoribosylpyrophosphate synthetase (gtcfc:1.3:4.1) (ec:2.7.6.1) (keggfc:1.3:4.1) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP0742 HP0742 Helicobacter pylori 210 -11538509 5500685464 prsa:hp0742 (sr:,campylobacter pylori) (ec:2.7.6.1) (de:pyrophosphate synthetase)) (db:swissprot) KPRS_HELPY P56184 HELICOBACTER PYLORI 210 -11538509 7000685701 prsa ribose-phosphate pyrophosphokinase::phosphoribosylpyrophosphate synthetase:phosphoribosylpyrophosphate synthetase (cl:ribose-phosphate pyrophosphokinase catalytic chain) (sr:strain 26695, , strain 26695) (sr:strain 26695,) (ec:2.7.6.1) (db:pir2.dat) F64612 F64612 Helicobacter pylori 210 -11538509 7500884707 hp0742 phosphoribosylpyrophosphate synthetase prsa (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:similar to egad:28600 percent identity: 56.55;) (le:63) (re:1019) (di:direct) HPAE000587 AE000587 g2313870 Helicobacter pylori 210 -11538509 7502852348 hp0742 phosphoribosylpyrophosphate synthetase prsa (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:similar to egad:28600 percent identity: 56.55;) (le:63) (re:1019) (di:direct) HPAE000587 AE000587 g2313870 Helicobacter pylori 26695 85962 -11538509

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897596	16573	38729	891	296

Description

6500734652 tkta:hp1088 transketolase a tkta:transketolase a (gtcfc:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (tigrfc:6.10) (db:gtc-helicobacter pylori) HP1088 HP1088 Helicobacter pylori 210 -11538510 7000690745 transketolase a (cl:transketolase:thiamine pyrophosphate-binding domain homology) (db:pir2.dat) H64655 H64655 Helicobacter pylori 210 -11538510 7500959510 hp1088 transketolase a tkta (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:similar to egad:28045 percent identity: 46.74;) (le:7784) (re:9709) (di:direct) HPAE000615 AE000615 g2314236 Helicobacter pylori 210 -11538510 7502852349 hp1088 transketolase a tkta (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:similar to egad:28045 percent identity: 46.74;) (le:7784) (re:9709) (di:direct) HPAE000615 AE000615 g2314236 Helicobacter pylori 26695 85962 -11538510

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897598	16574	38730	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897604	16575	38731	1260	419

Description

6500734653 g6pd:hp1101 glucose-6-phosphate dehydrogenase (gtcfc:1.3:6.16) (ec:1.1.1.49) (keggfc:1.3:6.9) (tigrfc:6.10) (db:gtc-helicobacter pylori) HP1101 HP1101 Helicobacter pylori 210 -11538511 5500685253 zwf:hp1101 (sr:,campylobacter pylori) (ec:1.1.1.49) (de:glucose-6-phosphate 1-dehydrogenase, (g6pd)) (db:swissprot) G6PD_HELPY P56110 HELICOBACTER PYLORI 210 -11538511 7000685339 probable glucose-6-phosphate 1-dehydrogenase (ec:1.1.1.49) (db:pir2.dat) E64657 E64657 Helicobacter pylori 210 -11538511 7500882003 hp1101 glucose-6-phosphate dehydrogenase g6pd (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to egad:13828 percent identity: 36.74;) (le:8682) (re:9959) (di:direct) HPAE000616 AE000616 g2314250 Helicobacter pylori 210 -11538511 7502852350 hp1101 glucose-6-phosphate dehydrogenase g6pd (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to egad:13828 percent identity: 36.74;) (le:8682) (re:9959) (di:direct) HPAE000616 AE000616 g2314250 Helicobacter pylori 26695 85962 -11538511

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897610	16576	38732	1197	398

Description

6500734654 devb:hp1102 glucose-6-phosphate 1-dehydrogenase (gtcfc:1.3:6.16) (ec:1.1.1.49) (keggfc:1.3:6.9) (tigrfc:6.10) (db:gtc-helicobacter pylori) HP1102 HP1102 Helicobacter pylori 210 -11538512 7000689962 probable glucose-6-phosphate 1-dehydrogenase (ec:1.1.1.49) (db:pir2.dat) F64657 F64657 Helicobacter pylori 210 -11538512 7500958749 hp1102 glucose-6-phosphate 1-dehydrogenase devb (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to egad:30065 percent identity: 29.21;) (le:9970) (re:10653) (di:direct) HPAE000616 AE000616 g2314251 Helicobacter pylori 210 -11538512 7502852351 hp1102 glucose-6-phosphate 1-dehydrogenase devb (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to egad:30065 percent identity: 29.21;) (le:9970) (re:10653) (di:direct) HPAE000616 AE000616 g2314251 Helicobacter pylori 26695 85962 -11538512

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897640	16577	38733	597	199

Description

6500734655 deob:hp1179 phosphopentomutase deob:phosphopentomutase (gtcfc:1.3:4.4) (ec:5.4.2.7) (keggfc:1.3) (tigrfc:8.5) (db:gtc-helicobacter pylori) HP1179 HP1179 Helicobacter pylori 210 -11538513 7000685007 deob:hp1179 (sr:,campylobacter pylori) (ec:5.4.2.7) (de:phosphopentomutase, (phosphodeoxyribomutase)) (db:swissprot) DEOB_HELPY P56195 HELICOBACTER PYLORI 210 -11538513 7000685008 phosphopentomutase (cl:phosphopentomutase) (db:pir2.dat) C64667 C64667 Helicobacter pylori 210 -11538513 7500880160 hp1179 phosphopentomutase deob (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:17059 percent identity: 55.91;) (le:10227) (re:11468) (di:complement) HPAE000623 AE000623 g2314336 Helicobacter pylori 210 -11538513 7502852352 hp1179 phosphopentomutase deob (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:17059 percent identity: 55.91;) (le:10227) (re:11468) (di:complement) HPAE000623 AE000623 g2314336 Helicobacter pylori 26695 85962 -11538513

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897644	16578	38734	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897650	16579	38735	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897654	16580	38736	333	110

Description

6500734656 rpe:hp1386 d-ribulose-5-phosphate 3 epimerase (gtcfc:1.3:1.4:2.4) (ec:5.1.3.1) (keggfc:1.3:1.4:2.3) (tigrfc:6.10) (db:gtc-helicobacter pylori) HP1386 HP1386 Helicobacter pylori 210 -11538514 5500685902 rpe:hp1386 (sr:,campylobacter pylori) (ec:5.1.3.1) (de:epimerase) (ppe) (r5p3e)) (db:swissprot) RPE_HELPY P56188 HELICOBACTER PYLORI 210 -11538514 7000686451 d-ribulose-5-phosphate 3 epimerase (cl:yeast ribulose-5-phosphate-epimerase) (db:pir2.dat) B64693 B64693 Helicobacter pylori 210 -11538514 7500890581 hp1386 d-ribulose-5-phosphate 3 epimerase rpe (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:similar to egad:37438 percent identity: 44.19;) (le:7319) (re:7972) (di:direct) HPAE000638 AE000638 g2314553 Helicobacter pylori 210 -11538514 7502852353 hp1386 d-ribulose-5-phosphate 3 epimerase rpe (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:similar to egad:37438 percent identity: 44.19;) (le:7319) (re:7972) (di:direct) HPAE000638 AE000638 g2314553 Helicobacter pylori 26695 85962 -11538514

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897656	16581	38737	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897661	16582	38738	1134	377

Description

6500734657 transaldolase tal:transaldolase:tal (gtcfc:1.3) (ec:2.2.1.2) (keggfc:1.3) (tigrfc:6.10) (db:gtc-helicobacter pylori) HP1495 HP1495 Helicobacter pylori 210 -11538515 5500686038 tal:hp1495 (sr:,campylobacter pylori) (ec:2.2.1.2) (de:transaldolase,) (db:swissprot) TAL_HELPY P56108 HELICOBACTER PYLORI 210 -11538515 7000686754 transaldolase (db:pir2.dat) G64706 G64706 Helicobacter pylori 210 -11538515 7500892745 hp1495 transaldolase tal (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:31920 percent identity: 33.54;) (le:4065) (re:5015) (di:direct) HPAE000648 AE000648 g2314674 Helicobacter pylori 210 -11538515 7502852354 hp1495 transaldolase tal (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:31920 percent identity: 33.54;) (le:4065) (re:5015) (di:direct) HPAE000648 AE000648 g2314674 Helicobacter pylori 26695 85962 -11538515

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897664	16583	38739	1146	381

Description

6500734658 tktb:hp0354 transketolase b tktb:transketolase b (gtcfc:1.3) (keggfc:14.2) (tigrfc:6.10) (db:gtc-helicobacter pylori) HP0354 HP0354 Helicobacter pylori 210 -11538516 7000690746 transketolase b (cl:hypothetical protein c2814) (db:pir2.dat) B64564 B64564 Helicobacter pylori 210 -11538516 7500959511 hp0354 transketolase b tktb (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:similar to egad:28438 percent identity: 39.74;) (le:4384) (re:6240) (di:direct) HPAE000552 AE000552 g2313455 Helicobacter pylori 210 -11538516 7502852355 hp0354 transketolase b tktb (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:similar to egad:28438 percent identity: 39.74;) (le:4384) (re:6240) (di:direct) HPAE000552 AE000552 g2313455 Helicobacter pylori 26695 85962 -11538516

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897667	16584	38740	1458	485

Description

6500734659 galu:hp0646 udp-glucose pyrophosphorylase (gtcfc:1.4:1.6:4.3:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (tigrfc:8.6) (db:gtc-helicobacter pylori) HP0646 HP0646 Helicobacter pylori 210 -11538517 7000690780 udp-glucose pyrophosphorylase (cl:escherichia coli utp--glucose-1-phosphate uridylyltransferase) (db:pir2.dat) F64600 F64600 Helicobacter pylori 210 -11538517 7500959543 hp0646 udp-glucose pyrophosphorylase galu (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to gp:1345068 percent identity: 65.56;) (le:8395) (re:9216) (di:direct) HPAE000578 AE000578 g2313766 Helicobacter pylori 210 -11538517 7502852356 hp0646 udp-glucose pyrophosphorylase galu (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to gp:1345068 percent identity: 65.56;) (le:8395) (re:9216) (di:direct) HPAE000578 AE000578 g2313766 Helicobacter pylori 26695 85962 -11538517

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897675	16585	38741	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897677	16586	38742	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897699	16587	38743	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897707	16588	38744	450	149

Description

6500734660 eda:hp1099 2-keto-3-deoxy-6-phosphogluconate aldolase (gtcfc:1.4:1.9:2.1:5.10) (keggfc:1.4:1.9:5.10) (tigrfc:6.6) (db:gtc-helicobacter pylori) HP1099 HP1099 Helicobacter pylori 210 -11538518 7000689589 2-keto-3-deoxy-6-phosphogluconate aldolase (cl:2-dehydro-3-deoxyphosphogluconate aldolase) (db:pir2.dat) C64657 C64657 Helicobacter pylori 210 -11538518 7500958409 hp1099 2-keto-3-deoxy-6-phosphogluconate aldolase (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to egad:16954 percent identity: 50.25;) (le:6145) (re:6771) (di:complement) HPAE000616 AE000616 g2314248 Helicobacter pylori 210 -11538518 7502852357 hp1099 2-keto-3-deoxy-6-phosphogluconate aldolase (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to egad:16954 percent identity: 50.25;) (le:6145) (re:6771) (di:complement) HPAE000616 AE000616 g2314248 Helicobacter pylori 26695 85962 -11538518

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897714	16589	38745	741	246

Description

6500734661 kdsa:hp0003 3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase:3-deoxy-d-manno-octulosonic acid 8-phosphatesynthetase (gtcfc:1.5:11.3) (ec:4.1.2.16) (keggfc:1.5) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0003 HP0003 Helicobacter pylori 210 -11538519 5500685455 kdsa:hp0003 (sr:,campylobacter pylori) (ec:4.1.2.16) (de:8-phosphate synthetase) (kdo 8-p synthase)) (db:swissprot) KDSA_HELPY P56060 HELICOBACTER PYLORI 210 -11538519 7000685675 3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase (db:pir2.dat) C64520 C64520 Helicobacter pylori 210 -11538519 7500884574 hp0003 3-deoxy-d-manno-octulosonic acid 8-phosphate (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to gp:1359596 percent identity: 53.41;) (le:1115) (re:1945) (di:complement) HPAE000523 AE000523 g2313080 Helicobacter pylori 210 -11538519 7502852358 hp0003 3-deoxy-d-manno-octulosonic acid 8-phosphate (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to gp:1359596 percent identity: 53.41;) (le:1115) (re:1945) (di:complement) HPAE000523 AE000523 g2313080 Helicobacter pylori 26695 85962 -11538519

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897720	16590	38746	204	67

Description

6500734662 pmi:alga:hp0043 mannose-6-phosphate isomerase:pmi or (gtcfc:1.5:4.3) (ec:5.3.1.8) (keggfc:1.5) (tigrfc:8.6) (db:gtc-helicobacter pylori) HP0043 HP0043 Helicobacter pylori 210 -11538520 7000690511 mannose-6-phosphate isomerase (cl:helicobacter mannose-6-phosphate isomerase) (db:pir2.dat) C64525 C64525 Helicobacter pylori 210 -11538520 7500954455 hp0043 mannose-6-phosphate isomerase pmi or alga (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:similar to pir:a25638 percent identity: 42.83;) (le:3007) (re:4419) (di:direct) HPAE000526 AE000526 g2313118 Helicobacter pylori 210 -11538520 7502852359 hp0043 mannose-6-phosphate isomerase pmi or alga (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:similar to pir:a25638 percent identity: 42.83;) (le:3007) (re:4419) (di:direct) HPAE000526 AE000526 g2313118 Helicobacter pylori 26695 85962 -11538520

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897724	16591	38747	471	156

Description

6500734663 rfbd:hp0044 gdp-d-mannose dehydratase (gtcfc:1.5:11.3) (ec:4.2.1.47) (keggfc:1.5) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0044 HP0044 Helicobacter pylori 210 -11538521 7000689957 gdp-d-mannose dehydratase (cl:gdp-d-mannose dehydratase) (db:pir2.dat) D64525 D64525 Helicobacter pylori 210 -11538521 7500958745 hp0044 gdp-d-mannose dehydratase rfbd (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:similar to egad:34254 percent identity: 62.07;) (le:4461) (re:5606) (di:direct) HPAE000526 AE000526 g2313119 Helicobacter pylori 210 -11538521 7502852360 hp0044 gdp-d-mannose dehydratase rfbd (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:similar to egad:34254 percent identity: 62.07;) (le:4461) (re:5606) (di:direct) HPAE000526 AE000526 g2313119 Helicobacter pylori 26695 85962 -11538521

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897728	16592	38748	471	156

Description

6500734664 kdsb:hp0230 ctp:cmp-3-deoxy-d-manno-octulosonate-cytidylyl-transferase (gtcfc:1.5:11.3) (ec:2.7.7.38) (keggfc:1.5) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0230 HP0230 Helicobacter pylori 210 -11538522 7000689874 ctp:cmp-3-deoxy-d-manno-octulosonate-cytidylyl-transferase (db:pir2.dat) F64548 F64548 Helicobacter pylori 210 -11538522 7500958675 hp0230 ctp:cmp-3-deoxy-d-manno-octulosonate-cytidylyl- (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to egad:27893 percent identity: 36.21;) (le:1741) (re:2472) (di:complement) HPAE000543 AE000543 g2313323 Helicobacter pylori 210 -11538522 7502852361 hp0230 ctp:cmp-3-deoxy-d-manno-octulosonate-cytidylyl- (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to egad:27893 percent identity: 36.21;) (le:1741) (re:2472) (di:complement) HPAE000543 AE000543 g2313323 Helicobacter pylori 26695 85962 -11538522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897729	16593	38749	2328	775

Description

6500734665 rfad:hp0859 adp-l-glycero-d-mannoheptose-6-epimerase (gtcfc:1.5:11.3) (ec:5.1.3.-) (keggfc:1.5) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0859 HP0859 Helicobacter pylori 210 -11538523 7000689622 adp-l-glycero-d-mannoheptose-6-epimerase (db:pir2.dat) C64627 C64627 Helicobacter pylori 210 -11538523 7500958441 hp0859 adp-l-glycero-d-mannoheptose-6-epimerase rfad (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:6946 percent identity: 32.73;) (le:12733) (re:13725) (di:complement) HPAE000596 AE000596 g2313991 Helicobacter pylori 210 -11538523 7502852362 hp0859 adp-l-glycero-d-mannoheptose-6-epimerase rfad (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:6946 percent identity: 32.73;) (le:12733) (re:13725) (di:complement) HPAE000596 AE000596 g2313991 Helicobacter pylori 26695 85962 -11538523

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897745	16594	38750	333	110

Description

6500734666 murg:hp1155 transferase:peptidoglycan synthesis (gtcfc:1.5:7.1:8.5:11.3:11.4) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1155 HP1155 Helicobacter pylori 210 -11538524 7000690744 transferase:peptidoglycan synthesis (db:pir2.dat) C64664 C64664 Helicobacter pylori 210 -11538524 7500959509 hp1155 transferase:peptidoglycan synthesis murg (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:28143 percent identity: 28.21;) (le:8631) (re:9692) (di:direct) HPAE000621 AE000621 g2314307 Helicobacter pylori 210 -11538524 7502852363 hp1155 transferase:peptidoglycan synthesis murg (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:28143 percent identity: 28.21;) (le:8631) (re:9692) (di:direct) HPAE000621 AE000621 g2314307 Helicobacter pylori 26695 85962 -11538524

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897746	16595	38751	612	203

Description

GTC ORF with score 442 to: (sr:burkholderia pickettii (strain:dtp0602) dna) (db:genpept-bct1) (de:burkholderia pickettii dna for hydroxyquinol-1, 2-dioxygenase andchlorophenol-4-hydroxylase,complete cds.) (le:2659) (re:3606) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897757	16596	38752	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897763	16597	38753	705	234

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897787	16598	38754	924	307

Description

6500734667 algc:hp1275 phosphomannomutase (gtcfc:1.5:11.3) (ec:5.4.2.8) (keggfc:1.5) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1275 HP1275 Helicobacter pylori 210 -11538525 7000690625 phosphomannomutase (db:pir2.dat) C64679 C64679 Helicobacter pylori 210 -11538525 7500959404 hp1275 phosphomannomutase algc {pseudomonas (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:21666 percent identity: 39.64;) (le:19496) (re:20875) (di:direct) HPAE000631 AE000631 g2314440 Helicobacter pylori 210 -11538525 7502852364 hp1275 phosphomannomutase algc {pseudomonas (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:21666 percent identity: 39.64;) (le:19496) (re:20875) (di:direct) HPAE000631 AE000631 g2314440 Helicobacter pylori 26695 85962 -11538525

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897794	16599	38755	3249	1082

Description

6500734668 udp-glucose 4-epimerase (gtcfc:1.6:4.3) (ec:5.1.3.2) (keggfc:1.6:4.3) (tigrfc:6.11) (db:gtc-helicobacter pylori) HP0360 HP0360 Helicobacter pylori 210 -11538526 7000690779 udp-glucose 4-epimerase (cl:udpglucose 4-epimerase homology) (db:pir2.dat) H64564 H64564 Helicobacter pylori 210 -11538526 7500959542 hp0360 udp-glucose 4-epimerase (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:similar to egad:21944 percent identity: 43.08;) (le:532) (re:1566) (di:direct) HPAE000553 AE000553 g2313462 Helicobacter pylori 210 -11538526 7502852365 hp0360 udp-glucose 4-epimerase (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:similar to egad:21944 percent identity: 43.08;) (le:532) (re:1566) (di:direct) HPAE000553 AE000553 g2313462 Helicobacter pylori 26695 85962 -11538526

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897803	16600	38756	747	248

Description

6500734669 laca:hp0574 galactosidase acetyltransferase (gtcfc:1.6) (keggfc:14.2) (tigrfc:6.11) (db:gtc-helicobacter pylori) HP0574 HP0574 Helicobacter pylori 210 -11538527 7000689956 galactosidase acetyltransferase (cl:galactoside o-acetyltransferase) (db:pir2.dat) F64591 F64591 Helicobacter pylori 210 -11538527 7500958744 hp0574 galactosidase acetyltransferase laca (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:31611 percent identity: 41.01;) (le:4312) (re:4767) (di:complement) HPAE000571 AE000571 g2313693 Helicobacter pylori 210 -11538527 7502852366 hp0574 galactosidase acetyltransferase laca (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:31611 percent identity: 41.01;) (le:4312) (re:4767) (di:complement) HPAE000571 AE000571 g2313693 Helicobacter pylori 26695 85962 -11538527

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897828	16601	38757	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897833	16602	38758	462	153

Description

GTC ORF with score 285 to: (fn:hydrolase) (sr:rattus norvegicus (strain:wistar) female liver cdna to mrna) (db:genpept-rod) (ec:3.4.14.4) (de:rattus norvegicus mrna for dipeptidyl peptidase iii, complete cds.) (le:15) (re:2498) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897859	16603	38759	1086	361

Description

6500734670 phenylacrylic acid decarboxylase (gtcfc:1.7:1.8:5.10:5.12:5.13:5.14:9.12:9.3:13.3) (ec:4.1.1.-) (keggfc:1.7:1.8:5.10:5.12:5.13:5.14:9.3:9.13) (tigrfc:14.4) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-ascorbate and aldarate metabolism:carbohydrate metabolism-pyruvate an... HP1476 HP1476 Helicobacter pylori 210 -11538528 7000690618 phenylacrylic acid decarboxylase (cl:dedf protein) (db:pir2.dat) D64704 D64704 Helicobacter pylori 210 -11538528 7500959396 hp1476 phenylacrylic acid decarboxylase (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:44285 percent identity: 39.67;) (le:10421) (re:10984) (di:complement) HPAE000647 AE000647 g2314652 Helicobacter pylori 210 -11538528 7502852367 hp1476 phenylacrylic acid decarboxylase (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:44285 percent identity: 39.67;) (le:10421) (re:10984) (di:complement) HPAE000647 AE000647 g2314652 Helicobacter pylori 26695 85962 -11538528

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897865	16604	38760	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897870	16605	38761	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897897	16606	38762	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897899	16607	38763	441	146

Description

6500734671 pabb:hp0293 para-aminobenzoate synthetase (gtcfc:1.8:5.15:5.9:9.12:9.6) (ec:4.1.3.-) (keggfc:1.8:5.9:5.15:9.13) (tigrfc:2.3) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:l-amino acid metabolism-phenylalanine--tyrosine and tryptophan biosynthesi... HP0293 HP0293 Helicobacter pylori 210 -11538529 7000690606 para-aminobenzoate synthetase (db:pir2.dat) E64556 E64556 Helicobacter pylori 210 -11538529 7500959386 hp0293 para-aminobenzoate synthetase pabb (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:similar to egad:17280 percent identity: 35.09;) (le:20379) (re:22058) (di:direct) HPAE000547 AE000547 g2313385 Helicobacter pylori 210 -11538529 7502852368 hp0293 para-aminobenzoate synthetase pabb (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:similar to egad:17280 percent identity: 35.09;) (le:20379) (re:22058) (di:direct) HPAE000547 AE000547 g2313385 Helicobacter pylori 26695 85962 -11538529

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897919	16608	38764	924	307

Description

6500734672 dld:hp1222 d-lactate dehydrogenase (gtcfc:1.1:1.8:2.8) (ec:1.1.2.4) (keggfc:1.8) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1222 HP1222 Helicobacter pylori 210 -11538530 7000689884 d-lactate dehydrogenase (db:pir2.dat) F64672 F64672 Helicobacter pylori 210 -11538530 7500958684 hp1222 d-lactate dehydrogenase dld (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:similar to egad:28178 percent identity: 26.99;) (le:9524) (re:12370) (di:complement) HPAE000627 AE000627 g2314381 Helicobacter pylori 210 -11538530 7502852369 hp1222 d-lactate dehydrogenase dld (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:similar to egad:28178 percent identity: 26.99;) (le:9524) (re:12370) (di:complement) HPAE000627 AE000627 g2314381 Helicobacter pylori 26695 85962 -11538530

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897923	16609	38765	594	197

Description

6500734673 fold:hp0577 methylene-tetrahydrofolate dehydrogenase (gtcfc:1.9:9.6) (ec:1.5.1.5) (keggfc:1.9:9.8) (tigrfc:2.3) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-glyoxylate and dicarboxylate metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP0577 HP0577 Helicobacter pylori 210 -11538531 7500881710 fold:hp0577 (sr:,campylobacter pylori) (ec:1.5.1.5:3.5.4.9) (de:methenyltetrahydrofolate cyclohydrolase,) (db:swissprot) FOLD_HELPY P56467 HELICOBACTER PYLORI 210 -11538531 7000690519 fold methylenetetrahydrofolate dehydrogenase nadp+:methenyltetrahydrofolate cyclohydrolase (cl:methylenetetrahydrofolate dehydrogenase (nad+):methylenetetrahydrofolate dehydrogenase (nad+) homology) (ec:1.5.1.5:3.5.4.9) (db:pir2.dat) A64592 A64592 Helicobacter pylori 210 -11538531 7500881712 hp0577 methylene-tetrahydrofolate dehydrogenase fold (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:29243 percent identity: 48.39;) (le:6367) (re:7245) (di:complement) HPAE000571 AE000571 g2313696 Helicobacter pylori 210 -11538531 7502852370 hp0577 methylene-tetrahydrofolate dehydrogenase fold (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:29243 percent identity: 48.39;) (le:6367) (re:7245) (di:complement) HPAE000571 AE000571 g2313696 Helicobacter pylori 26695 85962 -11538531

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897934	16610	38766	732	243

Description

6500734674 def:hp0793 polypeptide deformylase (gtcfc:1.9:5.4:10.6:10.7) (ec:3.5.1.31) (keggfc:1.9:5.4:10.1) (tigrfc:12.5) (db:gtc-helicobacter pylori) HP0793 HP0793 Helicobacter pylori 210 -11538532 7500880141 def:hp0793 (sr:,campylobacter pylori) (ec:3.5.1.31) (de:deformylase)) (db:swissprot) DEF_HELPY P56419 HELICOBACTER PYLORI 210 -11538532 7000690633 polypeptide deformylase (cl:polypeptide deformylase) (db:pir2.dat) A64619 A64619 Helicobacter pylori 210 -11538532 7500880143 hp0793 polypeptide deformylase def (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:similar to egad:10142 percent identity: 41.82;) (le:6979) (re:7503) (di:complement) HPAE000591 AE000591 g2313922 Helicobacter pylori 210 -11538532 7502852371 hp0793 polypeptide deformylase def (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:similar to egad:10142 percent identity: 41.82;) (le:6979) (re:7503) (di:complement) HPAE000591 AE000591 g2313922 Helicobacter pylori 26695 85962 -11538532

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897938	16611	38767	576	191

Description

6500734675 puru:hp1434 formyltetrahydrofolate hydrolase (gtcfc:1.9:4.1:9.6) (ec:3.5.1.10) (keggfc:1.9:9.8) (tigrfc:8.3) (db:gtc-helicobacter pylori) (gtcfc:carbohydrate metabolism-glyoxylate and dicarboxylate metabolism:nucleotide metabolism-purine metabolism:metabolism of cofactors and vitamins-biotin meta... HP1434 HP1434 Helicobacter pylori 210 -11538533 7000689952 formyltetrahydrofolate hydrolase (cl:phosphoribosylglycinamide formyltransferase:phosphoribosylglycinamide formyltransferase homology) (db:pir2.dat) B64699 B64699 Helicobacter pylori 210 -11538533 7500958740 hp1434 formyltetrahydrofolate hydrolase puru (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to egad:28570 percent identity: 49.10;) (le:85) (re:966) (di:complement) HPAE000644 AE000644 g2314610 Helicobacter pylori 210 -11538533 7502852372 hp1434 formyltetrahydrofolate hydrolase puru (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to egad:28570 percent identity: 49.10;) (le:85) (re:966) (di:complement) HPAE000644 AE000644 g2314610 Helicobacter pylori 26695 85962 -11538533

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897940	16612	38768	1317	438

Description

GTC ORF with score 394 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 37 kb genomic dna, clone c213.) (nt:similar to e.coli lipoate-protein ligase a:) (le:5158) (re:6249) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897954	16613	38769	453	150

Description

6500734676 icfa:hp0004 carbonic anhydrase icfa:carbonic anhydrase (gtcfc:1.9:2.6) (ec:4.2.1.1) (keggfc:2.5) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP0004 HP0004 Helicobacter pylori 210 -11538534 7000689693 carbonate dehydratase::carbonic anhydrase (cl:escherichia coli carbonate dehydratase) (ec:4.2.1.1) (db:pir1.dat) D64520 D64520 Helicobacter pylori 210 -11538534 7500958504 hp0004 carbonic anhydrase icfa (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to egad:9345 percent identity: 33.33;) (le:1932) (re:2597) (di:complement) HPAE000523 AE000523 g2313081 Helicobacter pylori 210 -11538534 7502852373 hp0004 carbonic anhydrase icfa (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to egad:9345 percent identity: 33.33;) (le:1932) (re:2597) (di:complement) HPAE000523 AE000523 g2313081 Helicobacter pylori 26695 85962 -11538534

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897960	16614	38770	2304	767

Description

GTC ORF with score 643 to: (db:genpept-bct1) (de:methanobacterium thermoautotrophicum from bases 559173 to 571236(section 50 of 148) of the complete genome.) (nt:function code:14.00 - unknown, ; similar to,) (le:3220) (re:5151) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897971	16615	38771	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897977	16616	38772	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897978	16617	38773	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897979	16618	38774	429	142

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897984	16619	38775	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897994	16620	38776	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501897995	16621	38777	3876	1292

Description

6500734677 hype:hp0047 hydrogenase expression/formation protein (gtcfc:1.9) (keggfc:14.2) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP0047 HP0047 Helicobacter pylori 210 -11538535 7000690002 hydrogenase expression/formation protein (cl:hydrogenase expression/formation protein hype) (db:pir2.dat) G64525 G64525 Helicobacter pylori 210 -11538535 7500958781 hp0047 hydrogenase expression/formation protein hype (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:similar to sp:p26412 percent identity: 39.70;) (le:7397) (re:8395) (di:complement) HPAE000526 AE000526 g2313121 Helicobacter pylori 210 -11538535 7502852374 hp0047 hydrogenase expression/formation protein hype (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:similar to sp:p26412 percent identity: 39.70;) (le:7397) (re:8395) (di:complement) HPAE000526 AE000526 g2313121 Helicobacter pylori 26695 85962 -11538535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898015	16622	38778	522	173

Description

6500734678 metx:hp0197 s-adenosylmethionine synthetase 2 (gtcfc:1.9:5.4:6.4) (ec:2.5.1.6) (keggfc:5.4:6.4) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP0197 HP0197 Helicobacter pylori 210 -11538536 7500885549 metk:hp0197 (sr:,campylobacter pylori) (ec:2.5.1.6) (de:adenosyltransferase) (adomet synthetase)) (db:swissprot) METK_HELPY P56460 HELICOBACTER PYLORI 210 -11538536 7000689076 methionine adenosyltransferase:2 (cl:methionine adenosyltransferase) (ec:2.5.1.6) (db:pir2.dat) E64544 E64544 Helicobacter pylori 210 -11538536 7500885551 hp0197 s-adenosylmethionine synthetase 2 metx (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:similar to egad:5695 percent identity: 62.10;) (le:63) (re:1220) (di:direct) HPAE000540 AE000540 g2313288 Helicobacter pylori 210 -11538536 7502852375 hp0197 s-adenosylmethionine synthetase 2 metx (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:similar to egad:5695 percent identity: 62.10;) (le:63) (re:1220) (di:direct) HPAE000540 AE000540 g2313288 Helicobacter pylori 26695 85962 -11538536

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898019	16623	38779	498	165

Description

7500958780 hypa:hp0869 hydrogenase expression/formation protein (gtcfc:1.9) (keggfc:14.2) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP0869 HP0869 Helicobacter pylori 210 -11538537 7000690001 hydrogenase expression/formation protein (cl:hydrogenase accessory protein) (db:pir2.dat) E64628 E64628 Helicobacter pylori 210 -11538537 7500958779 hp0869 hydrogenase expression/formation protein hypa (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:15266 percent identity: 28.07;) (le:20447) (re:20800) (di:complement) HPAE000596 AE000596 g2313996 Helicobacter pylori 210 -11538537 6500734679 hypa hydrogenase expression/formation protein (db:genpept) (de:helicobacter pylori, strain j99 section 70 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0869) (le:16847) (re:17200) (di:complement) AE001509 AE001509 g4155353 Helicobacter pylori J99 85963 -11538537 7502852376 hp0869 hydrogenase expression/formation protein hypa (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:15266 percent identity: 28.07;) (le:20447) (re:20800) (di:complement) HPAE000596 AE000596 g2313996 Helicobacter pylori 26695 85962 -11538537

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898020	16624	38780	630	209

Description

6500734680 hypd:hp0898 hydrogenase expression/formation protein (gtcfc:1.9) (keggfc:14.2) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP0898 HP0898 Helicobacter pylori 210 -11538538 7000689998 hydrogenase expression/formation protein (cl:hydrogenase expression/formation protein hypd) (db:pir2.dat) B64632 B64632 Helicobacter pylori 210 -11538538 7500958776 hp0898 hydrogenase expression/formation protein hypd (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:similar to egad:17454 percent identity: 47.80;) (le:5804) (re:6916) (di:complement) HPAE000599 AE000599 g2314033 Helicobacter pylori 210 -11538538 7502852377 hp0898 hydrogenase expression/formation protein hypd (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:similar to egad:17454 percent identity: 47.80;) (le:5804) (re:6916) (di:complement) HPAE000599 AE000599 g2314033 Helicobacter pylori 26695 85962 -11538538

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898024	16625	38781	252	83

Description

6500734681 hypc:hp0899 hydrogenase expression/formation protein (gtcfc:1.9) (keggfc:14.2) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP0899 HP0899 Helicobacter pylori 210 -11538539 7000689999 hydrogenase expression/formation protein (cl:hydrogenase expression/formation protein hypc) (db:pir2.dat) C64632 C64632 Helicobacter pylori 210 -11538539 7500958777 hp0899 hydrogenase expression/formation protein hypc (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:similar to egad:44379 percent identity: 38.46;) (le:6922) (re:7155) (di:complement) HPAE000599 AE000599 g2314034 Helicobacter pylori 210 -11538539 7502852378 hp0899 hydrogenase expression/formation protein hypc (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:similar to egad:44379 percent identity: 38.46;) (le:6922) (re:7155) (di:complement) HPAE000599 AE000599 g2314034 Helicobacter pylori 26695 85962 -11538539

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898043	16626	38782	405	134

Description

6500734682 hypb:hp0900 hydrogenase expression/formation protein (gtcfc:1.9) (keggfc:14.2) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP0900 HP0900 Helicobacter pylori 210 -11538540 7000690000 hydrogenase expression/formation protein (cl:hydrogenase expression/formation protein hypb) (db:pir2.dat) D64632 D64632 Helicobacter pylori 210 -11538540 7500958778 hp0900 hydrogenase expression/formation protein hypb (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:similar to egad:13918 percent identity: 41.44;) (le:7155) (re:7883) (di:complement) HPAE000599 AE000599 g2314035 Helicobacter pylori 210 -11538540 7502852379 hp0900 hydrogenase expression/formation protein hypb (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:similar to egad:13918 percent identity: 41.44;) (le:7155) (re:7883) (di:complement) HPAE000599 AE000599 g2314035 Helicobacter pylori 26695 85962 -11538540

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898054	16627	38783	3765	1254

Description

6500734683 hdha:hp1014 7-alpha-hydroxysteroid dehydrogenase (gtcfc:1.9) (keggfc:14.2) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP1014 HP1014 Helicobacter pylori 210 -11538541 7000689597 7-alpha-hydroxysteroid dehydrogenase (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) F64646 F64646 Helicobacter pylori 210 -11538541 7500958417 hp1014 7-alpha-hydroxysteroid dehydrogenase hdha (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:similar to egad:23950 percent identity: 33.18;) (le:10808) (re:11596) (di:direct) HPAE000609 AE000609 g2314157 Helicobacter pylori 210 -11538541 7502852380 hp1014 7-alpha-hydroxysteroid dehydrogenase hdha (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:similar to egad:23950 percent identity: 33.18;) (le:10808) (re:11596) (di:direct) HPAE000609 AE000609 g2314157 Helicobacter pylori 26695 85962 -11538541

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898055	16628	38784	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898057	16629	38785	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898064	16630	38786	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898074	16631	38787	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898089	16632	38788	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898095	16633	38789	990	330

Description

6500734684 carbonic anhydrase (gtcfc:1.9) (keggfc:14.2) (tigrfc:5.1) (db:gtc-helicobacter pylori) HP1186 HP1186 Helicobacter pylori 210 -11538542 7000689692 carbonic anhydrase (db:pir2.dat) B64668 B64668 Helicobacter pylori 210 -11538542 7500958503 hp1186 carbonic anhydrase (db:genpept-bct1) (de:helicobacter pylori section 102 of 134 of the complete genome.) (nt:similar to gp:1644374 percent identity: 36.97;) (le:6577) (re:7185) (di:direct) HPAE000624 AE000624 g2314346 Helicobacter pylori 210 -11538542 7502852381 hp1186 carbonic anhydrase (db:genpept) (de:helicobacter pylori 26695 section 102 of 134 of the completegenome.) (nt:similar to gp:1644374 percent identity: 36.97;) (le:6577) (re:7185) (di:direct) HPAE000624 AE000624 g2314346 Helicobacter pylori 26695 85962 -11538542

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898096	16634	38790	816	271

Description

6500734685 nadh-ubiquinone oxidoreductase subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP0037 HP0037 Helicobacter pylori 210 -11538543 7000690541 nadh dehydrogenase ubiquinone:chain nqo1 (ec:1.6.5.3) (db:pir2.dat) E64524 E64524 Helicobacter pylori 210 -11538543 7500959328 hp0037 nadh-ubiquinone oxidoreductase subunit (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to gp:343539 percent identity: 19.41;) (le:13427) (re:14482) (di:direct) HPAE000525 AE000525 g2313111 Helicobacter pylori 210 -11538543 7502852382 hp0037 nadh-ubiquinone oxidoreductase subunit (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to gp:343539 percent identity: 19.41;) (le:13427) (re:14482) (di:direct) HPAE000525 AE000525 g2313111 Helicobacter pylori 26695 85962 -11538543

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898098	16635	38791	963	320

Description

6500734686 fixn:hp0144 cytochrome c oxidase:heme-b and copper-binding subunit:membrane-bound:cytochrome c oxidase:heme b and copper-bindingsubunit:membrane-bound (gtcfc:2.1:2.8) (ec:1.9.3.1) (keggfc:2.1) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0144 HP0144 Helicobacter pylori 210 -11538544 7000689047 cytochrome-c oxidase:fixn chain:cb-type cytochrome-c oxidase 45k chain:cytochrome b410:fixn protein (cl:rhizobium cytochrome-c oxidase fixn chain:cytochrome-c oxidase chain i homology) (ec:1.9.3.1) (db:pir2.dat) H64537 H64537 Helicobacter pylori 210 -11538544 7500953919 hp0144 cytochrome c oxidase:heme b and copper-binding (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to egad:16112 percent identity: 43.88;) (le:115) (re:1581) (di:direct) HPAE000536 AE000536 g2313231 Helicobacter pylori 210 -11538544 7502852383 hp0144 cytochrome c oxidase:heme b and copper-binding (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to egad:16112 percent identity: 43.88;) (le:115) (re:1581) (di:direct) HPAE000536 AE000536 g2313231 Helicobacter pylori 26695 85962 -11538544

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898101	16636	38792	621	206

Description

6500734687 fixo:hp0145 cytochrome c oxidase:monoheme subunit:membrane-bound:cytochrome c oxidase:monoheme subunit:membrane-bound (gtcfc:2.1:2.8) (ec:1.9.3.1) (keggfc:2.1) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0145 HP0145 Helicobacter pylori 210 -11538545 7000689045 cytochrome-c oxidase:fixo chain:cb-type cytochrome-c oxidase 28k chain:cytochrome b410:fixo protein (cl:rhizobium cytochrome-c oxidase fixo chain) (ec:1.9.3.1) (db:pir2.dat) A64538 A64538 Helicobacter pylori 210 -11538545 7500953917 hp0145 cytochrome c oxidase:monoheme subunit (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to egad:20716 percent identity: 45.66;) (le:1594) (re:2292) (di:direct) HPAE000536 AE000536 g2313232 Helicobacter pylori 210 -11538545 7502852384 hp0145 cytochrome c oxidase:monoheme subunit (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to egad:20716 percent identity: 45.66;) (le:1594) (re:2292) (di:direct) HPAE000536 AE000536 g2313232 Helicobacter pylori 26695 85962 -11538545

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898126	16637	38793	696	231

Description

6500734688 ppa:hp0620 inorganic pyrophosphatase (gtcfc:2.1:13.10) (ec:3.6.1.1) (keggfc:2.1) (tigrfc:5.3) (db:gtc-helicobacter pylori) HP0620 HP0620 Helicobacter pylori 210 -11538546 5500685448 ppa:hp0620 (sr:,campylobacter pylori) (ec:3.6.1.1) (de:hydrolase) (ppase)) (db:swissprot) IPYR_HELPY P56153 HELICOBACTER PYLORI 210 -11538546 7000685644 inorganic pyrophosphatase (cl:inorganic pyrophosphatase) (db:pir2.dat) D64597 D64597 Helicobacter pylori 210 -11538546 7500884233 hp0620 inorganic pyrophosphatase ppa (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:similar to egad:21123 percent identity: 50.00;) (le:7295) (re:7816) (di:direct) HPAE000576 AE000576 g2313741 Helicobacter pylori 210 -11538546 7502852385 hp0620 inorganic pyrophosphatase ppa (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:similar to egad:21123 percent identity: 50.00;) (le:7295) (re:7816) (di:direct) HPAE000576 AE000576 g2313741 Helicobacter pylori 26695 85962 -11538546

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898137	16638	38794	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898157	16639	38795	249	82

Description

6500734689 atpb:hp0828 atp synthase f0:subunit a (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP0828 HP0828 Helicobacter pylori 210 -11538547 5500684900 atpb:hp0828 (sr:,campylobacter pylori) (ec:3.6.1.34) (de:atp synthase a chain, (protein 6)) (db:swissprot) ATP6_HELPY P56085 HELICOBACTER PYLORI 210 -11538547 7000684664 h+-transporting atp synthase:chain a (cl:h+-transporting atp synthase protein 6) (ec:3.6.1.34) (db:pir2.dat) D64623 D64623 Helicobacter pylori 210 -11538547 7500877364 hp0828 atp synthase f0:subunit a atpb (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:19494 percent identity: 37.73;) (le:3151) (re:3831) (di:complement) HPAE000594 AE000594 g2313962 Helicobacter pylori 210 -11538547 7502852386 hp0828 atp synthase f0:subunit a atpb (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:19494 percent identity: 37.73;) (le:3151) (re:3831) (di:complement) HPAE000594 AE000594 g2313962 Helicobacter pylori 26695 85962 -11538547

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898163	16640	38796	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898164	16641	38797	759	252

Description

GTC ORF with score 394 to: (fn:catalyzes conversion of 4-sulfobenzyl alcohol) (db:genpept-bct2) (de:comamonas testosteroni tsar (tsar), toluenesulfonatemethyl-monooxygenase oxygenase component (tsam), toluenesulfonatemethyl-monooxygenase reductase ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898165	16642	38798	375	124

Description

GTC ORF with score 140 to: (fn:catalyzes conversion of 4-sulfobenzyl alcohol) (db:genpept-bct2) (de:comamonas testosteroni tsar (tsar), toluenesulfonatemethyl-monooxygenase oxygenase component (tsam), toluenesulfonatemethyl-monooxygenase reductase ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898198	16643	38799	771	256

Description

6500734690 ppk:hp1010 polyphosphate kinase (gtcfc:2.1:13.10) (ec:2.7.4.1) (keggfc:2.1) (tigrfc:5.3) (db:gtc-helicobacter pylori) HP1010 HP1010 Helicobacter pylori 210 -11538548 7000690634 polyphosphate kinase (db:pir2.dat) B64646 B64646 Helicobacter pylori 210 -11538548 7500959413 hp1010 polyphosphate kinase ppk (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:similar to egad:40792 percent identity: 38.47;) (le:5444) (re:7471) (di:direct) HPAE000609 AE000609 g2314153 Helicobacter pylori 210 -11538548 7502852387 hp1010 polyphosphate kinase ppk (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:similar to egad:40792 percent identity: 38.47;) (le:5444) (re:7471) (di:direct) HPAE000609 AE000609 g2314153 Helicobacter pylori 26695 85962 -11538548

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898199	16644	38800	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898201	16645	38801	801	266

Description

6500734691 atpc:hp1131 atp synthase f1:subunit epsilon (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP1131 HP1131 Helicobacter pylori 210 -11538549 5500684909 atpc:hp1131 (sr:,campylobacter pylori) (ec:3.6.1.34) (de:atp synthase epsilon chain,) (db:swissprot) ATPE_HELPY P56084 HELICOBACTER PYLORI 210 -11538549 7000684675 atp synthase f1:subunit epsilon (cl:h+-transporting atp synthase epsilon chain) (db:pir2.dat) C64661 C64661 Helicobacter pylori 210 -11538549 7500877525 hp1131 atp synthase f1:subunit epsilon atpc (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:21617 percent identity: 32.73;) (le:5897) (re:6271) (di:complement) HPAE000619 AE000619 g2314282 Helicobacter pylori 210 -11538549 7502852388 hp1131 atp synthase f1:subunit epsilon atpc (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:21617 percent identity: 32.73;) (le:5897) (re:6271) (di:complement) HPAE000619 AE000619 g2314282 Helicobacter pylori 26695 85962 -11538549

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898203	16646	38802	288	95

Description

GTC ORF with score 108 to: (fn:nuclear polyadenylated rna-binding protein) (sr:saccharomyces cerevisiae (strain bj926) (library: lambda zap) dna) (db:genpept-pln1) (de:saccharomyces cerevisiae nuclear polyadenylate rna-binding protein(nab2) gene, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898205	16647	38803	465	154

Description

6500734692 atpd:hp1132 atp synthase f1:subunit beta (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP1132 HP1132 Helicobacter pylori 210 -11538550 5500684908 atpd:hp1132 (sr:,campylobacter pylori) (ec:3.6.1.34) (de:atp synthase beta chain,) (db:swissprot) ATPB_HELPY P55988 HELICOBACTER PYLORI 210 -11538550 7000684670 atp synthase f1:subunit beta (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (db:pir2.dat) D64661 D64661 Helicobacter pylori 210 -11538550 7500877487 hp1132 atp synthase f1:subunit beta atpd (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:30846 percent identity: 85.56;) (le:6279) (re:7688) (di:complement) HPAE000619 AE000619 g2314283 Helicobacter pylori 210 -11538550 7502852389 hp1132 atp synthase f1:subunit beta atpd (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:30846 percent identity: 85.56;) (le:6279) (re:7688) (di:complement) HPAE000619 AE000619 g2314283 Helicobacter pylori 26695 85962 -11538550

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898208	16648	38804	801	267

Description

6500734693 atpg:hp1133 atp synthase f1:subunit gamma (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP1133 HP1133 Helicobacter pylori 210 -11538551 5500684911 atpg:hp1133 (sr:,campylobacter pylori) (ec:3.6.1.34) (de:atp synthase gamma chain,) (db:swissprot) ATPG_HELPY P56082 HELICOBACTER PYLORI 210 -11538551 7000684680 h+-transporting atp synthase:gamma chain (cl:h+-transporting atp synthase gamma chain) (ec:3.6.1.34) (db:pir2.dat) E64661 E64661 Helicobacter pylori 210 -11538551 7500877552 hp1133 atp synthase f1:subunit gamma atpg (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:12200 percent identity: 37.85;) (le:7711) (re:8616) (di:complement) HPAE000619 AE000619 g2314284 Helicobacter pylori 210 -11538551 7502852390 hp1133 atp synthase f1:subunit gamma atpg (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:12200 percent identity: 37.85;) (le:7711) (re:8616) (di:complement) HPAE000619 AE000619 g2314284 Helicobacter pylori 26695 85962 -11538551

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898223	16649	38805	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898237	16650	38806	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898259	16651	38807	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898264	16652	38808	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898271	16653	38809	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898289	16654	38810	1845	615

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898290	16655	38811	378	125

Description

6500734694 atpa:hp1134 atp synthase f1:subunit alpha (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP1134 HP1134 Helicobacter pylori 210 -11538552 5500684907 atpa:hp1134 (sr:,campylobacter pylori) (ec:3.6.1.34) (de:atp synthase alpha chain,) (db:swissprot) ATPA_HELPY P55987 HELICOBACTER PYLORI 210 -11538552 7000684668 atp synthase f1:subunit alpha (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (db:pir2.dat) F64661 F64661 Helicobacter pylori 210 -11538552 7500877461 hp1134 atp synthase f1:subunit alpha atpa (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:14376 percent identity: 62.67;) (le:8631) (re:10142) (di:complement) HPAE000619 AE000619 g2314285 Helicobacter pylori 210 -11538552 7502852391 hp1134 atp synthase f1:subunit alpha atpa (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:14376 percent identity: 62.67;) (le:8631) (re:10142) (di:complement) HPAE000619 AE000619 g2314285 Helicobacter pylori 26695 85962 -11538552

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898294	16656	38812	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898320	16657	38813	957	318

Description

6500734695 atpf:hp1136 atp synthase f0:subunit b (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP1136 HP1136 Helicobacter pylori 210 -11538553 5500684910 atpf:hp1136 (sr:,campylobacter pylori) (ec:3.6.1.34) (de:atp synthase b chain,) (db:swissprot) ATPF_HELPY P56086 HELICOBACTER PYLORI 210 -11538553 7000684679 atp synthase f0:subunit b (db:pir2.dat) H64661 H64661 Helicobacter pylori 210 -11538553 7500877542 hp1136 atp synthase f0:subunit b atpf (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:17785 percent identity: 28.26;) (le:10706) (re:11221) (di:complement) HPAE000619 AE000619 g2314287 Helicobacter pylori 210 -11538553 7502852392 hp1136 atp synthase f0:subunit b atpf (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:17785 percent identity: 28.26;) (le:10706) (re:11221) (di:complement) HPAE000619 AE000619 g2314287 Helicobacter pylori 26695 85962 -11538553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898322	16658	38814	435	144

Description

GTC ORF with score 137 to: (sr:glomerella cingulata strain=icmp 11061) (db:genpept-pln1) (de:glomerella cingulata secreted aspartic proteinase precursor (gcsap)gene, complete cds.) (nt:degrades proteins; extracellular; gcsap) (le:105:905) (re:831:1401)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898325	16659	38815	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898333	16660	38816	651	217

Description

6500734696 atpf:hp1137 atp synthase f0:subunit b:atp synthase f0:subunit b:atpf (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP1137 HP1137 Helicobacter pylori 210 -11538554 7000689648 atp synthase f0:subunit b (db:pir2.dat) A64662 A64662 Helicobacter pylori 210 -11538554 7500958464 hp1137 atp synthase f0:subunit b atpf (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:10724 percent identity: 32.52;) (le:11225) (re:11659) (di:complement) HPAE000619 AE000619 g2314288 Helicobacter pylori 210 -11538554 7502852393 hp1137 atp synthase f0:subunit b atpf (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:10724 percent identity: 32.52;) (le:11225) (re:11659) (di:complement) HPAE000619 AE000619 g2314288 Helicobacter pylori 26695 85962 -11538554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898383	16661	38817	582	193

Description

6500734697 atpe:hp1212 atp synthase f0:subunit c (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP1212 HP1212 Helicobacter pylori 210 -11538555 5500684917 atpe:hp1212 (sr:,campylobacter pylori) (ec:3.6.1.34) (de:(dicyclohexylcarbodiimide-binding protein)) (db:swissprot) ATPL_HELPY P56087 HELICOBACTER PYLORI 210 -11538555 7000684682 atp synthase f0:subunit c (cl:h+-transporting atp synthase lipid-binding protein) (db:pir2.dat) D64671 D64671 Helicobacter pylori 210 -11538555 7500877575 hp1212 atp synthase f0:subunit c atpe (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:similar to egad:6190 percent identity: 41.25;) (le:483) (re:800) (di:complement) HPAE000627 AE000627 g2314374 Helicobacter pylori 210 -11538555 7502852394 hp1212 atp synthase f0:subunit c atpe (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:similar to egad:6190 percent identity: 41.25;) (le:483) (re:800) (di:complement) HPAE000627 AE000627 g2314374 Helicobacter pylori 26695 85962 -11538555

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898384	16662	38818	462	153

Description

6500734698 nqo7:hp1260 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo7 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1260 HP1260 Helicobacter pylori 210 -11538556 7000690550 nadh dehydrogenase ubiquinone:chain nqo7 (cl:nadh dehydrogenase (ubiquinone) chain 3) (ec:1.6.5.3) (db:pir2.dat) D64677 D64677 Helicobacter pylori 210 -11538556 7500959337 hp1260 nadh-ubiquinone oxidoreductase:nqo7 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to gp:633586 percent identity: 40.71;) (le:3103) (re:3504) (di:direct) HPAE000631 AE000631 g2314427 Helicobacter pylori 210 -11538556 7502852395 hp1260 nadh-ubiquinone oxidoreductase:nqo7 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to gp:633586 percent identity: 40.71;) (le:3103) (re:3504) (di:direct) HPAE000631 AE000631 g2314427 Helicobacter pylori 26695 85962 -11538556

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898398	16663	38819	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898399	16664	38820	885	294

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898409	16665	38821	1419	472

Description

GTC ORF with score 173 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus glycoprotein m, dnareplication protein, glycoprotein, dna replication protein, fliceinhibitory ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898415	16666	38822	618	205

Description

6500734699 nqo6:hp1261 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo6 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1261 HP1261 Helicobacter pylori 210 -11538557 7000689401 nadh dehydrogenase ubiquinone:chain nqo6 (cl:psbg protein) (ec:1.6.5.3) (db:pir2.dat) E64677 E64677 Helicobacter pylori 210 -11538557 7500955369 hp1261 nadh-ubiquinone oxidoreductase:nqo6 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:25562 percent identity: 62.16;) (le:3504) (re:3983) (di:direct) HPAE000631 AE000631 g2314428 Helicobacter pylori 210 -11538557 7502852396 hp1261 nadh-ubiquinone oxidoreductase:nqo6 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:25562 percent identity: 62.16;) (le:3504) (re:3983) (di:direct) HPAE000631 AE000631 g2314428 Helicobacter pylori 26695 85962 -11538557

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898422	16667	38823	402	133

Description

GTC ORF with score 120 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana bac t10m13 from chromosome iv short arm, mapsat 11.6 cm, complete sequence.) (nt:similar to plant and fission yeast hexose (glucose)) (le:24652:25815:26216) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898424	16668	38824	255	84

Description

6500734700 nqo5:hp1262 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo5 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1262 HP1262 Helicobacter pylori 210 -11538558 7000690549 nadh dehydrogenase ubiquinone:chain nqo5 (ec:1.6.5.3) (db:pir2.dat) F64677 F64677 Helicobacter pylori 210 -11538558 7500959336 hp1262 nadh-ubiquinone oxidoreductase:nqo5 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:6724 percent identity: -1.00;) (le:3980) (re:4780) (di:direct) HPAE000631 AE000631 g2314429 Helicobacter pylori 210 -11538558 7502852397 hp1262 nadh-ubiquinone oxidoreductase:nqo5 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:6724 percent identity: -1.00;) (le:3980) (re:4780) (di:direct) HPAE000631 AE000631 g2314429 Helicobacter pylori 26695 85962 -11538558

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898430	16669	38825	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898438	16670	38826	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898446	16671	38827	585	194

Description

6500734701 nqo4:hp1263 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo4 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1263 HP1263 Helicobacter pylori 210 -11538559 7000690548 nadh dehydrogenase ubiquinone:chain nqo4 (cl:nadh dehydrogenase (ubiquinone) 49k protein) (ec:1.6.5.3) (db:pir2.dat) G64677 G64677 Helicobacter pylori 210 -11538559 7500959335 hp1263 nadh-ubiquinone oxidoreductase:nqo4 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to pir:s46437 percent identity: 44.65;) (le:4782) (re:6011) (di:direct) HPAE000631 AE000631 g2314430 Helicobacter pylori 210 -11538559 7502852398 hp1263 nadh-ubiquinone oxidoreductase:nqo4 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to pir:s46437 percent identity: 44.65;) (le:4782) (re:6011) (di:direct) HPAE000631 AE000631 g2314430 Helicobacter pylori 26695 85962 -11538559

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898459	16672	38828	288	95

Description

6500734702 nqo8:hp1267 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo8 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1267 HP1267 Helicobacter pylori 210 -11538560 7000690551 nadh dehydrogenase ubiquinone:chain nqo8 (cl:nadh dehydrogenase (ubiquinone) chain 1) (ec:1.6.5.3) (db:pir2.dat) C64678 C64678 Helicobacter pylori 210 -11538560 7500959338 hp1267 nadh-ubiquinone oxidoreductase:nqo8 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:18733 percent identity: 42.43;) (le:9755) (re:10744) (di:direct) HPAE000631 AE000631 g2314432 Helicobacter pylori 210 -11538560 7502852399 hp1267 nadh-ubiquinone oxidoreductase:nqo8 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:18733 percent identity: 42.43;) (le:9755) (re:10744) (di:direct) HPAE000631 AE000631 g2314432 Helicobacter pylori 26695 85962 -11538560

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898460	16673	38829	534	177

Description

6500734703 nqo9:hp1268 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo9 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1268 HP1268 Helicobacter pylori 210 -11538561 7000690552 nadh dehydrogenase ubiquinone:chain nqo9 (ec:1.6.5.3) (db:pir2.dat) D64678 D64678 Helicobacter pylori 210 -11538561 7500959339 hp1268 nadh-ubiquinone oxidoreductase:nqo9 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:25564 percent identity: 41.18;) (le:10755) (re:11417) (di:direct) HPAE000631 AE000631 g2314433 Helicobacter pylori 210 -11538561 7502852400 hp1268 nadh-ubiquinone oxidoreductase:nqo9 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:25564 percent identity: 41.18;) (le:10755) (re:11417) (di:direct) HPAE000631 AE000631 g2314433 Helicobacter pylori 26695 85962 -11538561

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898462	16674	38830	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898470	16675	38831	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898472	16676	38832	462	153

Description

6500734704 nqo10:hp1269 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo10 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1269 HP1269 Helicobacter pylori 210 -11538562 7000690542 nadh dehydrogenase ubiquinone:chain nqo10 (ec:1.6.5.3) (db:pir2.dat) E64678 E64678 Helicobacter pylori 210 -11538562 7500959329 hp1269 nadh-ubiquinone oxidoreductase:nqo10 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:8599 percent identity: -1.00;) (le:11410) (re:11958) (di:direct) HPAE000631 AE000631 g2314434 Helicobacter pylori 210 -11538562 7502852401 hp1269 nadh-ubiquinone oxidoreductase:nqo10 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:8599 percent identity: -1.00;) (le:11410) (re:11958) (di:direct) HPAE000631 AE000631 g2314434 Helicobacter pylori 26695 85962 -11538562

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898480	16677	38833	312	103

Description

6500734705 nqo11:hp1270 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo11 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1270 HP1270 Helicobacter pylori 210 -11538563 7000690543 nadh dehydrogenase ubiquinone:chain nqo11 (cl:nadh dehydrogenase (ubiquinone) chain 41) (ec:1.6.5.3) (db:pir2.dat) F64678 F64678 Helicobacter pylori 210 -11538563 7500959330 hp1270 nadh-ubiquinone oxidoreductase:nqo11 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:15485 percent identity: 42.57;) (le:11955) (re:12257) (di:direct) HPAE000631 AE000631 g2314435 Helicobacter pylori 210 -11538563 7502852402 hp1270 nadh-ubiquinone oxidoreductase:nqo11 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:15485 percent identity: 42.57;) (le:11955) (re:12257) (di:direct) HPAE000631 AE000631 g2314435 Helicobacter pylori 26695 85962 -11538563

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898508	16678	38834	579	192

Description

6500734706 nqo12:hp1271 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo12 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1271 HP1271 Helicobacter pylori 210 -11538564 7000690544 nadh dehydrogenase ubiquinone:chain nqo12 (ec:1.6.5.3) (db:pir2.dat) G64678 G64678 Helicobacter pylori 210 -11538564 7500959331 hp1271 nadh-ubiquinone oxidoreductase:nqo12 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:14410 percent identity: 43.16;) (le:12260) (re:14098) (di:direct) HPAE000631 AE000631 g2314436 Helicobacter pylori 210 -11538564 7502852403 hp1271 nadh-ubiquinone oxidoreductase:nqo12 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:14410 percent identity: 43.16;) (le:12260) (re:14098) (di:direct) HPAE000631 AE000631 g2314436 Helicobacter pylori 26695 85962 -11538564

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898509	16679	38835	933	310

Description

6500734707 nqo13:hp1272 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo13 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1272 HP1272 Helicobacter pylori 210 -11538565 7000690545 nadh dehydrogenase ubiquinone:chain nqo13 (cl:nadh dehydrogenase (ubiquinone) chain 4) (ec:1.6.5.3) (db:pir2.dat) H64678 H64678 Helicobacter pylori 210 -11538565 7500959332 hp1272 nadh-ubiquinone oxidoreductase:nqo13 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:42981 percent identity: 40.25;) (le:14102) (re:15640) (di:direct) HPAE000631 AE000631 g2314437 Helicobacter pylori 210 -11538565 7502852404 hp1272 nadh-ubiquinone oxidoreductase:nqo13 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:42981 percent identity: 40.25;) (le:14102) (re:15640) (di:direct) HPAE000631 AE000631 g2314437 Helicobacter pylori 26695 85962 -11538565

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898511	16680	38836	483	160

Description

6500734708 nqo14:hp1273 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo14 subunit (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1273 HP1273 Helicobacter pylori 210 -11538566 7000690546 nadh dehydrogenase ubiquinone:chain nqo14 (cl:nadh dehydrogenase (ubiquinone) chain 2) (ec:1.6.5.3) (db:pir2.dat) A64679 A64679 Helicobacter pylori 210 -11538566 7500959333 hp1273 nadh-ubiquinone oxidoreductase:nqo14 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:22579 percent identity: 31.20;) (le:15627) (re:17099) (di:direct) HPAE000631 AE000631 g2314438 Helicobacter pylori 210 -11538566 7502852405 hp1273 nadh-ubiquinone oxidoreductase:nqo14 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:22579 percent identity: 31.20;) (le:15627) (re:17099) (di:direct) HPAE000631 AE000631 g2314438 Helicobacter pylori 26695 85962 -11538566

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898535	16681	38837	1785	594

Description

6500734709 glycerol-3-phosphate dehydrogenase nadp+:glycerol-3-phosphate dehydrogenase:nad:p+ (gtcfc:2.1:8.1) (ec:1.1.1.94) (keggfc:8.1) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP0961 HP0961 Helicobacter pylori 210 -11538567 7000689971 glycerol-3-phosphate dehydrogenase nad+ (cl:glycerol-3-phosphate dehydrogenase) (ec:1.1.1.8) (db:pir2.dat) A64640 A64640 Helicobacter pylori 210 -11538567 7500958756 hp0961 glycerol-3-phosphate dehydrogenase nad p + (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:30466 percent identity: 36.76;) (le:13128) (re:14066) (di:complement) HPAE000604 AE000604 g2314097 Helicobacter pylori 210 -11538567 7502852406 hp0961 glycerol-3-phosphate dehydrogenase nad p + (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:30466 percent identity: 36.76;) (le:13128) (re:14066) (di:complement) HPAE000604 AE000604 g2314097 Helicobacter pylori 26695 85962 -11538567

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898543	16682	38838	900	299

Description

6500734710 nqo3:hp1266 nadh-ubiquinone oxidoreductase:subunit:nadh-ubiquinone oxidoreductase:nqo3 subunit (gtcfc:2.1) (keggfc:14.2) (tigrfc:6.1) (db:gtc-helicobacter pylori) HP1266 HP1266 Helicobacter pylori 210 -11538568 7000690547 nadh dehydrogenase ubiquinone:chain nqo3 (ec:1.6.5.3) (db:pir2.dat) B64678 B64678 Helicobacter pylori 210 -11538568 7500959334 hp1266 nadh-ubiquinone oxidoreductase:nqo3 subunit (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to gp:1279867 percent identity: 31.64;) (le:7224) (re:9758) (di:direct) HPAE000631 AE000631 g2314431 Helicobacter pylori 210 -11538568 7502852407 hp1266 nadh-ubiquinone oxidoreductase:nqo3 subunit (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to gp:1279867 percent identity: 31.64;) (le:7224) (re:9758) (di:direct) HPAE000631 AE000631 g2314431 Helicobacter pylori 26695 85962 -11538568

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898552	16683	38839	1917	638

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898574	16684	38840	411	136

Description

6500734711 6-phosphogluconate dehydratase (gtcfc:2.1:5.7:9.5) (ec:4.2.1.9) (keggfc:5.7:9.5) (tigrfc:6.6) (db:gtc-helicobacter pylori) HP1100 HP1100 Helicobacter pylori 210 -11538569 5500685139 edd:hp1100 (sr:,campylobacter pylori) (ec:4.2.1.12) (de:dehydratase)) (db:swissprot) EDD_HELPY P56111 HELICOBACTER PYLORI 210 -11538569 7000685138 edd phosphogluconate dehydratase (cl:dihydroxy-acid dehydratase) (ec:4.2.1.12) (db:pir2.dat) D64657 D64657 Helicobacter pylori 210 -11538569 7500880837 hp1100 6-phosphogluconate dehydratase (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to egad:8682 percent identity: 50.67;) (le:6790) (re:8616) (di:complement) HPAE000616 AE000616 g2314249 Helicobacter pylori 210 -11538569 7502852408 hp1100 6-phosphogluconate dehydratase (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to egad:8682 percent identity: 50.67;) (le:6790) (re:8616) (di:complement) HPAE000616 AE000616 g2314249 Helicobacter pylori 26695 85962 -11538569

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898576	16685	38841	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898578	16686	38842	2028	675

Description

6500734712 glya:hp0183 serine hydroxymethyltransferase (gtcfc:2.2:5.3:5.5:5.9:6.5:9.3:9.6) (ec:2.1.2.1) (keggfc:2.2:5.3:5.9:6.5:9.3:9.8) (tigrfc:1.6) (db:gtc-helicobacter pylori) (gtcfc:energy metabolism-methane metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:l-amino acid metabo... HP0183 HP0183 Helicobacter pylori 210 -11538570 5500685292 glya:hp0183 (sr:,campylobacter pylori) (ec:2.1.2.1) (de:(shmt)) (db:swissprot) GLYA_HELPY P56089 HELICOBACTER PYLORI 210 -11538570 7000685433 serine hydroxymethyltransferase (cl:glycine hydroxymethyltransferase) (db:pir2.dat) G64542 G64542 Helicobacter pylori 210 -11538570 7500882597 hp0183 serine hydroxymethyltransferase glya (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:similar to egad:17680 percent identity: 53.96;) (le:8567) (re:9817) (di:direct) HPAE000538 AE000538 g2313271 Helicobacter pylori 210 -11538570 7502852409 hp0183 serine hydroxymethyltransferase glya (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:similar to egad:17680 percent identity: 53.96;) (le:8567) (re:9817) (di:direct) HPAE000538 AE000538 g2313271 Helicobacter pylori 26695 85962 -11538570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898626	16687	38843	423	140

Description

6500734713 catalase (gtcfc:2.2:5.14:12.12) (ec:1.11.1.6) (keggfc:2.2:5.14) (tigrfc:4.6) (db:gtc-helicobacter pylori) HP0875 HP0875 Helicobacter pylori 210 -11538571 1500685929 kata:hp0875 (sr:,campylobacter pylori) (ec:1.11.1.6) (de:catalase,) (db:swissprot) CATA_HELPY P77872 HELICOBACTER PYLORI 210 -11538571 7000684755 catalase (cl:catalase) (ec:1.11.1.6) (db:pir2.dat) C64629 C64629 Helicobacter pylori 210 -11538571 7500878203 hp0875 catalase (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:similar to gp:1561776 percent identity: 99.41;) (le:2924) (re:4441) (di:complement) HPAE000597 AE000597 g2314010 Helicobacter pylori 210 -11538571 7502852410 hp0875 catalase (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:similar to gp:1561776 percent identity: 99.41;) (le:2924) (re:4441) (di:complement) HPAE000597 AE000597 g2314010 Helicobacter pylori 26695 85962 -11538571

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898628	16688	38844	1089	362

Description

6500734714 short chain alcohol dehydrogenase (gtcfc:1.1) (keggfc:14.2) (tigrfc:6.7) (db:gtc-helicobacter pylori) HP0357 HP0357 Helicobacter pylori 210 -11538572 7000690700 short chain alcohol dehydrogenase (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) E64564 E64564 Helicobacter pylori 210 -11538572 7500959467 hp0357 short chain alcohol dehydrogenase (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:similar to egad:28429 percent identity: 57.55;) (le:8967) (re:9719) (di:complement) HPAE000552 AE000552 g2313457 Helicobacter pylori 210 -11538572 7502852411 hp0357 short chain alcohol dehydrogenase (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:similar to egad:28429 percent identity: 57.55;) (le:8967) (re:9719) (di:complement) HPAE000552 AE000552 g2313457 Helicobacter pylori 26695 85962 -11538572

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898629	16689	38845	747	248

Description

GTC ORF with score 141 to: (sr:p.aeruginosa (strain 8830) dna) (db:genpept-bct1) (de:p.aeruginosa alginate regulatory proteins algr2 and algr3, completecds.) (nt:alginate regulatory protein algr3) (le:2080) (re:3102) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898632	16690	38846	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898641	16691	38847	786	261

Description

6500734715 yxjd:hp0691 3-oxoadipate coa-transferase subunit a (gtcfc:2.2:5.13) (ec:2.8.3.6) (keggfc:5.13) (tigrfc:6.7) (db:gtc-helicobacter pylori) HP0691 HP0691 Helicobacter pylori 210 -11538573 5500685957 scoa:hp0691 (sr:,campylobacter pylori) (ec:2.8.3.5) (de:(succinyl coa:3-oxoacid coa-transferase) (oxct a)) (db:swissprot) SCOA_HELPY P56006 HELICOBACTER PYLORI 210 -11538573 7000686570 3-oxoadipate coa-transferase subunit a (cl:3-oxoadipate coa-transferase alpha chain:3-oxoadipate coa-transferase alpha chain homology) (db:pir2.dat) C64606 C64606 Helicobacter pylori 210 -11538573 7500891381 hp0691 3-oxoadipate coa-transferase subunit a yxjd (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:similar to egad:30770 percent identity: 65.52;) (le:4505) (re:5203) (di:direct) HPAE000582 AE000582 g2313815 Helicobacter pylori 210 -11538573 7502852412 hp0691 3-oxoadipate coa-transferase subunit a yxjd (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:similar to egad:30770 percent identity: 65.52;) (le:4505) (re:5203) (di:direct) HPAE000582 AE000582 g2313815 Helicobacter pylori 26695 85962 -11538573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898673	16692	38848	546	181

Description

6500734716 yxje:hp0692 3-oxoadipate coa-transferase subunit b (gtcfc:2.2:5.13) (ec:2.8.3.6) (keggfc:5.13) (tigrfc:6.7) (db:gtc-helicobacter pylori) HP0692 HP0692 Helicobacter pylori 210 -11538574 5500685959 scob:hp0692 (sr:,campylobacter pylori) (ec:2.8.3.5) (de:(succinyl coa:3-oxoacid coa-transferase) (oxct b)) (db:swissprot) SCOB_HELPY P56007 HELICOBACTER PYLORI 210 -11538574 7000686572 3-oxoadipate coa-transferase subunit b (cl:3-oxoadipate coa-transferase beta chain:3-oxoadipate coa-transferase beta chain homology) (db:pir2.dat) D64606 D64606 Helicobacter pylori 210 -11538574 7500891384 hp0692 3-oxoadipate coa-transferase subunit b yxje (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:similar to egad:30771 percent identity: 73.17;) (le:5200) (re:5823) (di:direct) HPAE000582 AE000582 g2313816 Helicobacter pylori 210 -11538574 7502852413 hp0692 3-oxoadipate coa-transferase subunit b yxje (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:similar to egad:30771 percent identity: 73.17;) (le:5200) (re:5823) (di:direct) HPAE000582 AE000582 g2313816 Helicobacter pylori 26695 85962 -11538574

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898677	16693	38849	1092	364

Description

6500734717 pta:hp0905 phosphotransacetylase (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.7) (db:gtc-helicobacter pylori) HP0905 HP0905 Helicobacter pylori 210 -11538575 7000690627 phosphotransacetylase (db:pir2.dat) A64633 A64633 Helicobacter pylori 210 -11538575 7500959406 hp0905 phosphotransacetylase pta (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:similar to egad:30391 percent identity: 26.92;) (le:10618) (re:11289) (di:complement) HPAE000599 AE000599 g2314036 Helicobacter pylori 210 -11538575 7502852414 hp0905 phosphotransacetylase pta (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:similar to egad:30391 percent identity: 26.92;) (le:10618) (re:11289) (di:complement) HPAE000599 AE000599 g2314036 Helicobacter pylori 26695 85962 -11538575

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898680	16694	38850	879	292

Description

6500734718 delta-1-pyrroline-5-carboxylate dehydrogenase (gtcfc:2.3:5.1:5.10:6.6) (ec:1.5.1.12) (keggfc:5.1:5.10) (tigrfc:6.2) (db:gtc-helicobacter pylori) HP0056 HP0056 Helicobacter pylori 210 -11538576 7000689885 delta-1-pyrroline-5-carboxylate dehydrogenase (db:pir2.dat) H64526 H64526 Helicobacter pylori 210 -11538576 7500958685 hp0056 delta-1-pyrroline-5-carboxylate dehydrogenase (db:genpept-bct1) (de:helicobacter pylori section 5 of 134 of the complete genome.) (nt:similar to gp:1653455 percent identity: 32.22;) (le:6587) (re:10144) (di:complement) HPAE000527 AE000527 g2313134 Helicobacter pylori 210 -11538576 7502852415 hp0056 delta-1-pyrroline-5-carboxylate dehydrogenase (db:genpept) (de:helicobacter pylori 26695 section 5 of 134 of the complete genome.) (nt:similar to gp:1653455 percent identity: 32.22;) (le:6587) (re:10144) (di:complement) HPAE000527 AE000527 g2313134 Helicobacter pylori 26695 85962 -11538576

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898684	16695	38851	519	172

Description

6500734719 sdaa:hp0132 l-serine deaminase sdaa:l-serine deaminase (gtcfc:2.3:5.3:5.5:6.6) (ec:4.2.1.13) (keggfc:5.3:5.5) (tigrfc:6.2) (db:gtc-helicobacter pylori) HP0132 HP0132 Helicobacter pylori 210 -11538577 5500685962 sdaa:hp0132 (sr:,campylobacter pylori) (ec:4.2.1.13) (de:l-serine dehydratase, (l-serine deaminase) (sdh) (l-sd)) (db:swissprot) SDHL_HELPY P56072 HELICOBACTER PYLORI 210 -11538577 7000686577 l-serine dehydratase::l-serine deaminase (cl:microbial l-serine dehydratase) (ec:4.2.1.13) (db:pir2.dat) D64536 D64536 Helicobacter pylori 210 -11538577 7500891423 hp0132 l-serine deaminase sdaa (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:similar to egad:24102 percent identity: 45.81;) (le:587) (re:1954) (di:complement) HPAE000535 AE000535 g2313218 Helicobacter pylori 210 -11538577 7502852416 hp0132 l-serine deaminase sdaa (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:similar to egad:24102 percent identity: 45.81;) (le:587) (re:1954) (di:complement) HPAE000535 AE000535 g2313218 Helicobacter pylori 26695 85962 -11538577

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898687	16696	38852	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898698	16697	38853	228	75

Description

6500734720 aime:hp0294 aliphatic amidase aime:aliphatic amidase (gtcfc:2.3:6.6) (keggfc:14.2) (tigrfc:6.2) (db:gtc-helicobacter pylori) HP0294 HP0294 Helicobacter pylori 210 -11538578 7000689627 aliphatic amidase (db:pir2.dat) F64556 F64556 Helicobacter pylori 210 -11538578 7500958445 hp0294 aliphatic amidase aime (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:19858 percent identity: 75.44;) (le:127) (re:1146) (di:direct) HPAE000548 AE000548 g2313392 Helicobacter pylori 210 -11538578 7502852417 hp0294 aliphatic amidase aime (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:19858 percent identity: 75.44;) (le:127) (re:1146) (di:direct) HPAE000548 AE000548 g2313392 Helicobacter pylori 26695 85962 -11538578

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898699	16698	38854	360	119

Description

6500734721 ansb:hp0723 l-asparaginase ii ansb:l-asparaginase ii (gtcfc:2.3:2.6:5.2:6.5:6.6) (ec:3.5.1.1) (keggfc:2.5:5.2:6.5) (tigrfc:6.2) (db:gtc-helicobacter pylori) HP0723 HP0723 Helicobacter pylori 210 -11538579 7000689141 l-asparaginase ii (cl:asparaginase) (db:pir2.dat) C64610 C64610 Helicobacter pylori 210 -11538579 7500954312 hp0723 l-asparaginase ii ansb (db:genpept-bct1) (de:helicobacter pylori section 63 of 134 of the complete genome.) (nt:similar to egad:33256 percent identity: 54.13;) (le:4272) (re:5264) (di:complement) HPAE000585 AE000585 g2313847 Helicobacter pylori 210 -11538579 7502852418 hp0723 l-asparaginase ii ansb (db:genpept) (de:helicobacter pylori 26695 section 63 of 134 of the complete genome.) (nt:similar to egad:33256 percent identity: 54.13;) (le:4272) (re:5264) (di:complement) HPAE000585 AE000585 g2313847 Helicobacter pylori 26695 85962 -11538579

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898708	16699	38855	1125	375

Description

6500734722 dada:hp0943 d-amino acid dehydrogenase (gtcfc:6.6) (ec:1.4.99.1) (keggfc:2.5:5.13) (tigrfc:6.2) (db:gtc-helicobacter pylori) HP0943 HP0943 Helicobacter pylori 210 -11538580 7502852419 hp0943 (sr:,campylobacter pylori) (de:hypothetical oxidoreductase hp0943) (db:swissprot) Y943_HELPY O25597 HELICOBACTER PYLORI 210 -11538580 7000689883 d-amino acid dehydrogenase (db:pir2.dat) G64637 G64637 Helicobacter pylori 210 -11538580 7500958683 hp0943 d-amino acid dehydrogenase dada (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:similar to egad:20287 percent identity: 26.21;) (le:7425) (re:8657) (di:complement) HPAE000603 AE000603 g2314081 Helicobacter pylori 210 -11538580 7502852420 hp0943 d-amino acid dehydrogenase dada (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:similar to egad:20287 percent identity: 26.21;) (le:7425) (re:8657) (di:complement) HPAE000603 AE000603 g2314081 Helicobacter pylori 26695 85962 -11538580

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898715	16700	38856	930	309

Description

GTC ORF with score 234 to: (fn:degradation and synthesis of lactone) (sr:fusarium oxysporum (strain:aku 3702) cdna to mrna) (db:genpept-pln2) (de:fusarium oxysporum mrna for lactonohydrolase, complete cds.) (le:8) (re:1210) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898741	16701	38857	1002	333

Description

6500734723 aime:hp1238 aliphatic amidase aime:aliphatic amidase (gtcfc:2.3:6.6) (keggfc:14.2) (tigrfc:6.2) (db:gtc-helicobacter pylori) HP1238 HP1238 Helicobacter pylori 210 -11538581 7000689628 aliphatic amidase (db:pir2.dat) F64674 F64674 Helicobacter pylori 210 -11538581 7500958446 hp1238 aliphatic amidase aime (db:genpept-bct1) (de:helicobacter pylori section 107 of 134 of the complete genome.) (nt:similar to egad:19858 percent identity: 37.19;) (le:1914) (re:2918) (di:direct) HPAE000629 AE000629 g2314402 Helicobacter pylori 210 -11538581 7502852421 hp1238 aliphatic amidase aime (db:genpept) (de:helicobacter pylori 26695 section 107 of 134 of the completegenome.) (nt:similar to egad:19858 percent identity: 37.19;) (le:1914) (re:2918) (di:direct) HPAE000629 AE000629 g2314402 Helicobacter pylori 26695 85962 -11538581

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898769	16702	38858	1110	369

Description

6500734724 ald:hp1398 alanine dehydrogenase (gtcfc:2.3:2.5:6.6) (ec:1.4.1.1) (keggfc:2.4) (tigrfc:6.2) (db:gtc-helicobacter pylori) (gtcfc:energy metabolism-glyoxylate cycle:energy metabolism-reductive carboxylate cycle (co2 fixation):metabolism of other amino acids-d-amino acid metabolism) (keg... HP1398 HP1398 Helicobacter pylori 210 -11538582 7000689623 alanine dehydrogenase (cl:alanine dehydrogenase:alanine dehydrogenase homology) (db:pir2.dat) F64694 F64694 Helicobacter pylori 210 -11538582 7500958442 hp1398 alanine dehydrogenase ald (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:similar to egad:15508 percent identity: 39.55;) (le:7904) (re:9046) (di:complement) HPAE000639 AE000639 g2314564 Helicobacter pylori 210 -11538582 7502852422 hp1398 alanine dehydrogenase ald (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:similar to egad:15508 percent identity: 39.55;) (le:7904) (re:9046) (di:complement) HPAE000639 AE000639 g2314564 Helicobacter pylori 26695 85962 -11538582

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898775	16703	38859	219	72

Description

6500734725 rocf:hp1399 arginase rocf:arginase (gtcfc:2.3:5.10:5.16:6.6) (ec:3.5.3.1) (keggfc:5.10:5.16) (tigrfc:6.2) (db:gtc-helicobacter pylori) HP1399 HP1399 Helicobacter pylori 210 -11538583 7000689642 arginase (db:pir2.dat) G64694 G64694 Helicobacter pylori 210 -11538583 7500958459 hp1399 arginase rocf (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:similar to egad:14086 percent identity: 31.80;) (le:9248) (re:10216) (di:direct) HPAE000639 AE000639 g2314565 Helicobacter pylori 210 -11538583 7502852423 hp1399 arginase rocf (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:similar to egad:14086 percent identity: 31.80;) (le:9248) (re:10216) (di:direct) HPAE000639 AE000639 g2314565 Helicobacter pylori 26695 85962 -11538583

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898784	16704	38860	408	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898788	16705	38861	483	160

Description

6500734726 gdha:hp0380 glutamate dehydrogenase (gtcfc:2.6:5.1) (ec:1.4.1.4) (keggfc:2.5:5.1) (tigrfc:1.4) (db:gtc-helicobacter pylori) HP0380 HP0380 Helicobacter pylori 210 -11538584 5500685094 gdha:hp0380 (sr:,campylobacter pylori) (ec:1.4.1.4) (de:nadp-specific glutamate dehydrogenase, (nadp-gdh)) (db:swissprot) DHE4_HELPY P55990 HELICOBACTER PYLORI 210 -11538584 7000685041 glutamate dehydrogenase (cl:glutamate dehydrogenase (nad(p)+)) (db:pir2.dat) D64567 D64567 Helicobacter pylori 210 -11538584 7500880253 hp0380 glutamate dehydrogenase gdha (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:similar to egad:29505 percent identity: 59.05;) (le:9983) (re:11329) (di:complement) HPAE000554 AE000554 g2313483 Helicobacter pylori 210 -11538584 7502852424 hp0380 glutamate dehydrogenase gdha (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:similar to egad:29505 percent identity: 59.05;) (le:9983) (re:11329) (di:complement) HPAE000554 AE000554 g2313483 Helicobacter pylori 26695 85962 -11538584

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898794	16706	38862	1173	390

Description

6500734727 glna:hp0512 glutamine synthetase (gtcfc:2.6:5.1:11.4) (ec:6.3.1.2) (keggfc:2.5:5.1:7.3) (tigrfc:1.4) (db:gtc-helicobacter pylori) HP0512 HP0512 Helicobacter pylori 210 -11538585 5500685280 glna:hp0512 (sr:,campylobacter pylori) (ec:6.3.1.2) (de:glutamine synthetase, (glutamate--ammonia ligase)) (db:swissprot) GLNA_HELPY P94845 HELICOBACTER PYLORI 210 -11538585 7000685407 glutamine synthetase (cl:glutamate--ammonia ligase) (db:pir2.dat) H64583 H64583 Helicobacter pylori 210 -11538585 7500882465 hp0512 glutamine synthetase glna (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:similar to egad:37126 percent identity: 48.59;) (le:8006) (re:9451) (di:complement) HPAE000565 AE000565 g2313621 Helicobacter pylori 210 -11538585 7502852425 hp0512 glutamine synthetase glna (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:similar to egad:37126 percent identity: 48.59;) (le:8006) (re:9451) (di:complement) HPAE000565 AE000565 g2313621 Helicobacter pylori 26695 85962 -11538585

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898802	16707	38863	549	182

Description

6500734728 aspa:hp0649 aspartate ammonia-lyase (gtcfc:2.6:5.2) (ec:4.3.1.1) (keggfc:2.5:5.2) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0649 HP0649 Helicobacter pylori 210 -11538586 5500684894 aspa:hp0649 (sr:,campylobacter pylori) (ec:4.3.1.1) (de:aspartate ammonia-lyase, (aspartase)) (db:swissprot) ASPA_HELPY P56149 HELICOBACTER PYLORI 210 -11538586 7000684647 aspartate ammonia-lyase (cl:fumarate hydratase) (db:pir2.dat) A64601 A64601 Helicobacter pylori 210 -11538586 7500877257 hp0649 aspartate ammonia-lyase aspa (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:23805 percent identity: 55.53;) (le:10964) (re:12370) (di:direct) HPAE000578 AE000578 g2313768 Helicobacter pylori 210 -11538586 7502852426 hp0649 aspartate ammonia-lyase aspa (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:23805 percent identity: 55.53;) (le:10964) (re:12370) (di:direct) HPAE000578 AE000578 g2313768 Helicobacter pylori 26695 85962 -11538586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898803	16708	38864	564	187

Description

6500734729 metb:hp0106 cystathionine gamma-synthase (gtcfc:2.7:5.2:5.3:5.4:5.5:6.4) (ec:4.2.99.9) (keggfc:2.6:5.3:5.4:5.5:6.4) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0106 HP0106 Helicobacter pylori 210 -11538587 5500685546 metb:hp0106 (sr:,campylobacter pylori) (ec:4.2.99.9) (de:(thiol)-lyase)) (db:swissprot) METB_HELPY P56069 HELICOBACTER PYLORI 210 -11538587 7000685835 cystathionine gamma-synthase (cl:o-succinylhomoserine (thiol)-lyase) (db:pir2.dat) B64533 B64533 Helicobacter pylori 210 -11538587 7500885517 hp0106 cystathionine gamma-synthase metb (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:similar to egad:28740 percent identity: 47.66;) (le:5999) (re:7141) (di:complement) HPAE000532 AE000532 g2313189 Helicobacter pylori 210 -11538587 7502852427 hp0106 cystathionine gamma-synthase metb (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:similar to egad:28740 percent identity: 47.66;) (le:5999) (re:7141) (di:complement) HPAE000532 AE000532 g2313189 Helicobacter pylori 26695 85962 -11538587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898815	16709	38865	612	203

Description

6500734730 cysk:hp0107 cysteine synthetase (gtcfc:2.7:5.3:5.5:6.4) (ec:4.2.99.8) (keggfc:2.6:5.5:6.4) (tigrfc:1.6) (db:gtc-helicobacter pylori) HP0107 HP0107 Helicobacter pylori 210 -11538588 5500685066 cysk:hp0107 (sr:,campylobacter pylori) (ec:4.2.99.8) (de:(o-acetylserine (thiol)-lyase) (csase)) (db:swissprot) CYSK_HELPY P56067 HELICOBACTER PYLORI 210 -11538588 7000684970 cysteine synthetase (cl:threonine dehydratase) (db:pir2.dat) C64533 C64533 Helicobacter pylori 210 -11538588 7500879912 hp0107 cysteine synthetase cysk (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:similar to egad:23030 percent identity: 45.72;) (le:7166) (re:8086) (di:complement) HPAE000532 AE000532 g2313190 Helicobacter pylori 210 -11538588 7502852428 hp0107 cysteine synthetase cysk (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:similar to egad:23030 percent identity: 45.72;) (le:7166) (re:8086) (di:complement) HPAE000532 AE000532 g2313190 Helicobacter pylori 26695 85962 -11538588

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898817	16710	38866	339	112

Description

6500734731 cyse:hp1210 serine acetyltransferase:sat (gtcfc:2.7:5.3:5.5) (ec:2.3.1.30) (keggfc:2.6:5.5) (tigrfc:1.6) (db:gtc-helicobacter pylori) HP1210 HP1210 Helicobacter pylori 210 -11538589 500684861 cyse:hp1210 (sr:,campylobacter pylori) (ec:2.3.1.30) (de:serine acetyltransferase, (sat)) (db:swissprot) CYSE_HELPY P71405 HELICOBACTER PYLORI 210 -11538589 7000684968 serine o-acetyltransferase (cl:bacillus serine acetyltransferase:serine acetyltransferase homology) (ec:2.3.1.30) (db:pir2.dat) B64671 B64671 Helicobacter pylori 210 -11538589 7500879906 hp1210 serine acetyltransferase cyse (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to gp:1518452 percent identity: 98.25;) (le:9838) (re:10353) (di:complement) HPAE000626 AE000626 g2314370 Helicobacter pylori 210 -11538589 7502852429 hp1210 serine acetyltransferase cyse (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to gp:1518452 percent identity: 98.25;) (le:9838) (re:10353) (di:complement) HPAE000626 AE000626 g2314370 Helicobacter pylori 26695 85962 -11538589

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898818	16711	38867	846	281

Description

6500734732 frdc:hp0193 fumarate reductase:cytochrome b subunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP0193 HP0193 Helicobacter pylori 210 -11538590 5500685232 frdc:hp0193 (sr:,campylobacter pylori) (de:fumarate reductase cytochrome b subunit) (db:swissprot) FRDC_HELPY O06912 HELICOBACTER PYLORI 210 -11538590 7000685319 fumarate reductase:cytochrome b subunit (cl:fumarate reductase cytochrome b) (db:pir2.dat) A64544 A64544 Helicobacter pylori 210 -11538590 7500881745 hp0193 fumarate reductase:cytochrome b subunit frdc (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:similar to egad:10459 percent identity: 58.75;) (le:7028) (re:7795) (di:complement) HPAE000539 AE000539 g2313280 Helicobacter pylori 210 -11538590 7502852430 hp0193 fumarate reductase:cytochrome b subunit frdc (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:similar to egad:10459 percent identity: 58.75;) (le:7028) (re:7795) (di:complement) HPAE000539 AE000539 g2313280 Helicobacter pylori 26695 85962 -11538590

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898829	16712	38868	285	94

Description

6500734733 ferredoxin oxidoreductase:alpha subunit (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP0589 HP0589 Helicobacter pylori 210 -11538591 7000689916 2-oxoacid--ferredoxin oxidoreductase:alpha chain:2-oxoacid:ferredoxin oxidoreductase coa-acetylating (cl:helicobacter pylori 2-oxoacid ferredoxin oxidoreductase:2-oxoacid ferredoxin oxidoreductase homology) (ec:1.2.7.-) (db:pir2.dat) E64593 E64593 Helicobacter pylori 210 -11538591 7500953992 hp0589 ferredoxin oxidoreductase:alpha subunit (db:genpept-bct1) (de:helicobacter pylori section 50 of 134 of the complete genome.) (nt:similar to egad:44451 percent identity: 42.74;) (le:5322) (re:6449) (di:direct) HPAE000572 AE000572 g2313707 Helicobacter pylori 210 -11538591 7502852431 hp0589 ferredoxin oxidoreductase:alpha subunit (db:genpept) (de:helicobacter pylori 26695 section 50 of 134 of the complete genome.) (nt:similar to egad:44451 percent identity: 42.74;) (le:5322) (re:6449) (di:direct) HPAE000572 AE000572 g2313707 Helicobacter pylori 26695 85962 -11538591

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898838	16713	38869	549	182

Description

6500734734 ferredoxin oxidoreductase:beta subunit (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP0590 HP0590 Helicobacter pylori 210 -11538592 7000689035 pyruvate synthase:beta chain (cl:pyruvate synthase beta chain) (ec:1.2.7.1) (db:pir2.dat) F64593 F64593 Helicobacter pylori 210 -11538592 7500953840 hp0590 ferredoxin oxidoreductase:beta subunit (db:genpept-bct1) (de:helicobacter pylori section 50 of 134 of the complete genome.) (nt:similar to egad:44705 percent identity: 43.18;) (le:6451) (re:7272) (di:direct) HPAE000572 AE000572 g2313708 Helicobacter pylori 210 -11538592 7502852432 hp0590 ferredoxin oxidoreductase:beta subunit (db:genpept) (de:helicobacter pylori 26695 section 50 of 134 of the complete genome.) (nt:similar to egad:44705 percent identity: 43.18;) (le:6451) (re:7272) (di:direct) HPAE000572 AE000572 g2313708 Helicobacter pylori 26695 85962 -11538592

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898846	16714	38870	810	269

Description

6500734735 ferredoxin oxidoreductase:gamma subunit (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP0591 HP0591 Helicobacter pylori 210 -11538593 7000689917 probable 2-oxoglutarate synthase:gamma chain (ec:1.2.7.3) (db:pir2.dat) G64593 G64593 Helicobacter pylori 210 -11538593 7500958711 hp0591 ferredoxin oxidoreductase:gamma subunit (db:genpept-bct1) (de:helicobacter pylori section 50 of 134 of the complete genome.) (nt:similar to egad:44704 percent identity: 33.33;) (le:7272) (re:7832) (di:direct) HPAE000572 AE000572 g2313709 Helicobacter pylori 210 -11538593 7502852433 hp0591 ferredoxin oxidoreductase:gamma subunit (db:genpept) (de:helicobacter pylori 26695 section 50 of 134 of the complete genome.) (nt:similar to egad:44704 percent identity: 33.33;) (le:7272) (re:7832) (di:direct) HPAE000572 AE000572 g2313709 Helicobacter pylori 26695 85962 -11538593

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898863	16715	38871	1155	384

Description

6500734736 glpc:hp0666 anaerobic glycerol-3-phosphate dehydrogenase:subunit c:anaerobic glycerol-3-phosphate dehydrogenase:subunit c (gtcfc:2.8:8.1) (ec:1.1.99.5) (keggfc:8.1) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP0666 HP0666 Helicobacter pylori 210 -11538594 7000689636 anaerobic glycerol-3-phosphate dehydrogenase:subunit c (db:pir2.dat) B64603 B64603 Helicobacter pylori 210 -11538594 7500958453 hp0666 anaerobic glycerol-3-phosphate dehydrogenase (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:18277 percent identity: 27.16;) (le:14321) (re:15622) (di:direct) HPAE000579 AE000579 g2313788 Helicobacter pylori 210 -11538594 7502852434 hp0666 anaerobic glycerol-3-phosphate dehydrogenase (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:18277 percent identity: 27.16;) (le:14321) (re:15622) (di:direct) HPAE000579 AE000579 g2313788 Helicobacter pylori 26695 85962 -11538594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898867	16716	38872	1767	588

Description

6500734737 pyruvate ferredoxin oxidoreductase:gamma subunit (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP1108 HP1108 Helicobacter pylori 210 -11538595 7000690670 pyruvate ferredoxin oxidoreductase:gamma subunit (db:pir2.dat) D64658 D64658 Helicobacter pylori 210 -11538595 7500959442 hp1108 pyruvate ferredoxin oxidoreductase:gamma (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to egad:41274 percent identity: 37.16;) (le:4921) (re:5481) (di:direct) HPAE000617 AE000617 g2314259 Helicobacter pylori 210 -11538595 7502852435 hp1108 pyruvate ferredoxin oxidoreductase:gamma (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to egad:41274 percent identity: 37.16;) (le:4921) (re:5481) (di:direct) HPAE000617 AE000617 g2314259 Helicobacter pylori 26695 85962 -11538595

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898875	16717	38873	636	211

Description

7500959441 pyruvate ferredoxin oxidoreductase:delta subunit (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP1109 HP1109 Helicobacter pylori 210 -11538596 7000690668 pyruvate ferredoxin oxidoreductase:delta subunit (db:pir2.dat) E64658 E64658 Helicobacter pylori 210 -11538596 7000690669 hp1109 pyruvate ferredoxin oxidoreductase:delta (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to gp:1197392 percent identity: 46.97;) (le:5497) (re:5889) (di:direct) HPAE000617 AE000617 g2314260 Helicobacter pylori 210 -11538596 7500959440 pord pord subunit of pyruvate:flavodoxin (db:genpept-bct2) (de:helicobacter pylori pyruvate:flavodoxin oxidoreductase subunitsporc, pord, pora, and porb genes, complete cds; andadenylosuccinate lyase (purb) gene, partial cds.) (nt:ferredoxin-like protein,containing conserved) (le:1160) (re:15... AF021092 AF021092 g2935171 Helicobacter pylori 210 -11538596 7502852436 pord pyruvate ferrodoxin oxidoreductase (db:genpept) (de:helicobacter pylori, strain j99 section 92 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1109) (le:6698) (re:7090) (di:direct) AE001531 AE001531 g4155625 Helicobacter pylori J99 85963 -11538596 6500734738 hp1109 pyruvate ferredoxin oxidoreductase:delta (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to gp:1197392 percent identity: 46.97;) (le:5497) (re:5889) (di:direct) HPAE000617 AE000617 g2314260 Helicobacter pylori 26695 85962 -11538596

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898877	16718	38874	306	101

Description

6500734739 pyruvate ferredoxin oxidoreductase:alpha subunit (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP1110 HP1110 Helicobacter pylori 210 -11538597 7000690667 pyruvate synthase:alpha chain (cl:pyruvate synthase alpha chain) (ec:1.2.7.1) (db:pir2.dat) F64658 F64658 Helicobacter pylori 210 -11538597 7500959439 hp1110 pyruvate ferredoxin oxidoreductase:alpha (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to egad:41278 percent identity: 41.03;) (le:5899) (re:7122) (di:direct) HPAE000617 AE000617 g2314261 Helicobacter pylori 210 -11538597 7502852437 hp1110 pyruvate ferredoxin oxidoreductase:alpha (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to egad:41278 percent identity: 41.03;) (le:5899) (re:7122) (di:direct) HPAE000617 AE000617 g2314261 Helicobacter pylori 26695 85962 -11538597

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898892	16719	38875	1098	365

Description

6500734740 pyruvate ferredoxin oxidoreductase:beta subunit (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.3) (db:gtc-helicobacter pylori) HP1111 HP1111 Helicobacter pylori 210 -11538598 7000689036 probable pyruvate synthase:beta chain (cl:pyruvate synthase beta chain) (ec:1.2.7.1) (db:pir2.dat) G64658 G64658 Helicobacter pylori 210 -11538598 7500953841 hp1111 pyruvate ferredoxin oxidoreductase:beta (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to egad:41282 percent identity: 43.67;) (le:7135) (re:8079) (di:direct) HPAE000617 AE000617 g2314262 Helicobacter pylori 210 -11538598 7502852438 hp1111 pyruvate ferredoxin oxidoreductase:beta (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to egad:41282 percent identity: 43.67;) (le:7135) (re:8079) (di:direct) HPAE000617 AE000617 g2314262 Helicobacter pylori 26695 85962 -11538598

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898893	16720	38876	336	111

Description

6500734741 atph:hp1135 atp synthase f1:subunit delta (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.4) (db:gtc-helicobacter pylori) HP1135 HP1135 Helicobacter pylori 210 -11538599 7000689649 atp synthase f1:subunit delta (db:pir2.dat) G64661 G64661 Helicobacter pylori 210 -11538599 7500958465 hp1135 atp synthase f1:subunit delta atph (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:9581 percent identity: 24.64;) (le:10163) (re:10705) (di:complement) HPAE000619 AE000619 g2314286 Helicobacter pylori 210 -11538599 7502852439 hp1135 atp synthase f1:subunit delta atph (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:9581 percent identity: 24.64;) (le:10163) (re:10705) (di:complement) HPAE000619 AE000619 g2314286 Helicobacter pylori 26695 85962 -11538599

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898897	16721	38877	270	89

Description

6500734742 ccoq:hp0146 cbb3-type cytochrome c oxidase subunit q (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0146 HP0146 Helicobacter pylori 210 -11538600 7000689700 fixq protein homolog:cbb3-type cytochrome-c oxidase chain q (db:pir2.dat) B64538 B64538 Helicobacter pylori 210 -11538600 7500958511 hp0146 cbb3-type cytochrome c oxidase subunit q ccoq (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to gp:1377867 percent identity: 44.19;) (le:2300) (re:2521) (di:direct) HPAE000536 AE000536 g2313239 Helicobacter pylori 210 -11538600 7502852440 hp0146 cbb3-type cytochrome c oxidase subunit q ccoq (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to gp:1377867 percent identity: 44.19;) (le:2300) (re:2521) (di:direct) HPAE000536 AE000536 g2313239 Helicobacter pylori 26695 85962 -11538600

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898902	16722	38878	1320	439

Description

6500734743 fixp:hp0147 cytochrome c oxidase:diheme subunit:membrane-bound:cytochrome c oxidase:diheme subunit:membrane-bound (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0147 HP0147 Helicobacter pylori 210 -11538601 7000689878 cytochrome-c oxidase:chain fixp (ec:1.9.3.1) (db:pir2.dat) C64538 C64538 Helicobacter pylori 210 -11538601 7500958679 hp0147 cytochrome c oxidase:diheme subunit (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to egad:12764 percent identity: 32.98;) (le:2523) (re:3383) (di:direct) HPAE000536 AE000536 g2313233 Helicobacter pylori 210 -11538601 7502852441 hp0147 cytochrome c oxidase:diheme subunit (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to egad:12764 percent identity: 32.98;) (le:2523) (re:3383) (di:direct) HPAE000536 AE000536 g2313233 Helicobacter pylori 26695 85962 -11538601

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898926	16723	38879	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898933	16724	38880	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898938	16725	38881	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898941	16726	38882	774	257

Description

6500734744 ccda:hp0265 cytochrome c biogenesis protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0265 HP0265 Helicobacter pylori 210 -11538602 7000689876 cytochrome c biogenesis protein (db:pir2.dat) A64553 A64553 Helicobacter pylori 210 -11538602 7500958677 hp0265 cytochrome c biogenesis protein ccda (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to egad:29881 percent identity: 35.44;) (le:10621) (re:11343) (di:direct) HPAE000545 AE000545 g2313357 Helicobacter pylori 210 -11538602 7502852442 hp0265 cytochrome c biogenesis protein ccda (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to egad:29881 percent identity: 35.44;) (le:10621) (re:11343) (di:direct) HPAE000545 AE000545 g2313357 Helicobacter pylori 26695 85962 -11538602

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898965	16727	38883	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898968	16728	38884	624	207

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898974	16729	38885	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898977	16730	38886	768	255

Description

6500734745 ferredoxin (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0277 HP0277 Helicobacter pylori 210 -11538603 7000689010 ferredoxin (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) E64554 E64554 Helicobacter pylori 210 -11538603 7500953754 hp0277 ferredoxin (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:similar to egad:13273 percent identity: 52.50;) (le:6700) (re:6954) (di:direct) HPAE000546 AE000546 g2313367 Helicobacter pylori 210 -11538603 7502852443 hp0277 ferredoxin (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:similar to egad:13273 percent identity: 52.50;) (le:6700) (re:6954) (di:direct) HPAE000546 AE000546 g2313367 Helicobacter pylori 26695 85962 -11538603

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898985	16731	38887	726	241

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501898992	16732	38888	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899001	16733	38889	456	151

Description

6500734746 ycf5:hp0378 cytochrome c biogenesis protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0378 HP0378 Helicobacter pylori 210 -11538604 7000689877 cytochrome c biogenesis protein (db:pir2.dat) B64567 B64567 Helicobacter pylori 210 -11538604 7500958678 hp0378 cytochrome c biogenesis protein ycf5 (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:similar to sp:p48257 percent identity: 37.55;) (le:5873) (re:8683) (di:direct) HPAE000554 AE000554 g2313481 Helicobacter pylori 210 -11538604 7502852444 hp0378 cytochrome c biogenesis protein ycf5 (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:similar to sp:p48257 percent identity: 37.55;) (le:5873) (re:8683) (di:direct) HPAE000554 AE000554 g2313481 Helicobacter pylori 26695 85962 -11538604

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899005	16734	38890	726	241

Description

6500734747 ferrodoxin-like protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0588 HP0588 Helicobacter pylori 210 -11538605 7000689919 ferrodoxin-like protein (db:pir2.dat) D64593 D64593 Helicobacter pylori 210 -11538605 7500958713 hp0588 ferrodoxin-like protein (db:genpept-bct1) (de:helicobacter pylori section 50 of 134 of the complete genome.) (nt:similar to egad:12984 percent identity: 42.59;) (le:4981) (re:5322) (di:direct) HPAE000572 AE000572 g2313706 Helicobacter pylori 210 -11538605 7502852445 hp0588 ferrodoxin-like protein (db:genpept) (de:helicobacter pylori 26695 section 50 of 134 of the complete genome.) (nt:similar to egad:12984 percent identity: 42.59;) (le:4981) (re:5322) (di:direct) HPAE000572 AE000572 g2313706 Helicobacter pylori 26695 85962 -11538605

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899011	16735	38891	1014	337

Description

6500734748 hyda:hp0631 quinone-reactive ni/fe hydrogenase:small subunit:quinone-reactive ni/fe hydrogenase:smallsubunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0631 HP0631 Helicobacter pylori 210 -11538606 7000690674 quinone-reactive ni/fe hydrogenase:small subunit (cl:hydrogenase (nife) small chain) (db:pir2.dat) G64598 G64598 Helicobacter pylori 210 -11538606 7500959446 hp0631 quinone-reactive ni/fe hydrogenase:small (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:similar to egad:14634 percent identity: 68.95;) (le:6438) (re:7592) (di:direct) HPAE000577 AE000577 g2313749 Helicobacter pylori 210 -11538606 7502852446 hp0631 quinone-reactive ni/fe hydrogenase:small (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:similar to egad:14634 percent identity: 68.95;) (le:6438) (re:7592) (di:direct) HPAE000577 AE000577 g2313749 Helicobacter pylori 26695 85962 -11538606

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899025	16736	38892	420	139

Description

6500734749 hydb:hp0632 quinone-reactive ni/fe hydrogenase:large subunit:quinone-reactive ni/fe hydrogenase:largesubunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0632 HP0632 Helicobacter pylori 210 -11538607 7000690673 quinone-reactive ni/fe hydrogenase:large subunit (cl:hydrogenase (nife) large chain) (db:pir2.dat) H64598 H64598 Helicobacter pylori 210 -11538607 7500959445 hp0632 quinone-reactive ni/fe hydrogenase:large (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:similar to egad:23634 percent identity: 68.54;) (le:7602) (re:9338) (di:direct) HPAE000577 AE000577 g2313750 Helicobacter pylori 210 -11538607 7502852447 hp0632 quinone-reactive ni/fe hydrogenase:large (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:similar to egad:23634 percent identity: 68.54;) (le:7602) (re:9338) (di:direct) HPAE000577 AE000577 g2313750 Helicobacter pylori 26695 85962 -11538607

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899026	16737	38893	447	148

Description

6500734750 hydc:hp0633 quinone-reactive ni/fe hydrogenase:cytochrome b subunit:quinone-reactive ni/fe hydrogenase:cytochrome bsubunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0633 HP0633 Helicobacter pylori 210 -11538608 7000689419 hydrogenase:nife b-type cytochrome chain:quinone-reactive (cl:hyac protein) (ec:1.18.99.1) (db:pir2.dat) A64599 A64599 Helicobacter pylori 210 -11538608 7500955458 hp0633 quinone-reactive ni/fe hydrogenase:cytochrome b (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:similar to egad:6415 percent identity: 51.40;) (le:9351) (re:10025) (di:direct) HPAE000577 AE000577 g2313751 Helicobacter pylori 210 -11538608 7502852448 hp0633 quinone-reactive ni/fe hydrogenase:cytochrome b (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:similar to egad:6415 percent identity: 51.40;) (le:9351) (re:10025) (di:direct) HPAE000577 AE000577 g2313751 Helicobacter pylori 26695 85962 -11538608

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899032	16738	38894	438	145

Description

6500734751 hydd:hp0634 quinone-reactive ni/fe hydrogenase (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0634 HP0634 Helicobacter pylori 210 -11538609 7000690672 quinone-reactive ni/fe hydrogenase (db:pir2.dat) B64599 B64599 Helicobacter pylori 210 -11538609 7500959444 hp0634 quinone-reactive ni/fe hydrogenase hydd (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:similar to egad:6812 percent identity: 54.72;) (le:10022) (re:10558) (di:direct) HPAE000577 AE000577 g2313752 Helicobacter pylori 210 -11538609 7502852449 hp0634 quinone-reactive ni/fe hydrogenase hydd (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:similar to egad:6812 percent identity: 54.72;) (le:10022) (re:10558) (di:direct) HPAE000577 AE000577 g2313752 Helicobacter pylori 26695 85962 -11538609

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899033	16739	38895	228	75

Description

6500734752 nadph-flavin oxidoreductase:nad:ph-flavin oxidoreductase (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0642 HP0642 Helicobacter pylori 210 -11538610 7000689006 nad p h-flavin oxidoreductase (cl:nitroreductase) (ec:1.6.6.-) (db:pir2.dat) B64600 B64600 Helicobacter pylori 210 -11538610 7500953719 hp0642 nad p h-flavin oxidoreductase (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:28277 percent identity: 46.12;) (le:4280) (re:4933) (di:direct) HPAE000578 AE000578 g2313762 Helicobacter pylori 210 -11538610 7502852450 hp0642 nad p h-flavin oxidoreductase (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:28277 percent identity: 46.12;) (le:4280) (re:4933) (di:direct) HPAE000578 AE000578 g2313762 Helicobacter pylori 26695 85962 -11538610

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899034	16740	38896	228	75

Description

6500734753 oxygen-insensitive nadph nitroreductase:oxygen-insensitive nad:ph nitroreductase (gtcfc:2.8) (ec:1.-.-.-) (keggfc:14.1) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP0954 HP0954 Helicobacter pylori 210 -11538611 7000690603 oxygen-insensitive nad p h nitroreductase (cl:nitroreductase) (db:pir2.dat) B64639 B64639 Helicobacter pylori 210 -11538611 7500959383 hp0954 oxygen-insensitive nad p h nitroreductase (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:28277 percent identity: 32.73;) (le:7296) (re:7928) (di:complement) HPAE000604 AE000604 g2314091 Helicobacter pylori 210 -11538611 7502852451 hp0954 oxygen-insensitive nad p h nitroreductase (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:28277 percent identity: 32.73;) (le:7296) (re:7928) (di:complement) HPAE000604 AE000604 g2314091 Helicobacter pylori 26695 85962 -11538611

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899039	16741	38897	234	77

Description

6500734754 flda:hp1161 flavodoxin (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP1161 HP1161 Helicobacter pylori 210 -11538612 7502852452 flda:hp1161 (sr:,campylobacter pylori) (de:flavodoxin) (db:swissprot) FLAV_HELPY O25776 HELICOBACTER PYLORI 210 -11538612 7000689948 flavodoxin (cl:flavodoxin:flavodoxin homology) (db:pir2.dat) A64665 A64665 Helicobacter pylori 210 -11538612 7500958736 hp1161 flavodoxin flda (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:similar to egad:20964 percent identity: 46.99;) (le:553) (re:1047) (di:complement) HPAE000622 AE000622 g2314319 Helicobacter pylori 210 -11538612 7502852453 hp1161 flavodoxin flda (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:similar to egad:20964 percent identity: 46.99;) (le:553) (re:1047) (di:complement) HPAE000622 AE000622 g2314319 Helicobacter pylori 26695 85962 -11538612

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899043	16742	38898	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899067	16743	38899	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899069	16744	38900	639	212

Description

6500734755 cytochrome c553 (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP1227 HP1227 Helicobacter pylori 210 -11538613 7000689880 cytochrome c553 (db:pir2.dat) C64673 C64673 Helicobacter pylori 210 -11538613 7500958681 hp1227 cytochrome c553 (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to egad:17080 percent identity: 38.38;) (le:2701) (re:2991) (di:direct) HPAE000628 AE000628 g2314390 Helicobacter pylori 210 -11538613 7502852454 hp1227 cytochrome c553 (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to egad:17080 percent identity: 38.38;) (le:2701) (re:2991) (di:direct) HPAE000628 AE000628 g2314390 Helicobacter pylori 26695 85962 -11538613

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899070	16745	38901	948	315

Description

6500734756 cytochrome c551 peroxidase (gtcfc:2.8) (ec:1.11.1.5) (keggfc:14.1) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP1461 HP1461 Helicobacter pylori 210 -11538614 7000689879 cytochrome-c peroxidase::cytochrome c551 (cl:pseudomonas cytochrome-c peroxidase:pseudomonas cytochrome-c peroxidase homology) (ec:1.11.1.5) (db:pir2.dat) E64702 E64702 Helicobacter pylori 210 -11538614 7500958680 hp1461 cytochrome c551 peroxidase (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:similar to egad:38715 percent identity: 48.45;) (le:5137) (re:6189) (di:direct) HPAE000646 AE000646 g2314639 Helicobacter pylori 210 -11538614 7502852455 hp1461 cytochrome c551 peroxidase (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:similar to egad:38715 percent identity: 48.45;) (le:5137) (re:6189) (di:direct) HPAE000646 AE000646 g2314639 Helicobacter pylori 26695 85962 -11538614

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899072	16746	38902	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899088	16747	38903	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899090	16748	38904	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899097	16749	38905	507	168

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899117	16750	38906	813	270

Description

6500734757 ferrodoxin-like protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP1508 HP1508 Helicobacter pylori 210 -11538615 7000689920 ferrodoxin-like protein (db:pir2.dat) D64708 D64708 Helicobacter pylori 210 -11538615 7500958714 hp1508 ferrodoxin-like protein (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:similar to egad:40049 percent identity: 29.38;) (le:1261) (re:2637) (di:complement) HPAE000649 AE000649 g2314689 Helicobacter pylori 210 -11538615 7502852456 hp1508 ferrodoxin-like protein (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:similar to egad:40049 percent identity: 29.38;) (le:1261) (re:2637) (di:complement) HPAE000649 AE000649 g2314689 Helicobacter pylori 26695 85962 -11538615

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899119	16751	38907	1011	336

Description

6500734758 fbch:hp1539 ubiquinol cytochrome c oxidoreductase:cytochrome b subunit:ubiquinol cytochrome c oxidoreductase:cytochrome b subunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP1539 HP1539 Helicobacter pylori 210 -11538616 7000690774 ubiquinol cytochrome c oxidoreductase:cytochrome b subunit (cl:cytochrome b:cytochrome b homology:cytochrome b6 homology:plastoquinol--plastocyanin reductase 17k protein homology) (db:pir2.dat) C64712 C64712 Helicobacter pylori 210 -11538616 7500959538 hp1539 ubiquinol cytochrome c oxidoreductase (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:20781 percent identity: 39.32;) (le:965) (re:2203) (di:complement) HPAE000652 AE000652 g2314721 Helicobacter pylori 210 -11538616 7502852457 hp1539 ubiquinol cytochrome c oxidoreductase (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:20781 percent identity: 39.32;) (le:965) (re:2203) (di:complement) HPAE000652 AE000652 g2314721 Helicobacter pylori 26695 85962 -11538616

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899123	16752	38908	447	148

Description

6500734759 fbcf:hp1540 ubiquinol cytochrome c oxidoreductase:rieske 2fe-2s subunit:ubiquinol cytochrome c oxidoreductase:rieske2fe-2s subunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-helicobacter pylori) HP1540 HP1540 Helicobacter pylori 210 -11538617 7000690776 ubiquinol cytochrome c oxidoreductase:rieske 2fe-2s subunit (db:pir2.dat) D64712 D64712 Helicobacter pylori 210 -11538617 7500959539 hp1540 ubiquinol cytochrome c oxidoreductase:rieske (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:24965 percent identity: 39.22;) (le:2214) (re:2717) (di:complement) HPAE000652 AE000652 g2314722 Helicobacter pylori 210 -11538617 7502852458 hp1540 ubiquinol cytochrome c oxidoreductase:rieske (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:24965 percent identity: 39.22;) (le:2214) (re:2717) (di:complement) HPAE000652 AE000652 g2314722 Helicobacter pylori 26695 85962 -11538617

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899125	16753	38909	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899126	16754	38910	603	200

Description

6500734760 fabd:hp0090 malonyl coenzyme a-acyl carrier protein transacylase (gtcfc:3.1:3.2:8.1) (ec:2.3.1.39) (keggfc:3.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0090 HP0090 Helicobacter pylori 210 -11538618 7000690510 malonyl coenzyme a-acyl carrier protein transacylase (cl:(acyl-carrier-protein) s-malonyltransferase:(acyl-carrier-protein) s-malonyltransferase homology) (db:pir2.dat) B64531 B64531 Helicobacter pylori 210 -11538618 7500959304 hp0090 malonyl coenzyme a-acyl carrier protein (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:similar to egad:28795 percent identity: 35.39;) (le:9652) (re:10581) (di:complement) HPAE000530 AE000530 g2313169 Helicobacter pylori 210 -11538618 7502852459 hp0090 malonyl coenzyme a-acyl carrier protein (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:similar to egad:28795 percent identity: 35.39;) (le:9652) (re:10581) (di:complement) HPAE000530 AE000530 g2313169 Helicobacter pylori 26695 85962 -11538618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899134	16755	38911	339	113

Description

6500734761 fabi:hp0195 enoyl-acyl-carrier-protein reductase nadh:enoyl-:acyl-carrier-protein reductase:nadh (gtcfc:3.1:3.2:8.1) (ec:1.3.1.9) (keggfc:3.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0195 HP0195 Helicobacter pylori 210 -11538619 7000689912 enoyl-acyl-carrier-protein reductase (nadh),:enoyl-acp reductase:short-chain alcohol dehydrogenase homolog envm) (cl:enoyl-(acyl-carrier-protein) reductase (nadh):short-chain alcohol dehydrogenase homology) (ec:1.3.1.9) (db:pir2.dat) C64544 C64544 Helicobacter pylori 210 -11538619 7500953792 hp0195 enoyl-acyl-carrier-protein reductase nadh (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:similar to egad:14980 percent identity: 45.80;) (le:8724) (re:9551) (di:direct) HPAE000539 AE000539 g2313282 Helicobacter pylori 210 -11538619 7502852460 hp0195 enoyl-acyl-carrier-protein reductase nadh (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:similar to egad:14980 percent identity: 45.80;) (le:8724) (re:9551) (di:direct) HPAE000539 AE000539 g2313282 Helicobacter pylori 26695 85962 -11538619

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899159	16756	38912	369	122

Description

6500734762 fabh:hp0202 beta-ketoacyl-acyl carrier protein synthase iii (gtcfc:3.1:3.2:8.1) (ec:2.3.1.41) (keggfc:3.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0202 HP0202 Helicobacter pylori 210 -11538620 7000689658 beta-ketoacyl-acyl carrier protein synthase iii (cl:3-oxoacyl-(acyl-carrier-protein) synthase iii) (db:pir2.dat) B64545 B64545 Helicobacter pylori 210 -11538620 7500958472 hp0202 beta-ketoacyl-acyl carrier protein synthase iii (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:similar to egad:23257 percent identity: 44.38;) (le:3360) (re:4355) (di:direct) HPAE000540 AE000540 g2313291 Helicobacter pylori 210 -11538620 7502852461 hp0202 beta-ketoacyl-acyl carrier protein synthase iii (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:similar to egad:23257 percent identity: 44.38;) (le:3360) (re:4355) (di:direct) HPAE000540 AE000540 g2313291 Helicobacter pylori 26695 85962 -11538620

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899164	16757	38913	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899170	16758	38914	264	87

Description

6500734763 fabf:hp0558 beta ketoacyl-acyl carrier protein synthase ii (gtcfc:3.1:3.2:8.1) (ec:2.3.1.41) (keggfc:3.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0558 HP0558 Helicobacter pylori 210 -11538621 7000689656 fabf 3-oxoacyl-acyl-carrier-protein synthase, ii:beta ketoacyl-acyl carrier protein synthase ii) (cl:3-oxoacyl-(acyl-carrier-protein) synthase i:3-oxoacyl-(acyl-carrier-protein) synthase i homology) (ec:2.3.1.41) (db:pir2.dat) F64589 F64589 Helicobacter pylori 210 -11538621 7500958470 hp0558 beta ketoacyl-acyl carrier protein synthase ii (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:similar to egad:24745 percent identity: 50.00;) (le:1934) (re:3172) (di:complement) HPAE000570 AE000570 g2313676 Helicobacter pylori 210 -11538621 7502852462 hp0558 beta ketoacyl-acyl carrier protein synthase ii (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:similar to egad:24745 percent identity: 50.00;) (le:1934) (re:3172) (di:complement) HPAE000570 AE000570 g2313676 Helicobacter pylori 26695 85962 -11538621

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899177	16759	38915	213	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899179	16760	38916	501	166

Description

6500734764 fabg:hp0561 3-ketoacyl-acyl carrier protein reductase (gtcfc:3.1:3.2:8.1) (ec:1.1.1.100) (keggfc:3.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0561 HP0561 Helicobacter pylori 210 -11538622 7000689021 3-ketoacyl-acyl carrier protein reductase (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) A64590 A64590 Helicobacter pylori 210 -11538622 7500953784 hp0561 3-ketoacyl-acyl carrier protein reductase (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:similar to egad:18311 percent identity: 45.71;) (le:3947) (re:4690) (di:complement) HPAE000570 AE000570 g2313678 Helicobacter pylori 210 -11538622 7502852463 hp0561 3-ketoacyl-acyl carrier protein reductase (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:similar to egad:18311 percent identity: 45.71;) (le:3947) (re:4690) (di:complement) HPAE000570 AE000570 g2313678 Helicobacter pylori 26695 85962 -11538622

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899180	16761	38917	666	221

Description

6500734765 plsx:hp0201 fatty acid/phospholipid synthesis protein (gtcfc:3.1:3.2:8.1) (keggfc:14.2) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0201 HP0201 Helicobacter pylori 210 -11538623 7000689340 fatty acid/phospholipid synthesis protein (cl:phospholipid synthesis protein) (db:pir2.dat) A64545 A64545 Helicobacter pylori 210 -11538623 7500955061 hp0201 fatty acid/phospholipid synthesis protein (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:similar to egad:14994 percent identity: 37.80;) (le:2319) (re:3335) (di:direct) HPAE000540 AE000540 g2313290 Helicobacter pylori 210 -11538623 7502852464 hp0201 fatty acid/phospholipid synthesis protein (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:similar to egad:14994 percent identity: 37.80;) (le:2319) (re:3335) (di:direct) HPAE000540 AE000540 g2313290 Helicobacter pylori 26695 85962 -11538623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899181	16762	38918	933	310

Description

6500734766 cdsa:hp0215 cdp-diglyceride synthetase (gtcfc:3.1:3.2:8.1) (ec:2.7.7.41) (keggfc:8.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0215 HP0215 Helicobacter pylori 210 -11538624 7500878464 cdsa:hp0215 (sr:,campylobacter pylori) (ec:2.7.7.41) (de:synthase)) (db:swissprot) CDSA_HELPY O25004 HELICOBACTER PYLORI 210 -11538624 7000689701 cdp-diglyceride synthetase (db:pir2.dat) G64546 G64546 Helicobacter pylori 210 -11538624 7500878466 hp0215 cdp-diglyceride synthetase cdsa (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:similar to egad:17459 percent identity: 42.42;) (le:9253) (re:10053) (di:direct) HPAE000541 AE000541 g2313305 Helicobacter pylori 210 -11538624 7502852465 hp0215 cdp-diglyceride synthetase cdsa (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:similar to egad:17459 percent identity: 42.42;) (le:9253) (re:10053) (di:direct) HPAE000541 AE000541 g2313305 Helicobacter pylori 26695 85962 -11538624

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899187	16763	38919	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899195	16764	38920	513	170

Description

6500734767 fabe:hp0371 biotin carboxyl carrier protein (gtcfc:3.1:3.2:8.1) (keggfc:14.2) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0371 HP0371 Helicobacter pylori 210 -11538625 7000689663 biotin carboxyl carrier protein (cl:biotin carboxyl carrier protein:lipoyl/biotin-binding homology) (db:pir2.dat) C64566 C64566 Helicobacter pylori 210 -11538625 7500958477 hp0371 biotin carboxyl carrier protein fabe (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:similar to egad:14038 percent identity: 30.77;) (le:10012) (re:10482) (di:complement) HPAE000553 AE000553 g2313469 Helicobacter pylori 210 -11538625 7502852466 hp0371 biotin carboxyl carrier protein fabe (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:similar to egad:14038 percent identity: 30.77;) (le:10012) (re:10482) (di:complement) HPAE000553 AE000553 g2313469 Helicobacter pylori 26695 85962 -11538625

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899201	16765	38921	600	199

Description

6500734768 cfa:hp0416 cyclopropane fatty acid synthase (gtcfc:3.1:3.2:8.1) (ec:2.1.1.79) (keggfc:14.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0416 HP0416 Helicobacter pylori 210 -11538626 7000689875 cyclopropane fatty acid synthase (db:pir2.dat) H64571 H64571 Helicobacter pylori 210 -11538626 7500958676 hp0416 cyclopropane fatty acid synthase cfa (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to egad:21564 percent identity: 39.65;) (le:8041) (re:9210) (di:complement) HPAE000557 AE000557 g2313520 Helicobacter pylori 210 -11538626 7502852467 hp0416 cyclopropane fatty acid synthase cfa (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to egad:21564 percent identity: 39.65;) (le:8041) (re:9210) (di:complement) HPAE000557 AE000557 g2313520 Helicobacter pylori 26695 85962 -11538626

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899202	16766	38922	744	248

Description

6500734769 phospholipase a1 precursor dr-phospholipase a:phospholipase a1 precursor:dr-phospholipase a (gtcfc:3.1:3.2:8.1:8.4) (ec:3.1.1.32) (keggfc:8.1:8.4) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0499 HP0499 Helicobacter pylori 210 -11538627 7000690624 phospholipase a1 precursor (db:pir2.dat) C64582 C64582 Helicobacter pylori 210 -11538627 7500959403 hp0499 phospholipase a1 precursor dr-phospholipase a (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:20225 percent identity: 33.82;) (le:8664) (re:9731) (di:direct) HPAE000564 AE000564 g2313609 Helicobacter pylori 210 -11538627 7502852468 hp0499 phospholipase a1 precursor dr-phospholipase a (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:20225 percent identity: 33.82;) (le:8664) (re:9731) (di:direct) HPAE000564 AE000564 g2313609 Helicobacter pylori 26695 85962 -11538627

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899208	16767	38923	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899219	16768	38924	372	123

Description

6500734770 acpp:hp0559 acyl carrier protein (gtcfc:3.1:3.2:8.1) (keggfc:14.2) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0559 HP0559 Helicobacter pylori 210 -11538628 7500876361 acpp:hp0559 (sr:,campylobacter pylori) (de:acyl carrier protein (acp)) (db:swissprot) ACP_HELPY P56464 HELICOBACTER PYLORI 210 -11538628 7000689356 acpp acyl carrier protein (cl:acyl carrier protein:acyl carrier protein homology) (db:pir2.dat) G64589 G64589 Helicobacter pylori 210 -11538628 7500876363 hp0559 acyl carrier protein acpp (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:similar to egad:28793 percent identity: 55.26;) (le:3480) (re:3716) (di:complement) HPAE000570 AE000570 g2313677 Helicobacter pylori 210 -11538628 7502852469 hp0559 acyl carrier protein acpp (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:similar to egad:28793 percent identity: 55.26;) (le:3480) (re:3716) (di:complement) HPAE000570 AE000570 g2313677 Helicobacter pylori 26695 85962 -11538628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899226	16769	38925	534	178

Description

6500734771 dgka:hp0700 diacylglycerol kinase (gtcfc:3.1:3.2:8.1) (ec:2.7.1.107) (keggfc:8.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0700 HP0700 Helicobacter pylori 210 -11538629 7500884548 dgka:hp0700 (sr:,campylobacter pylori) (ec:2.7.1.107) (de:(dgk)) (db:swissprot) KDGL_HELPY P56411 HELICOBACTER PYLORI 210 -11538629 7000689888 diacylglycerol kinase (cl:diacylglycerol kinase) (db:pir2.dat) D64607 D64607 Helicobacter pylori 210 -11538629 7500884550 hp0700 diacylglycerol kinase dgka (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:similar to egad:13380 percent identity: 45.79;) (le:1274) (re:1660) (di:direct) HPAE000583 AE000583 g2313825 Helicobacter pylori 210 -11538629 7502852470 hp0700 diacylglycerol kinase dgka (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:similar to egad:13380 percent identity: 45.79;) (le:1274) (re:1660) (di:direct) HPAE000583 AE000583 g2313825 Helicobacter pylori 26695 85962 -11538629

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899227	16770	38926	1239	412

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899228	16771	38927	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899235	16772	38928	528	176

Description

GTC ORF with score 131 to: (de:(pn:glyceraldehyde-3-phosphate dehydrogenase) (gn:gapdh) (db:genpept-bct) (de:mycobacterium avium glyceraldehyde-3-phosphate dehydrogenasehomolog (gapdh) gene, complete cds; and phosphoglycerate kinasegene, partial cds.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899240	16773	38929	744	248

Description

GTC ORF with score 381 to: (fn:binds to cutinase gene promoter negative acting) (db:genpept-pln1) (de:fusarium solani cutinase negative acting protein (nap) mrna,complete cds.) (nt:nap; transcription factor; similar to s. cerevisiae) (le:144) (re:1667)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899249	16774	38930	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899250	16775	38931	204	67

Description

6500734772 acps:hp0808 holo-acp synthase acps:holo-acp synthase (gtcfc:3.1:3.2:8.1) (keggfc:14.2) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0808 HP0808 Helicobacter pylori 210 -11538630 7000689993 holo-acp synthase (cl:holo-acp synthase) (db:pir2.dat) H64620 H64620 Helicobacter pylori 210 -11538630 7500955964 hp0808 holo-acp synthase acps (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:13032 percent identity: 29.06;) (le:8783) (re:9142) (di:complement) HPAE000592 AE000592 g2313937 Helicobacter pylori 210 -11538630 7502852471 hp0808 holo-acp synthase acps (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:13032 percent identity: 29.06;) (le:8783) (re:9142) (di:complement) HPAE000592 AE000592 g2313937 Helicobacter pylori 26695 85962 -11538630

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899251	16776	38932	1413	470

Description

6500734773 cdh:hp0871 cdp-diglyceride hydrolase (gtcfc:3.1:3.2:8.1) (keggfc:14.2) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0871 HP0871 Helicobacter pylori 210 -11538631 7000689165 cdpdiacylglycerol pyrophosphatase::cdp-diglyceride hydrolase (cl:cdpdiacylglycerol pyrophosphatase) (ec:3.6.1.26) (db:pir2.dat) G64628 G64628 Helicobacter pylori 210 -11538631 7500954329 hp0871 cdp-diglyceride hydrolase cdh (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:similar to egad:16276 percent identity: 73.88;) (le:134) (re:868) (di:complement) HPAE000597 AE000597 g2314008 Helicobacter pylori 210 -11538631 7502852472 hp0871 cdp-diglyceride hydrolase cdh (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:similar to egad:16276 percent identity: 73.88;) (le:134) (re:868) (di:complement) HPAE000597 AE000597 g2314008 Helicobacter pylori 26695 85962 -11538631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899252	16777	38933	747	248

Description

6500734774 acpp:hp0962 acyl carrier protein (gtcfc:3.1:3.2:8.1) (keggfc:14.2) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP0962 HP0962 Helicobacter pylori 210 -11538632 7000689610 acyl carrier protein (cl:acyl carrier protein homology) (db:pir2.dat) B64640 B64640 Helicobacter pylori 210 -11538632 7500958428 hp0962 acyl carrier protein acpp (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:similar to egad:28793 percent identity: 56.34;) (le:96) (re:557) (di:complement) HPAE000605 AE000605 g2314104 Helicobacter pylori 210 -11538632 7502852473 hp0962 acyl carrier protein acpp (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:similar to egad:28793 percent identity: 56.34;) (le:96) (re:557) (di:complement) HPAE000605 AE000605 g2314104 Helicobacter pylori 26695 85962 -11538632

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899258	16778	38934	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899268	16779	38935	558	185

Description

6500734775 pgsa:hp1016 phosphatidylglycerophosphate synthase (gtcfc:3.1:3.2:8.1) (ec:2.7.8.5) (keggfc:8.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP1016 HP1016 Helicobacter pylori 210 -11538633 7000690620 cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (cl:cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase) (ec:2.7.8.5) (db:pir2.dat) H64646 H64646 Helicobacter pylori 210 -11538633 7500959399 hp1016 phosphatidylglycerophosphate synthase pgsa (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:similar to egad:19485 percent identity: 35.37;) (le:526) (re:1128) (di:direct) HPAE000610 AE000610 g2314161 Helicobacter pylori 210 -11538633 7502852474 hp1016 phosphatidylglycerophosphate synthase pgsa (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:similar to egad:19485 percent identity: 35.37;) (le:526) (re:1128) (di:direct) HPAE000610 AE000610 g2314161 Helicobacter pylori 26695 85962 -11538633

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899275	16780	38936	657	218

Description

6500734776 pssa:hp1071 phosphatidylserine synthase (gtcfc:3.1:3.2:5.3:8.1) (ec:2.7.8.8) (keggfc:5.3:8.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP1071 HP1071 Helicobacter pylori 210 -11538634 5500685775 pssa:ptr:hp1071 (sr:,campylobacter pylori) (ec:2.7.8.8) (de:(phosphatidylserine synthase)) (db:swissprot) PSS_HELPY Q48269 HELICOBACTER PYLORI 210 -11538634 7000686202 phosphatidylserine synthase (cl:bacillus subtilis cdpdiacylglycerol--serine o-phosphatidyltransferase:bacillus subtilis cdpdiacylglycerol--serine o-phosphatidyltransferase homology) (db:pir2.dat) G64653 G64653 Helicobacter pylori 210 -11538634 7500888873 hp1071 phosphatidylserine synthase pssa (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:similar to gp:1477770 percent identity: 99.58;) (le:3706) (re:4419) (di:direct) HPAE000614 AE000614 g2314220 Helicobacter pylori 210 -11538634 7502852475 hp1071 phosphatidylserine synthase pssa (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:similar to gp:1477770 percent identity: 99.58;) (le:3706) (re:4419) (di:direct) HPAE000614 AE000614 g2314220 Helicobacter pylori 26695 85962 -11538634

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899287	16781	38937	357	119

Description

6500734777 plsc:hp1348 1-acyl-glycerol-3-phosphate acyltransferase (gtcfc:3.1:3.2:8.1) (ec:2.3.1.51) (keggfc:8.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP1348 HP1348 Helicobacter pylori 210 -11538635 7502852476 plsc:hp1348 (sr:,campylobacter pylori) (ec:2.3.1.51) (de:(lpaat)) (db:swissprot) PLSC_HELPY O25903 HELICOBACTER PYLORI 210 -11538635 7000689586 1-acyl-glycerol-3-phosphate acyltransferase (db:pir2.dat) D64688 D64688 Helicobacter pylori 210 -11538635 7500958407 hp1348 1-acyl-glycerol-3-phosphate acyltransferase (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:17997 percent identity: 31.96;) (le:773) (re:1495) (di:complement) HPAE000636 AE000636 g2314519 Helicobacter pylori 210 -11538635 7502852477 hp1348 1-acyl-glycerol-3-phosphate acyltransferase (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:17997 percent identity: 31.96;) (le:773) (re:1495) (di:complement) HPAE000636 AE000636 g2314519 Helicobacter pylori 26695 85962 -11538635

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899289	16782	38938	2148	715

Description

6500734778 psd:hp1357 phosphatidylserine decarboxylase proenzyme (gtcfc:3.1:3.2:5.3:8.1) (ec:4.1.1.65) (keggfc:5.3:8.1) (tigrfc:7.1) (db:gtc-helicobacter pylori) HP1357 HP1357 Helicobacter pylori 210 -11538636 7000690621 phosphatidylserine decarboxylase proenzyme (db:pir2.dat) E64689 E64689 Helicobacter pylori 210 -11538636 7500959400 hp1357 phosphatidylserine decarboxylase proenzyme (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:8174 percent identity: 33.19;) (le:11784) (re:12587) (di:complement) HPAE000636 AE000636 g2314525 Helicobacter pylori 210 -11538636 7502852478 hp1357 phosphatidylserine decarboxylase proenzyme (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:8174 percent identity: 33.19;) (le:11784) (re:12587) (di:complement) HPAE000636 AE000636 g2314525 Helicobacter pylori 26695 85962 -11538636

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899294	16783	38939	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899302	16784	38940	234	77

Description

6500734779 ispa:hp0929 geranyltranstransferase (gtcfc:3.4:9.12:9.13) (ec:2.5.1.10) (keggfc:3.4:9.11) (tigrfc:2.5) (db:gtc-helicobacter pylori) HP0929 HP0929 Helicobacter pylori 210 -11538637 7000689958 geranyltranstransferase (db:pir2.dat) A64636 A64636 Helicobacter pylori 210 -11538637 7500958746 hp0929 geranyltranstransferase ispa (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:28427 percent identity: 39.85;) (le:12444) (re:13355) (di:direct) HPAE000602 AE000602 g2314066 Helicobacter pylori 210 -11538637 7502852479 hp0929 geranyltranstransferase ispa (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:28427 percent identity: 39.85;) (le:12444) (re:13355) (di:direct) HPAE000602 AE000602 g2314066 Helicobacter pylori 26695 85962 -11538637

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899305	16785	38941	1680	559

Description

6500734780 prma:hp1068 ribosomal protein l11 methyltransferase (gtcfc:3.7:5.11:5.14:9.12:10.4) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1068 HP1068 Helicobacter pylori 210 -11538638 5500685761 prma:hsm:hp1068 (sr:,campylobacter pylori) (ec:2.1.1.-) (de:probable methyltransferase,) (db:swissprot) PRMA_HELPY O07678 HELICOBACTER PYLORI 210 -11538638 7000686180 prma ribosomal protein l11 methyltransferase (cl:ribosomal protein l11 methyltransferase:bioc homology) (ec:2.1.1.-) (db:pir2.dat) D64653 D64653 Helicobacter pylori 210 -11538638 7500888513 hp1068 ribosomal protein l11 methyltransferase prma (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:similar to egad:27991 percent identity: 38.42;) (le:551) (re:1552) (di:direct) HPAE000614 AE000614 g2314218 Helicobacter pylori 210 -11538638 7502852480 hp1068 ribosomal protein l11 methyltransferase prma (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:similar to egad:27991 percent identity: 38.42;) (le:551) (re:1552) (di:direct) HPAE000614 AE000614 g2314218 Helicobacter pylori 26695 85962 -11538638

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899306	16786	38942	561	186

Description

5000695894 ureb:hpub:hp0072 urease beta subunit:urea amidohydrolase (gtcfc:5.16:4.1) (ec:3.5.1.5) (keggfc:4.1:5.16) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0072 HP0072 Helicobacter pylori 210 -11538639 103835 ureb:hpub:hp0072 (sr:,campylobacter pylori) (ec:3.5.1.5) (de:urease beta subunit, (urea amidohydrolase)) (db:swissprot) URE2_HELPY P14917 HELICOBACTER PYLORI 210 -11538639 125022 ureb urease:62k chain:urease beta chain:urease chain b:urease large subunit (cl:urease 62k chain:urease 62k chain homology) (ec:3.5.1.5) (db:pir1.dat) URKCBP B38537 Helicobacter pylori 210 -11538639 324988 (sr:h.pylori dna) (db:genpept-bct1) (de:h.pylori urease (urea, ureb, urec, ured) genes, complete cds.) (nt:putative) (le:3379) (re:5088) (di:direct) HECUREABCD M60398 g149011 Helicobacter pylori 210 -11538639 324860 hp0072 urease beta subunit urea amidohydrolase (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:similar to egad:16403 percent identity: 100.00;) (le:127) (re:1836) (di:complement) HPAE000529 AE000529 g2313153 Helicobacter pylori 210 -11538639 7502852481 61 kda protein (db:genpept-pat) (de:c.jejuni gene for 61 kda protein.) (le:1) (re:1710) (di:direct) A07398 A07398 g412237 Campylobacter jejuni 197 -11538639 7502852482 61 kda protein (db:genpept-pat) (de:c.jejuni dna for 61 kda protein.) (le:1) (re:1710) (di:direct) A08818 A08818 g412248 Campylobacter jejuni 197 -11538639 7502852483 ureb urease beta subunit (db:genpept) (de:helicobacter pylori, strain j99 section 7 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0072) (le:143) (re:1852) (di:complement) AE001446 AE001446 g4154576 Helicobacter pylori J99 85963 -11538639 7502852484 hp0072 urease beta subunit urea amidohydrolase (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:similar to egad:16403 percent identity: 100.00;) (le:127) (re:1836) (di:complement) HPAE000529 AE000529 g2313153 Helicobacter pylori 26695 85962 -11538639 241365 (sr:h.pylori dna) (db:genpept-bct1) (de:h.pylori urease (urea, ureb, urec, ured) genes, complete cds.) (nt:putative) (le:3379) (re:5088) (di:direct) HECUREABCD M60398 g149011 Helicobacter pylori 210 -11538639 6500734781 ureb:hpub urease beta subunit:urea amidohydrolase (gtcfc:5.16:4.1) (ec:3.5.1.5) (keggfc:4.1:5.16) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0072 HP0072 Helicobacter pylori 210 -11538639 7500893844 ureb (de:cellular proces:u:urease beta subunit) (sr:strain j99) JHP67 JHP67 Helicobacter pylori 210 -11538639

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899321	16787	38943	462	153

Description

5000695895 urea:hpua:hp0073 urease alpha subunit:urea amidohydrolase (gtcfc:5.16:4.1) (ec:3.5.1.5) (keggfc:4.1:5.16) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0073 HP0073 Helicobacter pylori 210 -11538640 103815 urea:hpua:hp0073 (sr:,campylobacter pylori) (ec:3.5.1.5) (de:urease alpha subunit, (urea amidohydrolase)) (db:swissprot) URE1_HELPY P14916 HELICOBACTER PYLORI 210 -11538640 7000686899 urea urease:26k chain:urease alpha chain (cl:urease 26k chain:urease 11k chain homology:urease 12k chain homology) (ec:3.5.1.5) (db:pir1.dat) URKCAP A38537 Helicobacter pylori 210 -11538640 324987 urea (sr:h.pylori dna) (db:genpept-bct1) (de:h.pylori urease (urea, ureb, urec, ured) genes, complete cds.) (nt:putative) (le:2659) (re:3375) (di:direct) HECUREABCD M60398 g149010 Helicobacter pylori 210 -11538640 324859 hp0073 urease alpha subunit urea urea (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:similar to egad:7607 percent identity: 100.00;) (le:1840) (re:2556) (di:complement) HPAE000529 AE000529 g2313154 Helicobacter pylori 210 -11538640 7502852485 26 kda protein (db:genpept-pat) (de:c.jejuni gene for 26 kda protein.) (le:1) (re:717) (di:direct) A07396 A07396 g412235 Campylobacter jejuni 197 -11538640 7502852486 26 kda protein (db:genpept-pat) (de:c.jejuni dna for 26 kda protein.) (le:1) (re:717) (di:direct) A08816 A08816 g412246 Campylobacter jejuni 197 -11538640 7502852487 hp0073 urease alpha subunit urea urea (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:similar to egad:7607 percent identity: 100.00;) (le:1840) (re:2556) (di:complement) HPAE000529 AE000529 g2313154 Helicobacter pylori 26695 85962 -11538640 241364 urea (sr:h.pylori dna) (db:genpept-bct1) (de:h.pylori urease (urea, ureb, urec, ured) genes, complete cds.) (nt:putative) (le:2659) (re:3375) (di:direct) HECUREABCD M60398 g149010 Helicobacter pylori 210 -11538640 6500734782 urea:hpua urease alpha subunit:urea amidohydrolase (gtcfc:5.16:4.1) (ec:3.5.1.5) (keggfc:4.1:5.16) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0073 HP0073 Helicobacter pylori 210 -11538640

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899323	16788	38944	459	152

Description

6500734783 ndk:hp0198 nucleoside diphosphate kinase (gtcfc:4.1:4.2) (ec:2.7.4.6) (keggfc:4.1:4.2) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP0198 HP0198 Helicobacter pylori 210 -11538641 5500685605 ndk:hp0198 (sr:,campylobacter pylori) (ec:2.7.4.6) (de:nucleoside diphosphate kinase, (ndk) (ndp kinase)) (db:swissprot) NDK_HELPY P56075 HELICOBACTER PYLORI 210 -11538641 7000685952 nucleoside diphosphate kinase (cl:nucleoside-diphosphate kinase) (db:pir2.dat) F64544 F64544 Helicobacter pylori 210 -11538641 7500886375 hp0198 nucleoside diphosphate kinase ndk (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:similar to egad:13016 percent identity: 67.69;) (le:1287) (re:1700) (di:direct) HPAE000540 AE000540 g2313289 Helicobacter pylori 210 -11538641 7502852488 hp0198 nucleoside diphosphate kinase ndk (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:similar to egad:13016 percent identity: 67.69;) (le:1287) (re:1700) (di:direct) HPAE000540 AE000540 g2313289 Helicobacter pylori 26695 85962 -11538641

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899330	16789	38945	1431	476

Description

6500734784 pura:hp0255 adenylosuccinate synthetase (gtcfc:4.1:5.2) (ec:6.3.4.4) (keggfc:4.1:5.2) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP0255 HP0255 Helicobacter pylori 210 -11538642 5500685794 pura:hp0255 (sr:,campylobacter pylori) (ec:6.3.4.4) (de:adenylosuccinate synthetase, (imp--aspartate ligase)) (db:swissprot) PURA_HELPY P56137 HELICOBACTER PYLORI 210 -11538642 7000686242 adenylosuccinate synthetase (cl:adenylosuccinate synthase) (db:pir2.dat) G64551 G64551 Helicobacter pylori 210 -11538642 7500889081 hp0255 adenylosuccinate synthetase pura (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to egad:21582 percent identity: 44.58;) (le:80) (re:1315) (di:direct) HPAE000545 AE000545 g2313350 Helicobacter pylori 210 -11538642 7502852489 hp0255 adenylosuccinate synthetase pura (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to egad:21582 percent identity: 44.58;) (le:80) (re:1315) (di:direct) HPAE000545 AE000545 g2313350 Helicobacter pylori 26695 85962 -11538642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899333	16790	38946	930	309

Description

6500734785 gppa:hp0278 guanosine pentaphosphate phosphohydrolase (gtcfc:4.1:12.13) (keggfc:4.1) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0278 HP0278 Helicobacter pylori 210 -11538643 7000689980 guanosine pentaphosphate phosphohydrolase (db:pir2.dat) F64554 F64554 Helicobacter pylori 210 -11538643 7500958761 hp0278 guanosine pentaphosphate phosphohydrolase (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:similar to egad:15197 percent identity: 26.43;) (le:6964) (re:8418) (di:direct) HPAE000546 AE000546 g2313368 Helicobacter pylori 210 -11538643 7502852490 hp0278 guanosine pentaphosphate phosphohydrolase (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:similar to egad:15197 percent identity: 26.43;) (le:6964) (re:8418) (di:direct) HPAE000546 AE000546 g2313368 Helicobacter pylori 26695 85962 -11538643

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899337	16791	38947	210	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899343	16792	38948	1158	385

Description

6500734786 gmk:hp0321 5-guanylate kinase (gtcfc:4.1) (ec:2.7.4.8) (keggfc:4.1) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP0321 HP0321 Helicobacter pylori 210 -11538644 5500685458 gmk:hp0321 (sr:,campylobacter pylori) (ec:2.7.4.8) (de:guanylate kinase, (gmp kinase)) (db:swissprot) KGUA_HELPY P56103 HELICOBACTER PYLORI 210 -11538644 7000685682 5-guanylate kinase (cl:guanylate kinase:guanylate kinase homology) (db:pir2.dat) A64560 A64560 Helicobacter pylori 210 -11538644 7500884604 hp0321 5-guanylate kinase gmk (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:28792 percent identity: 44.75;) (le:2934) (re:3554) (di:complement) HPAE000550 AE000550 g2313420 Helicobacter pylori 210 -11538644 7502852491 hp0321 5-guanylate kinase gmk (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:28792 percent identity: 44.75;) (le:2934) (re:3554) (di:complement) HPAE000550 AE000550 g2313420 Helicobacter pylori 26695 85962 -11538644

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899345	16793	38949	1002	333

Description

6500734787 nrdb:hp0364 ribonucleoside diphosphate reductase:beta subunit:ribonucleoside diphosphate reductase:betasubunit (gtcfc:4.1:4.2) (ec:1.17.4.1) (keggfc:4.1:4.2) (tigrfc:8.2) (db:gtc-helicobacter pylori) (tigrfc:2'-deoxyribonucleotide metabolism) HP0364 HP0364 Helicobacter pylori 210 -11538645 5500685836 nrdb:hp0364 (sr:,campylobacter pylori) (ec:1.17.4.1) (de:(ribonucleotide reductase)) (db:swissprot) RIR2_HELPY P55983 HELICOBACTER PYLORI 210 -11538645 7000686340 ribonucleoside diphosphate reductase:beta subunit (cl:ribonucleoside diphosphate reductase beta chain) (db:pir2.dat) D64565 D64565 Helicobacter pylori 210 -11538645 7500889806 hp0364 ribonucleoside diphosphate reductase:beta (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:similar to gp:1653942 percent identity: 39.02;) (le:3976) (re:5001) (di:complement) HPAE000553 AE000553 g2313466 Helicobacter pylori 210 -11538645 7502852492 hp0364 ribonucleoside diphosphate reductase:beta (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:similar to gp:1653942 percent identity: 39.02;) (le:3976) (re:5001) (di:complement) HPAE000553 AE000553 g2313466 Helicobacter pylori 26695 85962 -11538645

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899358	16794	38950	369	122

Description

6500734788 guaa:hp0409 gmp synthase guaa:gmp synthase (gtcfc:4.1:5.1) (ec:6.3.5.2) (keggfc:4.1:5.1) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP0409 HP0409 Helicobacter pylori 210 -11538646 7500882841 guaa:hp0409 (sr:,campylobacter pylori) (ec:6.3.5.2) (de:amidotransferase) (gmp synthetase)) (db:swissprot) GUAA_HELPY O25165 HELICOBACTER PYLORI 210 -11538646 7000689226 gmp synthase glutamine-hydrolyzing (cl:gmp synthase (glutamine-hydrolyzing):trpg homology) (ec:6.3.5.2) (db:pir2.dat) A64571 A64571 Helicobacter pylori 210 -11538646 7500882843 hp0409 gmp synthase guaa (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to gp:460064 percent identity: 56.14;) (le:612) (re:2138) (di:direct) HPAE000557 AE000557 g2313515 Helicobacter pylori 210 -11538646 7502852493 hp0409 gmp synthase guaa (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to gp:460064 percent identity: 56.14;) (le:612) (re:2138) (di:direct) HPAE000557 AE000557 g2313515 Helicobacter pylori 26695 85962 -11538646

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899366	16795	38951	639	212

Description

6500734789 dnan:hp0500 dna polymerase iii beta-subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0500 HP0500 Helicobacter pylori 210 -11538647 7502852494 dnan:hp0500 (sr:,campylobacter pylori) (ec:2.7.7.7) (de:dna polymerase iii, beta chain,) (db:swissprot) DP3B_HELPY O25242 HELICOBACTER PYLORI 210 -11538647 7000689901 dna polymerase iii beta-subunit (db:pir2.dat) D64582 D64582 Helicobacter pylori 210 -11538647 7500958697 hp0500 dna polymerase iii beta-subunit dnan (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:28015 percent identity: 26.03;) (le:9789) (re:10913) (di:direct) HPAE000564 AE000564 g2313610 Helicobacter pylori 210 -11538647 7502852495 hp0500 dna polymerase iii beta-subunit dnan (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:28015 percent identity: 26.03;) (le:9789) (re:10913) (di:direct) HPAE000564 AE000564 g2313610 Helicobacter pylori 26695 85962 -11538647

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899378	16796	38952	1113	370

Description

6500734790 apt:hp0572 adenine phosphoribosyltransferase (gtcfc:4.1:4.4) (ec:2.4.2.7) (keggfc:4.1) (tigrfc:8.5) (db:gtc-helicobacter pylori) HP0572 HP0572 Helicobacter pylori 210 -11538648 7500877006 apt:hp0572 (sr:,campylobacter pylori) (ec:2.4.2.7) (de:adenine phosphoribosyltransferase, (aprt)) (db:swissprot) APT_HELPY O25296 HELICOBACTER PYLORI 210 -11538648 7000689074 apt adenine phosphoribosyltransferase::amp pyrophosphorylase:transphosphoribosidase (cl:adenine phosphoribosyltransferase) (ec:2.4.2.7) (db:pir2.dat) D64591 D64591 Helicobacter pylori 210 -11538648 7500877008 hp0572 adenine phosphoribosyltransferase apt (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:21858 percent identity: 50.29;) (le:3331) (re:3870) (di:complement) HPAE000571 AE000571 g2313692 Helicobacter pylori 210 -11538648 7502852496 hp0572 adenine phosphoribosyltransferase apt (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:21858 percent identity: 50.29;) (le:3331) (re:3870) (di:complement) HPAE000571 AE000571 g2313692 Helicobacter pylori 26695 85962 -11538648

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899380	16797	38953	378	125

Description

6500734791 adenylate kinase adk:adenylate kinase:adk (gtcfc:4.1) (ec:2.7.4.3) (keggfc:4.1) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP0618 HP0618 Helicobacter pylori 210 -11538649 5500685451 adk:hp0618 (sr:,campylobacter pylori) (ec:2.7.4.3) (de:adenylate kinase, (atp-amp transphosphorylase)) (db:swissprot) KAD_HELPY P56104 HELICOBACTER PYLORI 210 -11538649 7000685660 adenylate kinase (cl:adenylate kinase) (db:pir2.dat) B64597 B64597 Helicobacter pylori 210 -11538649 7500884460 hp0618 adenylate kinase adk (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:similar to egad:18646 percent identity: 33.33;) (le:5391) (re:5966) (di:direct) HPAE000576 AE000576 g2313740 Helicobacter pylori 210 -11538649 7502852497 hp0618 adenylate kinase adk (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:similar to egad:18646 percent identity: 33.33;) (le:5391) (re:5966) (di:direct) HPAE000576 AE000576 g2313740 Helicobacter pylori 26695 85962 -11538649

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899381	16798	38954	654	217

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899385	16799	38955	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899407	16800	38956	759	252

Description

6500734792 dnax:hp0717 dna polymerase iii gamma and tau subunits (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0717 HP0717 Helicobacter pylori 210 -11538650 7000689904 dna polymerase iii gamma and tau subunits (db:pir2.dat) E64609 E64609 Helicobacter pylori 210 -11538650 7500958700 hp0717 dna polymerase iii gamma and tau subunits (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:similar to egad:21779 percent identity: 38.96;) (le:9317) (re:11053) (di:complement) HPAE000584 AE000584 g2313841 Helicobacter pylori 210 -11538650 7502852498 hp0717 dna polymerase iii gamma and tau subunits (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:similar to egad:21779 percent identity: 38.96;) (le:9317) (re:11053) (di:complement) HPAE000584 AE000584 g2313841 Helicobacter pylori 26695 85962 -11538650

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899412	16801	38957	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899419	16802	38958	2076	692

Description

6500734793 spot:hp0775 penta-phosphate guanosine-3-pyrophosphohydrola:penta-phosphateguanosine-3-pyrophosphohydrolase (gtcfc:4.1:12.13) (ec:3.1.7.2) (keggfc:4.1) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0775 HP0775 Helicobacter pylori 210 -11538651 7000690612 penta-phosphate guanosine-3-pyrophosphohydrolase (cl:guanosine 3',5'-bis(diphosphate) 3'-pyrophosphatase) (db:pir2.dat) G64616 G64616 Helicobacter pylori 210 -11538651 7500959391 hp0775 penta-phosphate (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:similar to egad:12642 percent identity: 36.75;) (le:7476) (re:9803) (di:complement) HPAE000589 AE000589 g2313901 Helicobacter pylori 210 -11538651 7502852499 hp0775 penta-phosphate (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:similar to egad:12642 percent identity: 36.75;) (le:7476) (re:9803) (di:complement) HPAE000589 AE000589 g2313901 Helicobacter pylori 26695 85962 -11538651

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899442	16803	38959	690	229

Description

6500734794 guab:hp0829 inosine-5-monophosphate dehydrogenase (gtcfc:4.1) (ec:1.1.1.205) (keggfc:4.1) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP0829 HP0829 Helicobacter pylori 210 -11538652 5500685435 guab:hp0829 (sr:,campylobacter pylori) (ec:1.1.1.205) (de:dehydrogenase) (impdh) (impd)) (db:swissprot) IMDH_HELPY P56088 HELICOBACTER PYLORI 210 -11538652 7000685630 imp dehydrogenase (cl:imp dehydrogenase:cbs homology) (ec:1.1.1.205) (db:pir2.dat) E64623 E64623 Helicobacter pylori 210 -11538652 7500884114 hp0829 inosine-5-monophosphate dehydrogenase guab (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:37946 percent identity: 58.49;) (le:3953) (re:5398) (di:complement) HPAE000594 AE000594 g2313963 Helicobacter pylori 210 -11538652 7502852500 hp0829 inosine-5-monophosphate dehydrogenase guab (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:37946 percent identity: 58.49;) (le:3953) (re:5398) (di:complement) HPAE000594 AE000594 g2313963 Helicobacter pylori 26695 85962 -11538652

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899453	16804	38960	2172	723

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899454	16805	38961	3504	1168

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899463	16806	38962	2106	701

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899472	16807	38963	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899505	16808	38964	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899506	16809	38965	1122	373

Description

GTC ORF with score 241 to: (or:Homo sapiens) (sr:human) (db:genpept-pri3) (de:homo sapiens h-bcs1 (bcs1) mrna, nuclear gene encodingmitochondrial protein, complete cds.) (nt:mitochondrial protein; similar to bcs1p of) (le:114) (re:1373) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899511	16810	38966	597	198

Description

GTC ORF with score 175 to: (or:Homo sapiens) (sr:human) (db:genpept-pri3) (de:homo sapiens h-bcs1 (bcs1) mrna, nuclear gene encodingmitochondrial protein, complete cds.) (nt:mitochondrial protein; similar to bcs1p of) (le:114) (re:1373) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899532	16811	38967	789	262

Description

6500734795 purb:hp1112 adenylosuccinate lyase (gtcfc:4.1:5.2) (ec:4.3.2.2) (keggfc:4.1:5.2) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP1112 HP1112 Helicobacter pylori 210 -11538653 7500889068 purb:hp1112 (sr:,campylobacter pylori) (ec:4.3.2.2) (de:adenylosuccinate lyase, (adenylosuccinase) (asl)) (db:swissprot) PUR8_HELPY P56468 HELICOBACTER PYLORI 210 -11538653 7000689189 adenylosuccinate lyase (c1:fumarate hydratase) (db:pir2.dat) H64658 H64658 Helicobacter pylori 210 -11538653 7500889070 hp1112 adenylosuccinate lyase purb (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to egad:15453 percent identity: 49.53;) (le:8189) (re:9511) (di:direct) HPAE000617 AE000617 g2314263 Helicobacter pylori 210 -11538653 7502852501 hp1112 adenylosuccinate lyase purb (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to egad:15453 percent identity: 49.53;) (le:8189) (re:9511) (di:direct) HPAE000617 AE000617 g2314263 Helicobacter pylori 26695 85962 -11538653

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899540	16812	38968	2013	670

Description

6500734796 deod:hp1178 purine-nucleoside phosphorylase (gtcfc:4.1:4.2:4.4:9.4) (ec:2.4.2.1) (keggfc:4.1:4.2:9.4) (tigrfc:8.5) (db:gtc-helicobacter pylori) HP1178 HP1178 Helicobacter pylori 210 -11538654 7500880174 deod:hp1178 (sr:,campylobacter pylori) (ec:2.4.2.1) (de:(pnp)) (db:swissprot) DEOD_HELPY P56463 HELICOBACTER PYLORI 210 -11538654 7000690662 purine-nucleoside phosphorylase (cl:purine-nucleoside phosphorylase pnp) (db:pir2.dat) B64667 B64667 Helicobacter pylori 210 -11538654 7500880176 hp1178 purine-nucleoside phosphorylase deod (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:13741 percent identity: 55.46;) (le:9529) (re:10230) (di:complement) HPAE000623 AE000623 g2314335 Helicobacter pylori 210 -11538654 7502852502 hp1178 purine-nucleoside phosphorylase deod (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:13741 percent identity: 55.46;) (le:9529) (re:10230) (di:complement) HPAE000623 AE000623 g2314335 Helicobacter pylori 26695 85962 -11538654

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899551	16813	38969	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899557	16814	38970	834	277

Description

6500734797 rpob:hp1198 dna-directed rna polymerase:beta subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-helicobacter pylori) HP1198 HP1198 Helicobacter pylori 210 -11538655 7000689909 dna-directed rna polymerase:beta subunit (db:pir2.dat) F64669 F64669 Helicobacter pylori 210 -11538655 7500958705 hp1198 dna-directed rna polymerase:beta subunit (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to egad:10840 percent identity: 47.78;) (le:9068) (re:17740) (di:complement) HPAE000625 AE000625 g2314357 Helicobacter pylori 210 -11538655 7502852503 hp1198 dna-directed rna polymerase:beta subunit (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to egad:10840 percent identity: 47.78;) (le:9068) (re:17740) (di:complement) HPAE000625 AE000625 g2314357 Helicobacter pylori 26695 85962 -11538655

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899567	16815	38971	270	89

Description

6500734798 pnp:hp1213 polynucleotide phosphorylase (gtcfc:4.1:4.2:10.9) (ec:2.7.7.8) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-helicobacter pylori) HP1213 HP1213 Helicobacter pylori 210 -11538656 7000690632 polynucleotide phosphorylase (cl:polyribonucleotide nucleotidyltransferase alpha chain) (db:pir2.dat) E64671 E64671 Helicobacter pylori 210 -11538656 7500959412 hp1213 polynucleotide phosphorylase pnp (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:similar to egad:28876 percent identity: 38.87;) (le:933) (re:2999) (di:complement) HPAE000627 AE000627 g2314375 Helicobacter pylori 210 -11538656 7502852504 hp1213 polynucleotide phosphorylase pnp (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:similar to egad:28876 percent identity: 38.87;) (le:933) (re:2999) (di:complement) HPAE000627 AE000627 g2314375 Helicobacter pylori 26695 85962 -11538656

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899573	16816	38972	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899574	16817	38973	240	79

Description

6500734799 purd:hp1218 glycinamide ribonucleotide synthetase (gtcfc:4.1) (ec:6.3.4.13) (keggfc:4.1) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP1218 HP1218 Helicobacter pylori 210 -11538657 7000689972 glycinamide ribonucleotide synthetase (cl:phosphoribosylamine--glycine ligase homology) (db:pir2.dat) B64672 B64672 Helicobacter pylori 210 -11538657 7500958757 hp1218 glycinamide ribonucleotide synthetase purd (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:similar to egad:29361 percent identity: 31.82;) (le:6512) (re:7786) (di:complement) HPAE000627 AE000627 g2314378 Helicobacter pylori 210 -11538657 7502852505 hp1218 glycinamide ribonucleotide synthetase purd (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:similar to egad:29361 percent identity: 31.82;) (le:6512) (re:7786) (di:complement) HPAE000627 AE000627 g2314378 Helicobacter pylori 26695 85962 -11538657

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899578	16818	38974	564	187

Description

6500734800 rpoa:hp1293 dna-directed rna polymerase:alpha subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-helicobacter pylori) HP1293 HP1293 Helicobacter pylori 210 -11538658 5500685909 rpoa:hp1293 (sr:,campylobacter pylori) (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA_HELPY P56001 HELICOBACTER PYLORI 210 -11538658 7000686459 dna-directed rna polymerase:alpha subunit (db:pir2.dat) E64681 E64681 Helicobacter pylori 210 -11538658 7500890601 hp1293 dna-directed rna polymerase:alpha subunit (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:15427 percent identity: 35.29;) (le:6130) (re:7164) (di:complement) HPAE000633 AE000633 g2314459 Helicobacter pylori 210 -11538658 7502852506 hp1293 dna-directed rna polymerase:alpha subunit (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:15427 percent identity: 35.29;) (le:6130) (re:7164) (di:complement) HPAE000633 AE000633 g2314459 Helicobacter pylori 26695 85962 -11538658

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899585	16819	38975	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899595	16820	38976	447	148

Description

6500734801 dnaq:hp1387 dna polymerase iii epsilon subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1387 HP1387 Helicobacter pylori 210 -11538659 7000689903 dna polymerase iii epsilon subunit (db:pir2.dat) C64693 C64693 Helicobacter pylori 210 -11538659 7500958699 hp1387 dna polymerase iii epsilon subunit dnaq (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:similar to egad:21587 percent identity: 35.05;) (le:7842) (re:8894) (di:direct) HPAE000638 AE000638 g2314554 Helicobacter pylori 210 -11538659 7502852507 hp1387 dna polymerase iii epsilon subunit dnaq (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:similar to egad:21587 percent identity: 35.05;) (le:7842) (re:8894) (di:direct) HPAE000638 AE000638 g2314554 Helicobacter pylori 26695 85962 -11538659

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899600	16821	38977	333	110

Description

6500734802 dnae:hp1460 dna polymerase iii alpha-subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1460 HP1460 Helicobacter pylori 210 -11538660 5500685118 dnae:hp1460 (sr:,campylobacter pylori) (ec:2.7.7.7) (de:dna polymerase iii, alpha chain,) (db:swissprot) DP3A_HELPY P56157 HELICOBACTER PYLORI 210 -11538660 7000685084 dna polymerase iii alpha-subunit (cl:dna-directed dna polymerase iii alpha chain) (db:pir2.dat) D64702 D64702 Helicobacter pylori 210 -11538660 7500880545 hp1460 dna polymerase iii alpha-subunit dnae (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:similar to egad:34108 percent identity: 42.03;) (le:1354) (re:4989) (di:complement) HPAE000646 AE000646 g2314638 Helicobacter pylori 210 -11538660 7502852508 hp1460 dna polymerase iii alpha-subunit dnae (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:similar to egad:34108 percent identity: 42.03;) (le:1354) (re:4989) (di:complement) HPAE000646 AE000646 g2314638 Helicobacter pylori 26695 85962 -11538660

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899612	16822	38978	1146	381

Description

6500734803 pola:hp1470 dna polymerase i pola:dna polymerase i (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1470 HP1470 Helicobacter pylori 210 -11538661 5500685120 pola:hp1470 (sr:,campylobacter pylori) (ec:2.7.7.7) (de:dna polymerase i, (pol i)) (db:swissprot) DPO1_HELPY P56105 HELICOBACTER PYLORI 210 -11538661 7000685088 dna polymerase i (cl:dna-directed dna polymerase i) (db:pir2.dat) F64703 F64703 Helicobacter pylori 210 -11538661 7500880575 hp1470 dna polymerase i pola (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:19848 percent identity: 39.97;) (le:2733) (re:5411) (di:complement) HPAE000647 AE000647 g2314647 Helicobacter pylori 210 -11538661 7502852509 hp1470 dna polymerase i pola (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:19848 percent identity: 39.97;) (le:2733) (re:5411) (di:complement) HPAE000647 AE000647 g2314647 Helicobacter pylori 26695 85962 -11538661

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899615	16823	38979	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899617	16824	38980	354	117

Description

6500734804 guac:hp0854 gmp reductase guac:gmp reductase (gtcfc:4.1) (keggfc:14.2) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP0854 HP0854 Helicobacter pylori 210 -11538662 7000689975 gmp reductase:homolog (ec:1.6.6.8) (db:pir2.dat) F64626 F64626 Helicobacter pylori 210 -11538662 7500958759 hp0854 gmp reductase guac (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to sp:p36959 percent identity: 31.76;) (le:6961) (re:7944) (di:direct) HPAE000596 AE000596 g2313987 Helicobacter pylori 210 -11538662 7502852510 hp0854 gmp reductase guac (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to sp:p36959 percent identity: 31.76;) (le:6961) (re:7944) (di:direct) HPAE000596 AE000596 g2313987 Helicobacter pylori 26695 85962 -11538662

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899625	16825	38981	867	288

Description

6500734805 punb:hp1530 purine nucleoside phosphorylase (gtcfc:4.1) (keggfc:14.2) (tigrfc:8.3) (db:gtc-helicobacter pylori) HP1530 HP1530 Helicobacter pylori 210 -11538663 7000690660 purine nucleoside phosphorylase (db:pir2.dat) B64711 B64711 Helicobacter pylori 210 -11538663 7500959435 hp1530 purine nucleoside phosphorylase punb (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:similar to gp:1638807 percent identity: 20.67;) (le:3353) (re:3895) (di:direct) HPAE000651 AE000651 g2314710 Helicobacter pylori 210 -11538663 7502852511 hp1530 purine nucleoside phosphorylase punb (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:similar to gp:1638807 percent identity: 20.67;) (le:3353) (re:3895) (di:direct) HPAE000651 AE000651 g2314710 Helicobacter pylori 26695 85962 -11538663

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899642	16826	38982	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899678	16827	38983	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899683	16828	38984	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899688	16829	38985	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899696	16830	38986	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899699	16831	38987	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899711	16832	38988	228	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899724	16833	38989	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899733	16834	38990	1422	473

Description

6500734806 pyrf:hp0005 orotidine 5-phosphate decarboxylase (gtcfc:4.2) (ec:4.1.1.23) (keggfc:4.2) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP0005 HP0005 Helicobacter pylori 210 -11538664 5500685072 pyrf:hp0005 (sr:,campylobacter pylori) (ec:4.1.1.23) (de:decarboxylase)) (db:swissprot) DCOP_HELPY P56155 HELICOBACTER PYLORI 210 -11538664 7000684992 orotidine 5-phosphate decarboxylase (db:pir2.dat) E64520 E64520 Helicobacter pylori 210 -11538664 7500880062 hp0005 orotidine 5-phosphate decarboxylase pyrf (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to egad:16927 percent identity: 38.97;) (le:2719) (re:3402) (di:direct) HPAE000523 AE000523 g2313082 Helicobacter pylori 210 -11538664 7502852512 hp0005 orotidine 5-phosphate decarboxylase pyrf (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to egad:16927 percent identity: 38.97;) (le:2719) (re:3402) (di:direct) HPAE000523 AE000523 g2313082 Helicobacter pylori 26695 85962 -11538664

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899734	16835	38991	498	165

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899737	16836	38992	789	263

Description

6500734807 pyrc:hp0266 dihydroorotase pyrc:dihydroorotase (gtcfc:4.2) (ec:3.5.2.3) (keggfc:4.2) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP0266 HP0266 Helicobacter pylori 210 -11538665 7000689891 dihydroorotase (db:pir2.dat) B64553 B64553 Helicobacter pylori 210 -11538665 7500958689 hp0266 dihydroorotase pyrc (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to gp:151524 percent identity: -1.00;) (le:11353) (re:12489) (di:direct) HPAE000545 AE000545 g2313358 Helicobacter pylori 210 -11538665 5000695921 hp0266 dihydroorotase pyrc (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to gp:151524 percent identity: -1.00;) (le:11353) (re:12489) (di:direct) HPAE000545 AE000545 g2313358 Helicobacter pylori 26695 85962 -11538665

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899754	16837	38993	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899766	16838	38994	321	106

Description

6500734808 pyrg:hp0349 ctp synthetase pyrg:ctp synthetase (gtcfc:4.2) (ec:6.3.4.2) (keggfc:4.2) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP0349 HP0349 Helicobacter pylori 210 -11538666 7500889176 pyrg:hp0349 (sr:,campylobacter pylori) (ec:6.3.4.2) (de:ctp synthase, (utp--ammonia ligase) (ctp synthetase)) (db:swissprot) PYRG_HELPY O25116 HELICOBACTER PYLORI 210 -11538666 7000689222 ctp synthetase (cl:ctp synthase) (db:pir2.dat) E64563 E64563 Helicobacter pylori 210 -11538666 7500889178 hp0349 ctp synthetase pyrg (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:similar to egad:28088 percent identity: 50.66;) (le:11133) (re:12749) (di:complement) HPAE000551 AE000551 g2313438 Helicobacter pylori 210 -11538666 7502852513 hp0349 ctp synthetase pyrg (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:similar to egad:28088 percent identity: 50.66;) (le:11133) (re:12749) (di:complement) HPAE000551 AE000551 g2313438 Helicobacter pylori 26695 85962 -11538666

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899784	16839	38995	747	248

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899808	16840	38996	474	157

Description

6500734809 dcd:hp0372 deoxycytidine triphosphate deaminase (gtcfc:4.2) (ec:3.5.4.13) (keggfc:4.2) (tigrfc:8.2) (db:gtc-helicobacter pylori) (tigrfc:2'-deoxyribonucleotide metabolism) HP0372 HP0372 Helicobacter pylori 210 -11538667 7000689161 dctp deaminase (cl:dctp deaminase) (ec:3.5.4.13) (db:pir2.dat) D64566 D64566 Helicobacter pylori 210 -11538667 7500954321 hp0372 deoxycytidine triphosphate deaminase dcd (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:similar to egad:28786 percent identity: 28.19;) (le:92) (re:664) (di:direct) HPAE000554 AE000554 g2313476 Helicobacter pylori 210 -11538667 7502852514 hp0372 deoxycytidine triphosphate deaminase dcd (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:similar to egad:28786 percent identity: 28.19;) (le:92) (re:664) (di:direct) HPAE000554 AE000554 g2313476 Helicobacter pylori 26695 85962 -11538667

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899822	16841	38997	2775	924

Description

6500734810 pyrc:hp0581 dihydroorotase pyrc:dihydroorotase (gtcfc:4.2) (ec:3.5.2.3) (keggfc:4.2) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP0581 HP0581 Helicobacter pylori 210 -11538668 7500889148 pyrc:hp0581 (sr:,campylobacter pylori) (ec:3.5.2.3) (de:dihydroorotase, (dhoase)) (db:swissprot) PYRC_HELPY P56465 HELICOBACTER PYLORI 210 -11538668 7000689892 dihydroorotase (db:pir2.dat) E64592 E64592 Helicobacter pylori 210 -11538668 7500889150 hp0581 dihydroorotase pyrc (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:21845 percent identity: 31.53;) (le:11016) (re:12035) (di:complement) HPAE000571 AE000571 g2313687 Helicobacter pylori 210 -11538668 7502852515 hp0581 dihydroorotase pyrc (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:21845 percent identity: 31.53;) (le:11016) (re:12035) (di:complement) HPAE000571 AE000571 g2313687 Helicobacter pylori 26695 85962 -11538668

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899831	16842	38998	405	134

Description

6500734811 trxb:hp0825 thioredoxin reductase (gtcfc:9.13) (ec:1.6.4.5) (keggfc:4.2) (tigrfc:8.2) (db:gtc-helicobacter pylori) (tigrfc:2'-deoxyribonucleotide metabolism) HP0825 HP0825 Helicobacter pylori 210 -11538669 7500893534 trxb:hp0825 (sr:,campylobacter pylori) (ec:1.6.4.5) (de:thioredoxin reductase,) (db:swissprot) TRXB_HELPY P56431 HELICOBACTER PYLORI 210 -11538669 7000690730 thioredoxin reductase nadph (cl:thioredoxin reductase:thioredoxin reductase homology) (ec:1.6.4.5) (db:pir1.dat) A64623 A64623 Helicobacter pylori 210 -11538669 7500893536 hp0825 thioredoxin reductase trxb (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:38393 percent identity: 45.90;) (le:400) (re:1335) (di:direct) HPAE000594 AE000594 g2313959 Helicobacter pylori 210 -11538669 7502852516 hp0825 thioredoxin reductase trxb (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:38393 percent identity: 45.90;) (le:400) (re:1335) (di:direct) HPAE000594 AE000594 g2313959 Helicobacter pylori 26695 85962 -11538669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899849	16843	38999	1314	437

Description

6500734812 gmha:hp0857 phosphoheptose isomerase (gtcfc:4.2:6.1:9.5:11.3) (ec:3.5.1.6) (keggfc:4.2:6.1:9.5) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0857 HP0857 Helicobacter pylori 210 -11538670 7000689194 phosphoheptose isomerase (cl:phosphoheptose isomerase) (ec:5.-.-.-) (db:pir2.dat) A64627 A64627 Helicobacter pylori 210 -11538670 7500954445 hp0857 phosphoheptose isomerase gmha (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:36989 percent identity: 44.50;) (le:10780) (re:11358) (di:complement) HPAE000596 AE000596 g2313989 Helicobacter pylori 210 -11538670 7502852517 hp0857 phosphoheptose isomerase gmha (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:36989 percent identity: 44.50;) (le:10780) (re:11358) (di:complement) HPAE000596 AE000596 g2313989 Helicobacter pylori 26695 85962 -11538670

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899872	16844	39000	657	218

Description

6500734813 dut:hp0865 deoxyuridine 5-triphosphate nucleotidohydrolase (gtcfc:4.2) (ec:3.6.1.23) (keggfc:4.2) (tigrfc:8.2) (db:gtc-helicobacter pylori) (tigrfc:2'-deoxyribonucleotide metabolism) HP0865 HP0865 Helicobacter pylori 210 -11538671 7000689886 deoxyuridine 5-triphosphate nucleotidohydrolase (db:pir2.dat) A64628 A64628 Helicobacter pylori 210 -11538671 7500958686 hp0865 deoxyuridine 5-triphosphate nucleotidohydrolase (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to sp:p43058 percent identity: 41.43;) (le:17938) (re:18375) (di:complement) HPAE000596 AE000596 g2313993 Helicobacter pylori 210 -11538671 7502852518 hp0865 deoxyuridine 5-triphosphate nucleotidohydrolase (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to sp:p43058 percent identity: 41.43;) (le:17938) (re:18375) (di:complement) HPAE000596 AE000596 g2313993 Helicobacter pylori 26695 85962 -11538671

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899874	16845	39001	753	250

Description

6500734814 pyrd:hp1011 dihydroorotate dehydrogenase (gtcfc:4.2) (ec:1.3.99.11) (keggfc:4.2) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP1011 HP1011 Helicobacter pylori 210 -11538672 7000689893 dihydroorotate dehydrogenase (db:pir2.dat) C64646 C64646 Helicobacter pylori 210 -11538672 7500958690 hp1011 dihydroorotate dehydrogenase pyrd (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:similar to egad:28401 percent identity: 41.52;) (le:7508) (re:8563) (di:direct) HPAE000609 AE000609 g2314154 Helicobacter pylori 210 -11538672 7502852519 hp1011 dihydroorotate dehydrogenase pyrd (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:similar to egad:28401 percent identity: 41.52;) (le:7508) (re:8563) (di:direct) HPAE000609 AE000609 g2314154 Helicobacter pylori 26695 85962 -11538672

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899877	16846	39002	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899891	16847	39003	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899905	16848	39004	417	138

Description

6500734815 pyrb:hp1084 aspartate transcarbamoylase (gtcfc:4.2:5.2) (ec:2.1.3.2) (keggfc:4.2:5.2) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP1084 HP1084 Helicobacter pylori 210 -11538673 7000689645 aspartate transcarbamoylase (cl:aspartate/ornithine carbamoyltransferase homology) (db:pir2.dat) D64655 D64655 Helicobacter pylori 210 -11538673 7500958462 hp1084 aspartate transcarbamoylase pyrb (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:similar to egad:16102 percent identity: 38.70;) (le:4717) (re:5640) (di:complement) HPAE000615 AE000615 g2314233 Helicobacter pylori 210 -11538673 7502852520 hp1084 aspartate transcarbamoylase pyrb (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:similar to egad:16102 percent identity: 38.70;) (le:4717) (re:5640) (di:complement) HPAE000615 AE000615 g2314233 Helicobacter pylori 26695 85962 -11538673

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899906	16849	39005	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899909	16850	39006	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899922	16851	39007	1983	660

Description

6500734816 pyre:hp1257 orotate phosphoribosyltransferase (gtcfc:4.2) (ec:2.4.2.10) (keggfc:4.2) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP1257 HP1257 Helicobacter pylori 210 -11538674 5500685799 pyre:hp1257 (sr:,campylobacter pylori) (ec:2.4.2.10) (de:orotate phosphoribosyltransferase, (oprt) (oprtase)) (db:swissprot) PYRE_HELPY P56162 HELICOBACTER PYLORI 210 -11538674 7000686252 orotate phosphoribosyltransferase (db:pir2.dat) A64677 A64677 Helicobacter pylori 210 -11538674 7500889168 hp1257 orotate phosphoribosyltransferase pyre (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:42983 percent identity: 35.52;) (le:1255) (re:1860) (di:direct) HPAE000631 AE000631 g2314424 Helicobacter pylori 210 -11538674 7502852521 hp1257 orotate phosphoribosyltransferase pyre (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:42983 percent identity: 35.52;) (le:1255) (re:1860) (di:direct) HPAE000631 AE000631 g2314424 Helicobacter pylori 26695 85962 -11538674

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899924	16852	39008	315	104

Description

6500734817 thymidylate kinase tmk:thymidylate kinase:tmk (gtcfc:4.2) (ec:2.7.4.9) (keggfc:4.2) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP1474 HP1474 Helicobacter pylori 210 -11538675 7000690733 thymidylate kinase (db:pir2.dat) B64704 B64704 Helicobacter pylori 210 -11538675 7500959498 hp1474 thymidylate kinase tmk (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:31526 percent identity: 33.85;) (le:9371) (re:9946) (di:complement) HPAE000647 AE000647 g2314650 Helicobacter pylori 210 -11538675 7502852522 hp1474 thymidylate kinase tmk (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:31526 percent identity: 33.85;) (le:9371) (re:9946) (di:complement) HPAE000647 AE000647 g2314650 Helicobacter pylori 26695 85962 -11538675

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899930	16853	39009	1026	341

Description

6500734818 pyrh:hp0777 uridine 5-monophosphate:ump kinase:uridine 5-monophosphate:ump kinase (gtcfc:4.2) (ec:2.7.4.-) (keggfc:14.1) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP0777 HP0777 Helicobacter pylori 210 -11538676 5500685801 pyrh:hp0777 (sr:,campylobacter pylori) (ec:2.7.4.-) (de:(ump kinase)) (db:swissprot) PYRH_HELPY P56106 HELICOBACTER PYLORI 210 -11538676 7000686253 uridine 5-monophosphate (cl:uridine 5'-monophosphate kinase) (db:pir2.dat) A64617 A64617 Helicobacter pylori 210 -11538676 7500889182 hp0777 uridine 5-monophosphate ump kinase pyrh (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:similar to egad:37344 percent identity: 50.43;) (le:10056) (re:10778) (di:complement) HPAE000589 AE000589 g2313902 Helicobacter pylori 210 -11538676 7502852523 hp0777 uridine 5-monophosphate ump kinase pyrh (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:similar to egad:37344 percent identity: 50.43;) (le:10056) (re:10778) (di:complement) HPAE000589 AE000589 g2313902 Helicobacter pylori 26695 85962 -11538676

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899933	16854	39010	1464	487

Description

6500734819 pyrab:hp0919 carbamoyl-phosphate synthase:glutamine-hydrolysing:carbamoyl-phosphate synthase:glutamine-hydrolysing (gtcfc:4.2:5.1) (ec:6.3.5.5) (keggfc:5.1) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP0919 HP0919 Helicobacter pylori 210 -11538677 7000689227 carbamoyl-phosphate synthase glutamine-hydrolyzing:large chain (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain:biotin carboxylase homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology) (ec:6.3.5.5) (db:pir2.dat) G64634 G64634 Helicobacter pylori 210 -11538677 7500954517 hp0919 carbamoyl-phosphate synthase (db:genpept-bct1) (de:helicobacter pylori section 79 of 134 of the complete genome.) (nt:similar to egad:19155 percent identity: 48.63;) (le:5405) (re:8662) (di:complement) HPAE000601 AE000601 g2314054 Helicobacter pylori 210 -11538677 7502852524 hp0919 carbamoyl-phosphate synthase (db:genpept) (de:helicobacter pylori 26695 section 79 of 134 of the complete genome.) (nt:similar to egad:19155 percent identity: 48.63;) (le:5405) (re:8662) (di:complement) HPAE000601 AE000601 g2314054 Helicobacter pylori 26695 85962 -11538677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899945	16855	39011	456	151

Description

6500734820 pyraa:hp1237 carbamoyl-phosphate synthetase (gtcfc:4.2:5.1) (ec:6.3.5.5) (keggfc:5.1) (tigrfc:8.4) (db:gtc-helicobacter pylori) HP1237 HP1237 Helicobacter pylori 210 -11538678 7000689691 carbamoyl-phosphate synthetase (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology:trpg homology) (db:pir2.dat) E64674 E64674 Helicobacter pylori 210 -11538678 7500958502 hp1237 carbamoyl-phosphate synthetase pyraa (db:genpept-bct1) (de:helicobacter pylori section 107 of 134 of the complete genome.) (nt:similar to egad:12319 percent identity: 39.68;) (le:621) (re:1748) (di:direct) HPAE000629 AE000629 g2314401 Helicobacter pylori 210 -11538678 7502852525 hp1237 carbamoyl-phosphate synthetase pyraa (db:genpept) (de:helicobacter pylori 26695 section 107 of 134 of the completegenome.) (nt:similar to egad:12319 percent identity: 39.68;) (le:621) (re:1748) (di:direct) HPAE000629 AE000629 g2314401 Helicobacter pylori 26695 85962 -11538678

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899948	16856	39012	1134	377

Description

6500734821 nrda:hp0680 ribonucleoside-diphosphate reductase 1 alpha subunit:ribonucleoside-diphosphate reductase 1 alphasubunit (gtcfc:4.2) (ec:1.17.4.-) (keggfc:14.1) (tigrfc:8.2) (db:gtc-helicobacter pylori) (tigrfc:2'-deoxyribonucleotide metabolism) HP0680 HP0680 Helicobacter pylori 210 -11538679 5500685835 nrda:hp0680 (sr:,campylobacter pylori) (ec:1.17.4.1) (de:(ribonucleotide reductase)) (db:swissprot) RIR1_HELPY P55982 HELICOBACTER PYLORI 210 -11538679 7000686336 ribonucleoside-diphosphate reductase:1 alpha chain (ec:1.17.4.1) (db:pir2.dat) H64604 H64604 Helicobacter pylori 210 -11538679 7500889799 hp0680 ribonucleoside-diphosphate reductase 1 alpha (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:similar to egad:8706 percent identity: 28.38;) (le:2462) (re:4828) (di:complement) HPAE000581 AE000581 g2313806 Helicobacter pylori 210 -11538679 7502852526 hp0680 ribonucleoside-diphosphate reductase 1 alpha (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:similar to egad:8706 percent identity: 28.38;) (le:2462) (re:4828) (di:complement) HPAE000581 AE000581 g2313806 Helicobacter pylori 26695 85962 -11538679

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899949	16857	39013	1128	375

Description

6500734822 slt:hp0645 soluble lytic murein transglycosylase (gtcfc:4.3:7.1:11.4) (ec:3.2.1.-) (keggfc:4.3:4.4) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0645 HP0645 Helicobacter pylori 210 -11538680 7000690714 soluble lytic murein transglycosylase (db:pir2.dat) E64600 E64600 Helicobacter pylori 210 -11538680 7500959480 hp0645 soluble lytic murein transglycosylase slt (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:23218 percent identity: 32.17;) (le:6716) (re:8398) (di:direct) HPAE000578 AE000578 g2313765 Helicobacter pylori 210 -11538680 7502852527 hp0645 soluble lytic murein transglycosylase slt (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:23218 percent identity: 32.17;) (le:6716) (re:8398) (di:direct) HPAE000578 AE000578 g2313765 Helicobacter pylori 26695 85962 -11538680

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899988	16858	39014	504	167

Description

6500734823 nolk:hp0045 nodulation protein nolk:nodulation protein (gtcfc:4.3) (keggfc:14.2) (tigrfc:8.6) (db:gtc-helicobacter pylori) HP0045 HP0045 Helicobacter pylori 210 -11538681 7000690561 nodulation protein (cl:hypothetical protein sll1213) (db:pir2.dat) E64525 E64525 Helicobacter pylori 210 -11538681 7500959346 hp0045 nodulation protein nolk (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:similar to egad:9251 percent identity: 44.26;) (le:5599) (re:6531) (di:direct) HPAE000526 AE000526 g2313120 Helicobacter pylori 210 -11538681 7502852528 hp0045 nodulation protein nolk (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:similar to egad:9251 percent identity: 44.26;) (le:5599) (re:6531) (di:direct) HPAE000526 AE000526 g2313120 Helicobacter pylori 26695 85962 -11538681

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501899999	16859	39015	876	291

Description

6500734824 glmu:hp0683 udp-n-acetylglucosamine pyrophosphorylase (gtcfc:4.3:7.1) (ec:2.7.7.23) (keggfc:4.4) (tigrfc:8.6) (db:gtc-helicobacter pylori) HP0683 HP0683 Helicobacter pylori 210 -11538682 7000690785 udp-n-acetylglucosamine pyrophosphorylase (db:pir2.dat) C64605 C64605 Helicobacter pylori 210 -11538682 7500959548 hp0683 udp-n-acetylglucosamine pyrophosphorylase (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:similar to egad:8169 percent identity: 40.05;) (le:6080) (re:7381) (di:complement) HPAE000581 AE000581 g2313807 Helicobacter pylori 210 -11538682 7502852529 hp0683 udp-n-acetylglucosamine pyrophosphorylase (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:similar to egad:8169 percent identity: 40.05;) (le:6080) (re:7381) (di:complement) HPAE000581 AE000581 g2313807 Helicobacter pylori 26695 85962 -11538682

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900005	16860	39016	450	149

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900007	16861	39017	324	107

Description

6500734825 cpdb:hp0104 2-3-cyclic-nucleotide 2-phosphodiesterase:2:3-cyclic-nucleotide 2-phosphodiesterase (gtcfc:4.4) (ec:3.1.4.16) (keggfc:14.1) (tigrfc:8.5) (db:gtc-helicobacter pylori) HP0104 HP0104 Helicobacter pylori 210 -11538683 7000689587 hp0104 2:3-cyclic-nucleotide 2-phosphodiesterase:precursor (cl:2',3'-cyclic-nucleotide 2'-phosphodiesterase:2',3'-cyclic-nucleotide 2'-phosphodiesterase homology:phosphoesterase core homology) (ec:3.1.4.16) (db:pir1.dat) H64532 H64532 Helicobacter pylori 210 -11538683 7500953285 hp0104 2:3-cyclic-nucleotide 2-phosphodiesterase (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:similar to egad:29207 percent identity: 31.83;) (le:3594) (re:5339) (di:complement) HPAE000532 AE000532 g2313187 Helicobacter pylori 210 -11538683 7502852530 hp0104 2:3-cyclic-nucleotide 2-phosphodiesterase (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:similar to egad:29207 percent identity: 31.83;) (le:3594) (re:5339) (di:complement) HPAE000532 AE000532 g2313187 Helicobacter pylori 26695 85962 -11538683

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900010	16862	39018	1368	456

Description

6500734826 gpt:hp0735 xanthine guanine phosphoribosyl transferase (gtcfc:4.4) (ec:2.4.2.22) (keggfc:14.1) (tigrfc:8.5) (db:gtc-helicobacter pylori) HP0735 HP0735 Helicobacter pylori 210 -11538684 7000690798 xanthine guanine phosphoribosyl transferase (db:pir2.dat) G64611 G64611 Helicobacter pylori 210 -11538684 7500959556 hp0735 xanthine guanine phosphoribosyl transferase (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:29445 percent identity: 27.12;) (le:7624) (re:8085) (di:complement) HPAE000586 AE000586 g2313857 Helicobacter pylori 210 -11538684 7502852531 hp0735 xanthine guanine phosphoribosyl transferase (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:29445 percent identity: 27.12;) (le:7624) (re:8085) (di:complement) HPAE000586 AE000586 g2313857 Helicobacter pylori 26695 85962 -11538684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900014	16863	39019	474	157

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900016	16864	39020	477	158

Description

6500734827 nade:hp0329 nh3-dependent nad+ synthetase:nh:3-dependent nad+ synthetase (gtcfc:5.1:9.4) (ec:6.3.5.1) (keggfc:5.1:9.4) (tigrfc:2.12) (db:gtc-helicobacter pylori) HP0329 HP0329 Helicobacter pylori 210 -11538685 7000690553 nh 3 -dependent nad+ synthetase (cl:ammonia-dependent nad+ synthetase) (db:pir2.dat) A64561 A64561 Helicobacter pylori 210 -11538685 7500959340 hp0329 nh 3 -dependent nad+ synthetase nade (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:43958 percent identity: 37.50;) (le:10314) (re:11096) (di:complement) HPAE000550 AE000550 g2313427 Helicobacter pylori 210 -11538685 7502852532 hp0329 nh 3 -dependent nad+ synthetase nade (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:43958 percent identity: 37.50;) (le:10314) (re:11096) (di:complement) HPAE000550 AE000550 g2313427 Helicobacter pylori 26695 85962 -11538685

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900047	16865	39021	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900062	16866	39022	297	98

Description

6500734828 spea:hp0422 arginine decarboxylase (gtcfc:5.1:5.10:13.11) (ec:4.1.1.19) (keggfc:5.1:5.10) (tigrfc:5.4) (db:gtc-helicobacter pylori) HP0422 HP0422 Helicobacter pylori 210 -11538686 7000689643 arginine decarboxylase (db:pir2.dat) F64572 F64572 Helicobacter pylori 210 -11538686 7500958460 hp0422 arginine decarboxylase spea (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to egad:20433 percent identity: 33.28;) (le:14762) (re:16609) (di:direct) HPAE000557 AE000557 g2313524 Helicobacter pylori 210 -11538686 7502852533 hp0422 arginine decarboxylase spea (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to egad:20433 percent identity: 33.28;) (le:14762) (re:16609) (di:direct) HPAE000557 AE000557 g2313524 Helicobacter pylori 26695 85962 -11538686

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900063	16867	39023	441	146

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900080	16868	39024	1434	478

Description

6500734829 gltx:hp0476 glutamyl-trna synthetase (gtcfc:5.1:9.10:10.6) (ec:6.1.1.17) (keggfc:5.1:9.10:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0476 HP0476 Helicobacter pylori 210 -11538687 5500686012 gltx:hp0476 (sr:,campylobacter pylori) (ec:6.1.1.17) (de:(glurs)) (db:swissprot) SYE_HELPY P96551 HELICOBACTER PYLORI 210 -11538687 7000686707 glutamate--trna ligase (cl:glutamate--trna ligase:glutamine--trna ligase homology) (ec:6.1.1.17) (db:pir2.dat) D64579 D64579 Helicobacter pylori 210 -11538687 7500892375 hp0476 glutamyl-trna synthetase gltx (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to egad:16197 percent identity: 43.14;) (le:4780) (re:6171) (di:complement) HPAE000562 AE000562 g2313587 Helicobacter pylori 210 -11538687 7502852534 hp0476 glutamyl-trna synthetase gltx (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to egad:16197 percent identity: 43.14;) (le:4780) (re:6171) (di:complement) HPAE000562 AE000562 g2313587 Helicobacter pylori 26695 85962 -11538687

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900098	16869	39025	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900099	16870	39026	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900121	16871	39027	684	227

Description

6500734830 glr:hp0549 glutamate racemase (gtcfc:5.1:6.7:11.4) (ec:5.1.1.3) (keggfc:5.1:6.6) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0549 HP0549 Helicobacter pylori 210 -11538688 5500685587 muri:glr:hp0549 (sr:,campylobacter pylori) (ec:5.1.1.3) (de:glutamate racemase,) (db:swissprot) MURI_HELPY P56068 HELICOBACTER PYLORI 210 -11538688 7000685890 glutamate racemase (cl:glutamate racemase) (ec:5.1.1.3) (db:pir2.dat) E64588 E64588 Helicobacter pylori 210 -11538688 7500886154 hp0549 glutamate racemase glr (db:genpept-bct1) (de:helicobacter pylori section 47 of 134 of the complete genome.) (nt:similar to egad:18529 percent identity: 36.61;) (le:5109) (re:5876) (di:complement) HPAE000569 AE000569 g2313665 Helicobacter pylori 210 -11538688 7502852535 hp0549 glutamate racemase glr (db:genpept) (de:helicobacter pylori 26695 section 47 of 134 of the complete genome.) (nt:similar to egad:18529 percent identity: 36.61;) (le:5109) (re:5876) (di:complement) HPAE000569 AE000569 g2313665 Helicobacter pylori 26695 85962 -11538688

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900130	16872	39028	1194	397

Description

6500734831 glms:hp1532 glucosamine fructose-6-phosphate aminotransferase:isomerizing:glucosamine fructose-6-phosphateaminotransferase:isomerizing (gtcfc:5.1:7.1) (ec:2.6.1.16) (keggfc:5.1) (tigrfc:5.2) (db:gtc-helicobacter pylori) HP1532 HP1532 Helicobacter pylori 210 -11538689 7000689961 glutamine--fructose-6-phosphate transaminase isomerizing::glucosamine fructose-6-phosphate aminotransferase misnomer (cl:glutamine--fructose-6-phosphate aminotransferase (isomerizing)) (ec:2.6.1.16) (db:pir2.dat) D64711 D64711 Helicobacter pylori 210 -11538689 7500958753 hp1532 glucosamine fructose-6-phosphate (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:similar to egad:29065 percent identity: 41.74;) (le:4178) (re:5971) (di:direct) HPAE000651 AE000651 g2314711 Helicobacter pylori 210 -11538689 7502852536 hp1532 glucosamine fructose-6-phosphate (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:similar to egad:29065 percent identity: 41.74;) (le:4178) (re:5971) (di:direct) HPAE000651 AE000651 g2314711 Helicobacter pylori 26695 85962 -11538689

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900138	16873	39029	459	152

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900156	16874	39030	405	134

Description

6500734832 proc:hp1158 pyrroline-5-carboxylate reductase (gtcfc:5.1:5.10:5.16) (ec:1.5.1.2) (keggfc:5.10:5.16) (tigrfc:1.4) (db:gtc-helicobacter pylori) HP1158 HP1158 Helicobacter pylori 210 -11538690 7500888539 proc:hp1158 (sr:,campylobacter pylori) (ec:1.5.1.2) (de:pyrroline-5-carboxylate reductase, (p5cr) (p5c reductase)) (db:swissprot) PROC_HELPY O25773 HELICOBACTER PYLORI 210 -11538690 7000690666 pyrroline-5-carboxylate reductase (db:pir2.dat) F64664 F64664 Helicobacter pylori 210 -11538690 7500888541 hp1158 pyrroline-5-carboxylate reductase proc (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:14418 percent identity: 28.85;) (le:15619) (re:16392) (di:direct) HPAE000621 AE000621 g2314308 Helicobacter pylori 210 -11538690 7502852537 hp1158 pyrroline-5-carboxylate reductase proc (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:14418 percent identity: 28.85;) (le:15619) (re:16392) (di:direct) HPAE000621 AE000621 g2314308 Helicobacter pylori 26695 85962 -11538690

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900171	16875	39031	501	166

Description

6500734833 pros:hp0238 prolyl-trna synthetase (gtcfc:5.10:10.6) (ec:6.1.1.15) (keggfc:5.10:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0238 HP0238 Helicobacter pylori 210 -11538691 5500686020 pros:hp0238 (sr:,campylobacter pylori) (ec:6.1.1.15) (de:prolyl-trna synthetase, (proline--trna ligase) (prors)) (db:swissprot) SYP_HELPY P56124 HELICOBACTER PYLORI 210 -11538691 7000686727 proline--trna ligase (cl:proline--trna ligase) (ec:6.1.1.15) (db:pir2.dat) F64549 F64549 Helicobacter pylori 210 -11538691 7500892545 hp0238 prolyl-trna synthetase pros (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to egad:20246 percent identity: 39.83;) (le:8947) (re:10680) (di:complement) HPAE000543 AE000543 g2313329 Helicobacter pylori 210 -11538691 7502852538 hp0238 prolyl-trna synthetase pros (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to egad:20246 percent identity: 39.83;) (le:8947) (re:10680) (di:complement) HPAE000543 AE000543 g2313329 Helicobacter pylori 26695 85962 -11538691

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900193	16876	39032	441	146

Description

6500734834 args:hp0319 arginyl-trna synthetase (gtcfc:5.10:10.6) (ec:6.1.1.19) (keggfc:5.10:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0319 HP0319 Helicobacter pylori 210 -11538692 5500686024 args:hp0319 (sr:,campylobacter pylori) (ec:6.1.1.19) (de:arginyl-trna synthetase, (arginine--trna ligase) (argrs)) (db:swissprot) SYR_HELPY P56128 HELICOBACTER PYLORI 210 -11538692 7000686728 arginine--trna ligase (cl:bacillus arginine--trna ligase) (ec:6.1.1.19) (db:pir2.dat) G64559 G64559 Helicobacter pylori 210 -11538692 7500892563 hp0319 arginyl-trna synthetase args (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:22401 percent identity: 35.82;) (le:995) (re:2620) (di:complement) HPAE000550 AE000550 g2313419 Helicobacter pylori 210 -11538692 7502852539 hp0319 arginyl-trna synthetase args (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:22401 percent identity: 35.82;) (le:995) (re:2620) (di:complement) HPAE000550 AE000550 g2313419 Helicobacter pylori 26695 85962 -11538692

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900199	16877	39033	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900201	16878	39034	699	232

Description

6500734835 amidase (gtcfc:5.10:5.13:5.14:6.5:11.4) (ec:3.5.1.4) (keggfc:5.10:5.13:5.14:6.5) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0830 HP0830 Helicobacter pylori 210 -11538693 5500684865 hp0830 (sr:,campylobacter pylori) (ec:3.5.1.4) (de:putative amidase,) (db:swissprot) AMID_HELPY P56114 HELICOBACTER PYLORI 210 -11538693 7000684569 amidase (cl:indoleacetamide hydrolase) (db:pir2.dat) F64623 F64623 Helicobacter pylori 210 -11538693 7500876804 hp0830 amidase (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:43777 percent identity: 40.57;) (le:5408) (re:6769) (di:complement) HPAE000594 AE000594 g2313964 Helicobacter pylori 210 -11538693 7502852540 hp0830 amidase (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:43777 percent identity: 40.57;) (le:5408) (re:6769) (di:complement) HPAE000594 AE000594 g2313964 Helicobacter pylori 26695 85962 -11538693

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900206	16879	39035	924	307

Description

6500734836 spee:hp0832 spermidine synthase (gtcfc:13.11) (ec:2.5.1.16) (keggfc:5.10:5.16:6.1) (tigrfc:5.4) (db:gtc-helicobacter pylori) HP0832 HP0832 Helicobacter pylori 210 -11538694 7000690715 spermidine synthase (db:pir2.dat) H64623 H64623 Helicobacter pylori 210 -11538694 7500959481 hp0832 spermidine synthase spee (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:44488 percent identity: 26.49;) (le:7420) (re:8208) (di:complement) HPAE000594 AE000594 g2313966 Helicobacter pylori 210 -11538694 7502852541 hp0832 spermidine synthase spee (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:44488 percent identity: 26.49;) (le:7420) (re:8208) (di:complement) HPAE000594 AE000594 g2313966 Helicobacter pylori 26695 85962 -11538694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900211	16880	39036	375	124

Description

6500734837 enva:hp1052 udp-3-0-acyl n-acetylglcosamine deacetylase (gtcfc:5.10:5.11:7.1:9.4:9.5:11.3) (ec:3.5.1.-) (keggfc:4.4:5.10:5.11:9.4:9.5) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1052 HP1052 Helicobacter pylori 210 -11538695 7000690778 udp-3-0-acyl n-acetylglcosamine deacetylase (cl:enva protein) (db:pir2.dat) D64651 D64651 Helicobacter pylori 210 -11538695 7500959540 hp1052 udp-3-0-acyl n-acetylglcosamine deacetylase (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:similar to egad:28159 percent identity: 44.64;) (le:67) (re:954) (di:complement) HPAE000613 AE000613 g2314201 Helicobacter pylori 210 -11538695 7502852542 hp1052 udp-3-0-acyl n-acetylglcosamine deacetylase (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:similar to egad:28159 percent identity: 44.64;) (le:67) (re:954) (di:complement) HPAE000613 AE000613 g2314201 Helicobacter pylori 26695 85962 -11538695

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900217	16881	39037	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900218	16882	39038	291	96

Description

6500734838 hiss:hp1190 histidyl-trna synthetase (gtcfc:5.11:10.6) (ec:6.1.1.21) (keggfc:5.11:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP1190 HP1190 Helicobacter pylori 210 -11538696 7500892439 hiss:hp1190 (sr:,campylobacter pylori) (ec:6.1.1.21) (de:(hisrs)) (db:swissprot) SYH_HELPY P56455 HELICOBACTER PYLORI 210 -11538696 7000689989 histidine--trna ligase (cl:helicobacter pylori histidine--trna ligase) (ec:6.1.1.21) (db:pir2.dat) F64668 F64668 Helicobacter pylori 210 -11538696 7500892441 hp1190 histidyl-trna synthetase hiss (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to egad:1631 percent identity: 32.39;) (le:1337) (re:2665) (di:complement) HPAE000625 AE000625 g2314351 Helicobacter pylori 210 -11538696 7502852543 hp1190 histidyl-trna synthetase hiss (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to egad:1631 percent identity: 32.39;) (le:1337) (re:2665) (di:complement) HPAE000625 AE000625 g2314351 Helicobacter pylori 26695 85962 -11538696

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900219	16883	39039	417	138

Description

6500734839 hema:hp0239 glutamyl-trna reductase (gtcfc:5.13:5.14:9.10) (ec:1.2.1.-) (keggfc:5.13:5.14:9.10) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP0239 HP0239 Helicobacter pylori 210 -11538697 5500685328 hema:hp0239 (sr:,campylobacter pylori) (ec:1.2.1.-) (de:glutamyl-trna reductase, (glutr)) (db:swissprot) HEM1_HELPY P56125 HELICOBACTER PYLORI 210 -11538697 7000685505 glutamyl-trna reductase (ec:1.2.1.-) (db:pir2.dat) G64549 G64549 Helicobacter pylori 210 -11538697 7500883136 hp0239 glutamyl-trna reductase hema (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to egad:30936 percent identity: 32.72;) (le:10684) (re:12033) (di:complement) HPAE000543 AE000543 g2313330 Helicobacter pylori 210 -11538697 7502852544 hp0239 glutamyl-trna reductase hema (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to egad:30936 percent identity: 32.72;) (le:10684) (re:12033) (di:complement) HPAE000543 AE000543 g2313330 Helicobacter pylori 26695 85962 -11538697

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900225	16884	39040	1245	415

Description

6500734840 trps:hp1253 tryptophanyl-trna synthetase (gtcfc:5.14:10.6) (ec:6.1.1.2) (keggfc:5.14:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP1253 HP1253 Helicobacter pylori 210 -11538698 7500892637 trps:hp1253 (sr:,campylobacter pylori) (ec:6.1.1.2) (de:(trprs)) (db:swissprot) SYW_HELPY P56396 HELICOBACTER PYLORI 210 -11538698 7000689204 tryptophan--trna ligase (cl:tryptophan--trna ligase) (ec:6.1.1.2) (db:pir2.dat) E64676 E64676 Helicobacter pylori 210 -11538698 7500892639 hp1253 tryptophanyl-trna synthetase trps (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to egad:17047 percent identity: 52.62;) (le:8751) (re:9770) (di:complement) HPAE000630 AE000630 g2314417 Helicobacter pylori 210 -11538698 7502852545 hp1253 tryptophanyl-trna synthetase trps (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to egad:17047 percent identity: 52.62;) (le:8751) (re:9770) (di:complement) HPAE000630 AE000630 g2314417 Helicobacter pylori 26695 85962 -11538698

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900268	16885	39041	273	90

Description

6500734841 arok:hp0157 shikimic acid kinase i (gtcfc:5.15) (ec:2.7.1.71) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP0157 HP0157 Helicobacter pylori 210 -11538699 5500684889 arok:hp0157 (sr:,campylobacter pylori) (ec:2.7.1.71) (de:shikimate kinase, (sk)) (db:swissprot) AROK_HELPY P56073 HELICOBACTER PYLORI 210 -11538699 7000684634 shikimic acid kinase i (cl:shikimate kinase:shikimate kinase homology) (db:pir2.dat) E64539 E64539 Helicobacter pylori 210 -11538699 7500877192 hp0157 shikimic acid kinase i arok (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to egad:28854 percent identity: 36.13;) (le:9931) (re:10419) (di:direct) HPAE000536 AE000536 g2313237 Helicobacter pylori 210 -11538699 7502852546 hp0157 shikimic acid kinase i arok (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to egad:28854 percent identity: 36.13;) (le:9931) (re:10419) (di:direct) HPAE000536 AE000536 g2313237 Helicobacter pylori 26695 85962 -11538699

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900272	16886	39042	480	159

Description

GTC ORF with score 222 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.cerevisiae hypothetical 105.9 kd) (le:35939:36599) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900273	16887	39043	504	167

Description

GTC ORF with score 187 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.cerevisiae hypothetical 105.9 kd) (le:35939:36599) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900274	16888	39044	1728	575

Description

6500734842 arob:hp0283 3-dehydroquinate synthase (gtcfc:5.15) (ec:4.6.1.3) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP0283 HP0283 Helicobacter pylori 210 -11538700 5500684882 arob:hp0283 (sr:,campylobacter pylori) (ec:4.6.1.3) (de:3-dehydroquinate synthase,) (db:swissprot) AROB_HELPY P56081 HELICOBACTER PYLORI 210 -11538700 7000684625 3-dehydroquinate synthase (cl:3-dehydroquinate synthase:3-dehydroquinate synthase homology) (db:pir2.dat) C64555 C64555 Helicobacter pylori 210 -11538700 7500877170 hp0283 3-dehydroquinate synthase arob (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:similar to egad:6437 percent identity: 38.12;) (le:2693) (re:3724) (di:direct) HPAE000547 AE000547 g2313379 Helicobacter pylori 210 -11538700 7502852547 hp0283 3-dehydroquinate synthase arob (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:similar to egad:6437 percent identity: 38.12;) (le:2693) (re:3724) (di:direct) HPAE000547 AE000547 g2313379 Helicobacter pylori 26695 85962 -11538700

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900283	16889	39045	642	213

Description

6500734843 aroa:hp0401 3-phosphoshikimate 1-carboxyvinyltransferase (gtcfc:5.15) (ec:2.5.1.19) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP0401 HP0401 Helicobacter pylori 210 -11538701 7000684622 aroa:hp0401 (sr:,campylobacter pylori) (ec:2.5.1.19) (de:(5-enolpyruvylshikimate-3-phosphate synthase) (epsp synthase)) (db:swissprot) AROA_HELPY P56197 HELICOBACTER PYLORI 210 -11538701 7000684623 3-phosphoshikimate 1-carboxyvinyltransferase (cl:3-phosphoshikimate 1-carboxyvinyltransferase:3-phosphoshikimate 1-carboxyvinyltransferase homology) (db:pir2.dat) A64570 A64570 Helicobacter pylori 210 -11538701 7500877165 hp0401 3-phosphoshikimate 1-carboxyvinyltransferase (db:genpept-bct1) (de:helicobacter pylori section 34 of 134 of the complete genome.) (nt:similar to egad:43030 percent identity: 53.56;) (le:905) (re:2194) (di:complement) HPAE000556 AE000556 g2313507 Helicobacter pylori 210 -11538701 7502852548 hp0401 3-phosphoshikimate 1-carboxyvinyltransferase (db:genpept) (de:helicobacter pylori 26695 section 34 of 134 of the complete genome.) (nt:similar to egad:43030 percent identity: 53.56;) (le:905) (re:2194) (di:complement) HPAE000556 AE000556 g2313507 Helicobacter pylori 26695 85962 -11538701

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900298	16890	39046	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900301	16891	39047	1302	433

Description

6500734844 phet:hp0402 phenylalanyl-trna synthetase:beta subunit (gtcfc:5.15:10.6) (ec:6.1.1.20) (keggfc:5.15:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0402 HP0402 Helicobacter pylori 210 -11538702 5500686014 phet:hp0402 (sr:,campylobacter pylori) (ec:6.1.1.20) (de:trna ligase beta chain) (phers)) (db:swissprot) SYFB_HELPY P56145 HELICOBACTER PYLORI 210 -11538702 7000686712 phenylalanine--trna ligase:beta chain (cl:phenylalanine--trna ligase beta chain) (ec:6.1.1.20) (db:pir2.dat) B64570 B64570 Helicobacter pylori 210 -11538702 7500892394 hp0402 phenylalanyl-trna synthetase:beta subunit (db:genpept-bct1) (de:helicobacter pylori section 34 of 134 of the complete genome.) (nt:similar to egad:6640 percent identity: 29.97;) (le:2210) (re:4504) (di:complement) HPAE000556 AE000556 g2313508 Helicobacter pylori 210 -11538702 7502852549 hp0402 phenylalanyl-trna synthetase:beta subunit (db:genpept) (de:helicobacter pylori 26695 section 34 of 134 of the complete genome.) (nt:similar to egad:6640 percent identity: 29.97;) (le:2210) (re:4504) (di:complement) HPAE000556 AE000556 g2313508 Helicobacter pylori 26695 85962 -11538702

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900307	16892	39048	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900309	16893	39049	711	236

Description

6500734845 phes:hp0403 phenylalanyl-trna synthetase:alpha subunit (gtcfc:5.15:10.6) (ec:6.1.1.20) (keggfc:5.15:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0403 HP0403 Helicobacter pylori 210 -11538703 5500686013 phes:hp0403 (sr:,campylobacter pylori) (ec:6.1.1.20) (de:-trna ligase alpha chain) (phers)) (db:swissprot) SYFA_HELPY P56146 HELICOBACTER PYLORI 210 -11538703 7000686711 phenylalanine--trna ligase:alpha chain (cl:phenylalanine--trna ligase alpha chain) (ec:6.1.1.20) (db:pir2.dat) C64570 C64570 Helicobacter pylori 210 -11538703 7500892386 hp0403 phenylalanyl-trna synthetase:alpha subunit (db:genpept-bct1) (de:helicobacter pylori section 34 of 134 of the complete genome.) (nt:similar to egad:28317 percent identity: 48.68;) (le:4504) (re:5490) (di:complement) HPAE000556 AE000556 g2313509 Helicobacter pylori 210 -11538703 7502852550 hp0403 phenylalanyl-trna synthetase:alpha subunit (db:genpept) (de:helicobacter pylori 26695 section 34 of 134 of the complete genome.) (nt:similar to egad:28317 percent identity: 48.68;) (le:4504) (re:5490) (di:complement) HPAE000556 AE000556 g2313509 Helicobacter pylori 26695 85962 -11538703

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900322	16894	39050	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900323	16895	39051	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900324	16896	39052	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900347	16897	39053	687	229

Description

6500734846 aroc:hp0663 chorismate synthase (gtcfc:5.15) (ec:4.6.1.4) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP0663 HP0663 Helicobacter pylori 210 -11538704 5500684883 aroc:hp0663 (sr:,campylobacter pylori) (ec:4.6.1.4) (de:phospholyase)) (db:swissprot) AROC_HELPY P56122 HELICOBACTER PYLORI 210 -11538704 7000684627 chorismate synthase (cl:chorismate synthase) (db:pir2.dat) G64602 G64602 Helicobacter pylori 210 -11538704 7500877175 hp0663 chorismate synthase aroc (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:28843 percent identity: 47.23;) (le:11301) (re:12398) (di:direct) HPAE000579 AE000579 g2313786 Helicobacter pylori 210 -11538704 7502852551 hp0663 chorismate synthase aroc (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:28843 percent identity: 47.23;) (le:11301) (re:12398) (di:direct) HPAE000579 AE000579 g2313786 Helicobacter pylori 26695 85962 -11538704

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900349	16898	39054	1002	333

Description

6500734847 tyrs:hp0774 tyrosyl-trna synthetase (gtcfc:5.15:10.6) (ec:6.1.1.1) (keggfc:5.15:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0774 HP0774 Helicobacter pylori 210 -11538705 7500892658 tyrs:hp0774 (sr:,campylobacter pylori) (ec:6.1.1.1) (de:tyrosyl-trna synthetase, (tyrosine--trna ligase) (tyrrs)) (db:swissprot) SYY_HELPY P56417 HELICOBACTER PYLORI 210 -11538705 7000689203 tyrosine--trna ligase::tyrosyl-trna synthetase (cl:tyrosine--trna ligase) (ec:6.1.1.1) (db:pir2.dat) F64616 F64616 Helicobacter pylori 210 -11538705 7500892660 hp0774 tyrosyl-trna synthetase tyrs (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:similar to egad:28601 percent identity: 54.68;) (le:6244) (re:7452) (di:complement) HPAE000589 AE000589 g2313900 Helicobacter pylori 210 -11538705 7502852552 hp0774 tyrosyl-trna synthetase tyrs (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:similar to egad:28601 percent identity: 54.68;) (le:6244) (re:7452) (di:complement) HPAE000589 AE000589 g2313900 Helicobacter pylori 26695 85962 -11538705

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900364	16899	39055	879	292

Description

6500734848 aroq:hp1038 3-dehydroquinase type ii:3-dehydroquinate dehydratase:3-dehydroquinase (gtcfc:5.15) (ec:4.2.1.10) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP1038 HP1038 Helicobacter pylori 210 -11538706 1500685863 aroq:hp1038 (sr:,campylobacter pylori) (ec:4.2.1.10) (de:3-dehydroquinate dehydratase, (3-dehydroquinase)) (db:swissprot) AROD_HELPY Q48255 HELICOBACTER PYLORI 210 -11538706 7500877179 hp1038 3-dehydroquinase type ii aroq (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to gp:1419553 percent identity: 99.40;) (le:8460) (re:8963) (di:complement) HPAE000611 AE000611 g2314182 Helicobacter pylori 210 -11538706 7502852553 hp1038 3-dehydroquinase type ii aroq (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to gp:1419553 percent identity: 99.40;) (le:8460) (re:8963) (di:complement) HPAE000611 AE000611 g2314182 Helicobacter pylori 26695 85962 -11538706 7000684629 3-dehydroquinase type ii (db:pir) F64649 F64649 Helicobacter pylori 210 -11538706

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900365	16900	39056	522	173

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900372	16901	39057	780	259

Description

6500734849 aroe:hp1249 shikimate 5-dehydrogenase (gtcfc:5.15) (ec:1.1.1.25) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP1249 HP1249 Helicobacter pylori 210 -11538707 5500684888 aroe:hp1249 (sr:,campylobacter pylori) (ec:1.1.1.25) (de:shikimate 5-dehydrogenase,) (db:swissprot) AROE_HELPY P56119 HELICOBACTER PYLORI 210 -11538707 7000684631 shikimate 5-dehydrogenase (cl:shikimate dehydrogenase homology) (db:pir2.dat) A64676 A64676 Helicobacter pylori 210 -11538707 7500877183 hp1249 shikimate 5-dehydrogenase aroe (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to egad:6487 percent identity: 36.63;) (le:4537) (re:5328) (di:complement) HPAE000630 AE000630 g2314414 Helicobacter pylori 210 -11538707 7502852554 hp1249 shikimate 5-dehydrogenase aroe (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to egad:6487 percent identity: 36.63;) (le:4537) (re:5328) (di:complement) HPAE000630 AE000630 g2314414 Helicobacter pylori 26695 85962 -11538707

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900378	16902	39058	327	108

Description

6500734850 trpa:hp1277 tryptophan synthase:alpha subunit (gtcfc:5.15) (ec:4.2.1.20) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP1277 HP1277 Helicobacter pylori 210 -11538708 5500686080 trpa:hp1277 (sr:,campylobacter pylori) (ec:4.2.1.20) (de:tryptophan synthase alpha chain,) (db:swissprot) TRPA_HELPY P56141 HELICOBACTER PYLORI 210 -11538708 7000686829 tryptophan synthase:alpha subunit (cl:tryptophan synthase alpha chain:tryptophan synthase alpha chain homology) (db:pir2.dat) E64679 E64679 Helicobacter pylori 210 -11538708 7500893438 hp1277 tryptophan synthase:alpha subunit trpa (db:genpept-bct1) (de:helicobacter pylori section 110 of 134 of the complete genome.) (nt:similar to egad:14644 percent identity: 46.54;) (le:735) (re:1523) (di:complement) HPAE000632 AE000632 g2314444 Helicobacter pylori 210 -11538708 7502852555 hp1277 tryptophan synthase:alpha subunit trpa (db:genpept) (de:helicobacter pylori 26695 section 110 of 134 of the completegenome.) (nt:similar to egad:14644 percent identity: 46.54;) (le:735) (re:1523) (di:complement) HPAE000632 AE000632 g2314444 Helicobacter pylori 26695 85962 -11538708

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900391	16903	39059	255	84

Description

6500734851 trpb:hp1278 tryptophan synthase:beta subunit (gtcfc:5.15) (ec:4.2.1.20) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP1278 HP1278 Helicobacter pylori 210 -11538709 5500686081 trpb:hp1278 (sr:,campylobacter pylori) (ec:4.2.1.20) (de:tryptophan synthase beta chain,) (db:swissprot) TRPB_HELPY P56142 HELICOBACTER PYLORI 210 -11538709 7000686831 trpb tryptophan synthase:beta chain (cl:tryptophan synthase beta chain:tryptophan synthase beta chain homology) (ec:4.2.1.20) (db:pir2.dat) F64679 F64679 Helicobacter pylori 210 -11538709 7500893449 hp1278 tryptophan synthase:beta subunit trpb (db:genpept-bct1) (de:helicobacter pylori section 110 of 134 of the complete genome.) (nt:similar to egad:22671 percent identity: 66.06;) (le:1520) (re:2701) (di:complement) HPAE000632 AE000632 g2314445 Helicobacter pylori 210 -11538709 7502852556 hp1278 tryptophan synthase:beta subunit trpb (db:genpept) (de:helicobacter pylori 26695 section 110 of 134 of the completegenome.) (nt:similar to egad:22671 percent identity: 66.06;) (le:1520) (re:2701) (di:complement) HPAE000632 AE000632 g2314445 Helicobacter pylori 26695 85962 -11538709

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900392	16904	39060	933	310

Description

6500734852 trpc:hp1279 anthranilate isomerase (gtcfc:5.15) (ec:5.3.1.24) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP1279 HP1279 Helicobacter pylori 210 -11538710 7000689637 anthranilate isomerase (cl:trpc-trpf bifunctional enzyme:trpc homology:trpf homology) (db:pir2.dat) G64679 G64679 Helicobacter pylori 210 -11538710 7500958454 hp1279 anthranilate isomerase trpc (db:genpept-bct1) (de:helicobacter pylori section 110 of 134 of the complete genome.) (nt:similar to egad:37478 percent identity: 47.01;) (le:2703) (re:4061) (di:complement) HPAE000632 AE000632 g2314446 Helicobacter pylori 210 -11538710 7502852557 hp1279 anthranilate isomerase trpc (db:genpept) (de:helicobacter pylori 26695 section 110 of 134 of the completegenome.) (nt:similar to egad:37478 percent identity: 47.01;) (le:2703) (re:4061) (di:complement) HPAE000632 AE000632 g2314446 Helicobacter pylori 26695 85962 -11538710

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900427	16905	39061	276	91

Description

6500734853 trpd:hp1281 anthranilate synthase component ii (gtcfc:5.15) (ec:2.4.2.18) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP1281 HP1281 Helicobacter pylori 210 -11538711 7000689639 anthranilate synthase component ii (cl:glutamine amidotransferase:trpg homology) (db:pir2.dat) A64680 A64680 Helicobacter pylori 210 -11538711 7500958456 hp1281 anthranilate synthase component ii trpd (db:genpept-bct1) (de:helicobacter pylori section 110 of 134 of the complete genome.) (nt:similar to egad:12757 percent identity: 40.21;) (le:5058) (re:5642) (di:complement) HPAE000632 AE000632 g2314447 Helicobacter pylori 210 -11538711 7502852558 hp1281 anthranilate synthase component ii trpd (db:genpept) (de:helicobacter pylori 26695 section 110 of 134 of the completegenome.) (nt:similar to egad:12757 percent identity: 40.21;) (le:5058) (re:5642) (di:complement) HPAE000632 AE000632 g2314447 Helicobacter pylori 26695 85962 -11538711

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900435	16906	39062	1131	376

Description

6500734854 trpe:hp1282 anthranilate synthase component i (gtcfc:5.15:9.12) (ec:4.1.3.27) (keggfc:5.15:9.13) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP1282 HP1282 Helicobacter pylori 210 -11538712 7000689638 anthranilate synthase component i (cl:anthranilate synthase component i) (db:pir2.dat) B64680 B64680 Helicobacter pylori 210 -11538712 7500958455 hp1282 anthranilate synthase component i trpe (db:genpept-bct1) (de:helicobacter pylori section 110 of 134 of the complete genome.) (nt:similar to egad:19709 percent identity: 47.89;) (le:5639) (re:7141) (di:complement) HPAE000632 AE000632 g2314448 Helicobacter pylori 210 -11538712 7502852559 hp1282 anthranilate synthase component i trpe (db:genpept) (de:helicobacter pylori 26695 section 110 of 134 of the completegenome.) (nt:similar to egad:19709 percent identity: 47.89;) (le:5639) (re:7141) (di:complement) HPAE000632 AE000632 g2314448 Helicobacter pylori 26695 85962 -11538712

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900444	16907	39063	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900447	16908	39064	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900472	16909	39065	1239	412

Description

6500734855 nada:hp1356 quinolinate synthetase a (gtcfc:5.15:9.4) (ec:4.6.1.3) (keggfc:5.15) (tigrfc:2.12) (db:gtc-helicobacter pylori) HP1356 HP1356 Helicobacter pylori 210 -11538713 7000690671 quinolinate synthetase a (cl:helicobacter pylori quinolinate synthetase a) (db:pir2.dat) D64689 D64689 Helicobacter pylori 210 -11538713 7500959443 hp1356 quinolinate synthetase a nada (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:44578 percent identity: 34.19;) (le:10784) (re:11794) (di:complement) HPAE000636 AE000636 g2314524 Helicobacter pylori 210 -11538713 7502852560 hp1356 quinolinate synthetase a nada (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:44578 percent identity: 34.19;) (le:10784) (re:11794) (di:complement) HPAE000636 AE000636 g2314524 Helicobacter pylori 26695 85962 -11538713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900477	16910	39066	924	307

Description

6500734856 tyra:hp1380 prephenate dehydrogenase (gtcfc:5.15) (ec:1.3.1.12) (keggfc:5.15) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP1380 HP1380 Helicobacter pylori 210 -11538714 7000690636 prephenate dehydrogenase (db:pir2.dat) D64692 D64692 Helicobacter pylori 210 -11538714 7500959415 hp1380 prephenate dehydrogenase tyra (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:similar to egad:8704 percent identity: 30.22;) (le:4164) (re:4961) (di:direct) HPAE000638 AE000638 g2314550 Helicobacter pylori 210 -11538714 7502852561 hp1380 prephenate dehydrogenase tyra (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:similar to egad:8704 percent identity: 30.22;) (le:4164) (re:4961) (di:direct) HPAE000638 AE000638 g2314550 Helicobacter pylori 26695 85962 -11538714

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900482	16911	39067	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900485	16912	39068	444	147

Description

GTC ORF with score 407 to: (sr:human) (db:genpept-pri3) (de:human beta-prime-adaptin (bam22) gene, exon 20 and partial cds.) (nt:candidate meningioma tumor suppressor) (le:u36250:164:u36251:249:u36252:147) (re:200:354:282) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900489	16913	39069	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900494	16914	39070	1041	346

Description

6500734857 dhs1:hp0134 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase:3-deoxy-d-arabino-heptulosonate 7-phosphatesynthase (gtcfc:5.15) (keggfc:14.2) (tigrfc:1.2) (db:gtc-helicobacter pylori) HP0134 HP0134 Helicobacter pylori 210 -11538715 7000689590
3-deoxy-d-arabino-heptulosonate 7-phosphate synthase (db:pir2.dat) F64536 F64536 Helicobacter pylori 210 -11538715 7500958411 hp0134
3-deoxy-d-arabino-heptulosonate 7-phosphate (db:genpept-bct1)
(de:helicobacter pylori section 13 of 134 of the complete genome.)
(nt:similar to egad:25290 percent identity: 54.61;) (le:3376) (re:4725)
(di:direct) HPAE000535 AE000535 g2313220 Helicobacter pylori 210 -11538715
7502852562 hp0134 3-deoxy-d-arabino-heptulosonate 7-phosphate (db:genpept)
(de:helicobacter pylori 26695 section 13 of 134 of the complete genome.)
(nt:similar to egad:25290 percent identity: 54.61;) (le:3376) (re:4725)
(di:direct) HPAE000535 AE000535 g2313220 Helicobacter pylori 26695 85962 -11538715

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900495	16915	39071	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900501	16916	39072	324	107

Description

6500734858 ureh:hp0067 urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0067 HP0067 Helicobacter pylori 210 -11538716 103906 ureh:hp0067 (sr:,campylobacter pylori) (de:urease accessory protein ureh) (db:swissprot) UREH_HELPY Q09067 HELICOBACTER PYLORI 210 -11538716 7000686904 ureh urease accessory protein ureh (db:pir2.dat) C64528 C64528 Helicobacter pylori 210 -11538716 7500893859 hp0067 urease accessory protein ureh (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:similar to egad:18938 percent identity: 96.23;) (le:10593) (re:11390) (di:complement) HPAE000528 AE000528 g2313139 Helicobacter pylori 210 -11538716 7502852563 hp0067 urease accessory protein ureh (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:similar to egad:18938 percent identity: 96.23;) (le:10593) (re:11390) (di:complement) HPAE000528 AE000528 g2313139 Helicobacter pylori 26695 85962 -11538716

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900502	16917	39073	387	128

Description

6500734859 ureg:hp0068 urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0068 HP0068 Helicobacter pylori 210 -11538717 103897 ureg:hp0068 (sr:,campylobacter pylori) (de:urease accessory protein ureg) (db:swissprot) UREG_HELPY Q09066 HELICOBACTER PYLORI 210 -11538717 7000686903 ureg urease accessory protein ureg (db:pir2.dat) D64528 D64528 Helicobacter pylori 210 -11538717 7500893856 hp0068 urease accessory protein ureg (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:similar to egad:22922 percent identity: 94.97;) (le:11390) (re:11989) (di:complement) HPAE000528 AE000528 g2313140 Helicobacter pylori 210 -11538717 7502852564 hp0068 urease accessory protein ureg (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:similar to egad:22922 percent identity: 94.97;) (le:11390) (re:11989) (di:complement) HPAE000528 AE000528 g2313140 Helicobacter pylori 26695 85962 -11538717

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900511	16918	39074	1389	462

Description

GTC ORF with score 349 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f6e13 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:106569:107096:107521) (re:106756:107402:108507) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900515	16919	39075	561	186

Description

6500734860 uref:hp0069 urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0069 HP0069 Helicobacter pylori 210 -11538718 103887 uref:hp0069 (sr:,campylobacter pylori) (de:urease accessory protein uref) (db:swissprot) UREF_HELPY Q09065 HELICOBACTER PYLORI 210 -11538718 7000686902 uref urease accessory protein uref:uref protein (db:pir2.dat) E64528 E64528 Helicobacter pylori 210 -11538718 7500893853 hp0069 urease accessory protein uref (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:similar to egad:14053 percent identity: 94.51;) (le:12018) (re:12782) (di:complement) HPAE000528 AE000528 g2313141 Helicobacter pylori 210 -11538718 7502852565 hp0069 urease accessory protein uref (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:similar to egad:14053 percent identity: 94.51;) (le:12018) (re:12782) (di:complement) HPAE000528 AE000528 g2313141 Helicobacter pylori 26695 85962 -11538718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900532	16920	39076	1656	551

Description

6500734861 uree:hp0070 urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0070 HP0070 Helicobacter pylori 210 -11538719 103879 uree:hp0070 (sr:,campylobacter pylori) (de:urease accessory protein uree) (db:swissprot) UREE_HELPY Q09064 HELICOBACTER PYLORI 210 -11538719 7500893851 hp0070 urease accessory protein uree (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:similar to egad:15506 percent identity: 97.06;) (le:12805) (re:13317) (di:complement) HPAE000528 AE000528 g2313142 Helicobacter pylori 210 -11538719 7502852566 hp0070 urease accessory protein uree (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:similar to egad:15506 percent identity: 97.06;) (le:12805) (re:13317) (di:complement) HPAE000528 AE000528 g2313142 Helicobacter pylori 26695 85962 -11538719

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900545	16921	39077	729	242

Description

6500734862 urei:hp0071 urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0071 HP0071 Helicobacter pylori 210 -11538720 103908 urei:hp0071 (sr:,campylobacter pylori) (de:urease accessory protein urei) (db:swissprot) UREI_HELPY Q09068 HELICOBACTER PYLORI 210 -11538720 7000686905 urei urease accessory protein urei (db:pir2.dat) A41834 G64528 Helicobacter pylori 210 -11538720 7500893860 hp0071 urease accessory protein urei (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:similar to egad:17574 percent identity: 98.46;) (le:13319) (re:13906) (di:complement) HPAE000528 AE000528 g2313143 Helicobacter pylori 210 -11538720 7502852567 hp0071 urease accessory protein urei (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:similar to egad:17574 percent identity: 98.46;) (le:13319) (re:13906) (di:complement) HPAE000528 AE000528 g2313143 Helicobacter pylori 26695 85962 -11538720

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900561	16922	39078	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900563	16923	39079	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900566	16924	39080	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900570	16925	39081	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900571	16926	39082	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900578	16927	39083	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900589	16928	39084	342	114

Description

6500734863 urec:hp0075 urease protein:urease operon protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.5) (db:gtc-helicobacter pylori) HP0075 HP0075 Helicobacter pylori 210 -11538721 103867 urec:hp0075 (sr:,campylobacter pylori) (de:putative urease operon urec protein) (db:swissprot) UREC_HELPY P25177 HELICOBACTER PYLORI 210 -11538721 7500893849 hp0075 urease protein urec (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:similar to egad:16135 percent identity: 97.98;) (le:3369) (re:4706) (di:complement) HPAE000529 AE000529 g2313156 Helicobacter pylori 210 -11538721 7502852568 hp0075 urease protein urec (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:similar to egad:16135 percent identity: 97.98;) (le:3369) (re:4706) (di:complement) HPAE000529 AE000529 g2313156 Helicobacter pylori 26695 85962 -11538721

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900590	16929	39085	702	233

Description

6500734864 pand:hp0034 aspartate 1-decarboxylase (gtcfc:5.2:6.1:9.5) (ec:4.1.1.11) (keggfc:5.2:6.1) (tigrfc:2.7) (db:gtc-helicobacter pylori) HP0034 HP0034 Helicobacter pylori 210 -11538722 5500685704 pand:hp0034 (sr:,campylobacter pylori) (ec:4.1.1.11) (de:decarboxylase)) (db:swissprot) PAND_HELPY P56065 HELICOBACTER PYLORI 210 -11538722 7000686084 aspartate 1-decarboxylase (cl:aspartate 1-decarboxylase) (db:pir2.dat) B64524 B64524 Helicobacter pylori 210 -11538722 7500887650 hp0034 aspartate 1-decarboxylase pand (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to egad:37749 percent identity: 50.00;) (le:11766) (re:12119) (di:direct) HPAE000525 AE000525 g2313109 Helicobacter pylori 210 -11538722 7502852569 hp0034 aspartate 1-decarboxylase pand (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to egad:37749 percent identity: 50.00;) (le:11766) (re:12119) (di:direct) HPAE000525 AE000525 g2313109 Helicobacter pylori 26695 85962 -11538722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900591	16930	39086	288	95

Description

6500734865 asps:hp0617 aspartyl-trna synthetase (gtcfc:5.2:10.6) (ec:6.1.1.12) (keggfc:5.2:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0617 HP0617 Helicobacter pylori 210 -11538723 7500892356 asps:hp0617 (sr:,campylobacter pylori) (ec:6.1.1.12) (de:(asprs)) (db:swissprot) SYD_HELPY P56459 HELICOBACTER PYLORI 210 -11538723 7000689213 aspartate--trna ligase (cl:lysine--trna ligase) (ec:6.1.1.12) (db:pir2.dat) A64597 A64597 Helicobacter pylori 210 -11538723 7500892358 hp0617 aspartyl-trna synthetase asps (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:similar to egad:9464 percent identity: 50.09;) (le:3641) (re:5374) (di:direct) HPAE000576 AE000576 g2313739 Helicobacter pylori 210 -11538723 7502852570 hp0617 aspartyl-trna synthetase asps (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:similar to egad:9464 percent identity: 50.09;) (le:3641) (re:5374) (di:direct) HPAE000576 AE000576 g2313739 Helicobacter pylori 26695 85962 -11538723

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900593	16931	39087	717	238

Description

6500734866 alr:hp0941 alanine racemase:biosynthetic (gtcfc:5.2:6.15) (ec:5.1.1.1) (keggfc:5.2:6.8) (tigrfc:1.5) (db:gtc-helicobacter pylori) HP0941 HP0941 Helicobacter pylori 210 -11538724 7502852571 alr:hp0941 (sr:,campylobacter pylori) (ec:5.1.1.1) (de:alanine racemase,) (db:swissprot) ALR_HELPY O25595 HELICOBACTER PYLORI 210 -11538724 7000689624 alanine racemase:biosynthetic (cl:alanine racemase) (db:pir2.dat) E64637 E64637 Helicobacter pylori 210 -11538724 7500958443 hp0941 alanine racemase:biosynthetic alr (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:similar to egad:9029 percent identity: 32.40;) (le:4892) (re:6025) (di:complement) HPAE000603 AE000603 g2314079 Helicobacter pylori 210 -11538724 7502852572 hp0941 alanine racemase:biosynthetic alr (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:similar to egad:9029 percent identity: 32.40;) (le:4892) (re:6025) (di:complement) HPAE000603 AE000603 g2314079 Helicobacter pylori 26695 85962 -11538724

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900597	16932	39088	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900603	16933	39089	1011	336

Description

GTC ORF with score 362 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid t11g6, complete sequence.) (nt:similar to rna recognition motif. (aka rrm, rbd, or) (le:25182:25367:26044:26863) (re:25292:25626:26669:27018) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900606	16934	39090	927	309

Description

6500734867 alas:hp1241 alanyl-trna synthetase (gtcfc:5.2:10.6) (ec:6.1.1.7) (keggfc:5.2:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP1241 HP1241 Helicobacter pylori 210 -11538725 7500892318 alas:hp1241 (sr:,campylobacter pylori) (ec:6.1.1.7) (de:alanyl-trna synthetase, (alanine--trna ligase) (alars)) (db:swissprot) SYA_HELPY P56452 HELICOBACTER PYLORI 210 -11538725 7000689625 alanine--trna ligase (cl:alanine--trna ligase) (ec:6.1.1.7) (db:pir2.dat) A64675 A64675 Helicobacter pylori 210 -11538725 7500892320 hp1241 alanyl-trna synthetase alas (db:genpept-bct1) (de:helicobacter pylori section 107 of 134 of the complete genome.) (nt:similar to egad:29299 percent identity: 44.92;) (le:3946) (re:6489) (di:complement) HPAE000629 AE000629 g2314404 Helicobacter pylori 210 -11538725 7502852573 hp1241 alanyl-trna synthetase alas (db:genpept) (de:helicobacter pylori 26695 section 107 of 134 of the completegenome.) (nt:similar to egad:29299 percent identity: 44.92;) (le:3946) (re:6489) (di:complement) HPAE000629 AE000629 g2314404 Helicobacter pylori 26695 85962 -11538725

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900609	16935	39091	189	62

Description

6500734868 thrc:hp0098 threonine synthase (gtcfc:5.2:5.3:9.3) (ec:4.2.99.2) (keggfc:5.3:9.3) (tigrfc:1.3) (db:gtc-helicobacter pylori) (gtcfc:l-amino acid metabolism-alanine and aspartate metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:metabolism of cofactors and vi... HP0098 HP0098 Helicobacter pylori 210 -11538726 7000690732 threonine synthase (cl:threonine synthase) (db:pir2.dat) B64532 B64532 Helicobacter pylori 210 -11538726 7500959497 hp0098 threonine synthase thrc (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:similar to egad:28741 percent identity: 32.89;) (le:5599) (re:7059) (di:complement) HPAE000531 AE000531 g2313178 Helicobacter pylori 210 -11538726 7502852574 hp0098 threonine synthase thrc (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:similar to egad:28741 percent identity: 32.89;) (le:5599) (re:7059) (di:complement) HPAE000531 AE000531 g2313178 Helicobacter pylori 26695 85962 -11538726

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900613	16936	39092	402	133

Description

6500734869 dape:hp0212 succinyl-diaminopimelate desuccinylase (gtcfc:5.2:5.8) (ec:3.5.1.18) (keggfc:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0212 HP0212 Helicobacter pylori 210 -11538727 7000690720 succinyl-diaminopimelate desuccinylase (db:pir2.dat) D64546 D64546 Helicobacter pylori 210 -11538727 7500959486 hp0212 succinyl-diaminopimelate desuccinylase dape (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:similar to egad:28756 percent identity: 42.32;) (le:4460) (re:5611) (di:complement) HPAE000541 AE000541 g2313302 Helicobacter pylori 210 -11538727 7502852575 hp0212 succinyl-diaminopimelate desuccinylase dape (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:similar to egad:28756 percent identity: 42.32;) (le:4460) (re:5611) (di:complement) HPAE000541 AE000541 g2313302 Helicobacter pylori 26695 85962 -11538727

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900614	16937	39093	564	187

Description

6500734870 lysa:hp0290 diaminopimelate decarboxylase:dap decarboxylase (gtcfc:5.2:5.8) (ec:4.1.1.20) (keggfc:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0290 HP0290 Helicobacter pylori 210 -11538728 5500685068 lysa:hp0290 (sr:,campylobacter pylori) (ec:4.1.1.20) (de:diaminopimelate decarboxylase, (dap decarboxylase)) (db:swissprot) DCDA_HELPY P56129 HELICOBACTER PYLORI 210 -11538728 7000684988 diaminopimelate decarboxylase (cl:diaminopimelate decarboxylase) (ec:4.1.1.20) (db:pir2.dat) B64556 B64556 Helicobacter pylori 210 -11538728 7500880049 hp0290 diaminopimelate decarboxylase dap (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:similar to egad:29494 percent identity: 42.68;) (le:17981) (re:19198) (di:direct) HPAE000547 AE000547 g2313384 Helicobacter pylori 210 -11538728 7502852576 hp0290 diaminopimelate decarboxylase dap (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:similar to egad:29494 percent identity: 42.68;) (le:17981) (re:19198) (di:direct) HPAE000547 AE000547 g2313384 Helicobacter pylori 26695 85962 -11538728

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900635	16938	39094	306	101

Description

6500734871 dapb:hp0510 dihydrodipicolinate reductase (gtcfc:5.2:5.8) (ec:1.3.1.26) (keggfc:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0510 HP0510 Helicobacter pylori 210 -11538729 5500685067 dapb:hp0510 (sr:,campylobacter pylori) (ec:1.3.1.26) (de:dihydrodipicolinate reductase,) (db:swissprot) DAPB_HELPY P94844 HELICOBACTER PYLORI 210 -11538729 7000684982 dihydrodipicolinate reductase (cl:dihydrodipicolinate reductase) (db:pir2.dat) F64583 F64583 Helicobacter pylori 210 -11538729 7500879996 hp0510 dihydrodipicolinate reductase dapb (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:similar to gp:1763301 percent identity: 95.28;) (le:6381) (re:7145) (di:direct) HPAE000565 AE000565 g2313620 Helicobacter pylori 210 -11538729 7502852577 hp0510 dihydrodipicolinate reductase dapb (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:similar to gp:1763301 percent identity: 95.28;) (le:6381) (re:7145) (di:direct) HPAE000565 AE000565 g2313620 Helicobacter pylori 26695 85962 -11538729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900643	16939	39095	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900663	16940	39096	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900668	16941	39097	321	106

Description

GTC ORF with score 257 to: (sr:baker's yeast) (db:genpept-pln2) (de:saccharomyces cerevisiae putative transmembrane protein hum1p(hum1) gene, complete cds.) (nt:novel protein; putative transmembrane protein;) (le:1) (re:1236) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900676	16942	39098	351	116

Description

GTC ORF with score 254 to: (sr:baker's yeast) (db:genpept-pln2) (de:saccharomyces cerevisiae putative transmembrane protein hum1p(hum1) gene, complete cds.) (nt:novel protein; putative transmembrane protein;) (le:1) (re:1236) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900677	16943	39099	447	148

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900683	16944	39100	840	279

Description

6500734872 dapf:hp0566 diaminopimelate epimerase (gtcfc:5.2:5.8) (ec:5.1.1.7) (keggfc:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0566 HP0566 Helicobacter pylori 210 -11538730 7502852578 dapf:hp0566 (sr:,campylobacter pylori) (ec:5.1.1.7) (de:diaminopimelate epimerase, (dap epimerase)) (db:swissprot) DAPF_HELPY O25290 HELICOBACTER PYLORI 210 -11538730 7000689889 diaminopimelate epimerase (db:pir2.dat) F64590 F64590 Helicobacter pylori 210 -11538730 7500958687 hp0566 diaminopimelate epimerase dapf (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:similar to egad:27917 percent identity: 30.00;) (le:7490) (re:8311) (di:complement) HPAE000570 AE000570 g2313673 Helicobacter pylori 210 -11538730 7502852579 hp0566 diaminopimelate epimerase dapf (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:similar to egad:27917 percent identity: 30.00;) (le:7490) (re:8311) (di:complement) HPAE000570 AE000570 g2313673 Helicobacter pylori 26695 85962 -11538730

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900692	16945	39101	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900698	16946	39102	1827	609

Description

6500734873 dapd:hp0626 tetrahydrodipicolinate n-succinyltransferase (gtcfc:5.2:5.8) (ec:2.3.1.117) (keggfc:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0626 HP0626 Helicobacter pylori 210 -11538731 7000690724 tetrahydrodipicolinate n-succinyltransferase (db:pir2.dat) B64598 B64598 Helicobacter pylori 210 -11538731 7500959490 hp0626 tetrahydrodipicolinate n-succinyltransferase (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:similar to egad:21144 percent identity: 36.11;) (le:1172) (re:2377) (di:direct) HPAE000577 AE000577 g2313754 Helicobacter pylori 210 -11538731 7502852580 hp0626 tetrahydrodipicolinate n-succinyltransferase (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:similar to egad:21144 percent identity: 36.11;) (le:1172) (re:2377) (di:direct) HPAE000577 AE000577 g2313754 Helicobacter pylori 26695 85962 -11538731

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900699	16947	39103	1344	447

Description

6500734874 aspb:hp0672 solute-binding signature and mitochondrial signature protein:solute-binding signature and mitochondrialsignature protein (gtcfc:5.2) (keggfc:14.2) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0672 HP0672 Helicobacter pylori 210 -11538732 7500959017 hypothetical protein hp0672 (cl:aspartate transaminase) (db:pir2.dat) H64603 H64603 Helicobacter pylori 210 -11538732 7500959018 hp0672 solute-binding signature and mitochondrial (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:similar to egad:37753 percent identity: 47.31;) (le:7278) (re:8450) (di:direct) HPAE000580 AE000580 g2313794 Helicobacter pylori 210 -11538732 7502852581 hp0672 solute-binding signature and mitochondrial (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:similar to egad:37753 percent identity: 47.31;) (le:7278) (re:8450) (di:direct) HPAE000580 AE000580 g2313794 Helicobacter pylori 26695 85962 -11538732

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900722	16948	39104	1494	497

Description

GTC ORF with score 144 to: (fn:ubiquitin-dependent proteolytic protein) (sr:human) (db:genpept) (de:homo sapiens ubiquitin fusion-degradation 1 like protein (ufd1l)mrna, complete cds.) (nt:ubiquitin like protein) (le:79) (re:1110) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900729	16949	39105	1230	409

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900734	16950	39106	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900747	16951	39107	294	98

Description

6500734875 metl:hp0822 homoserine dehydrogenase (gtcfc:5.2:5.3:5.8) (ec:1.1.1.3) (keggfc:5.3:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP0822 HP0822 Helicobacter pylori 210 -11538733 7500880268 hom:hp0822 (sr:,campylobacter pylori) (ec:1.1.1.3) (de:homoserine dehydrogenase, (hdh)) (db:swissprot) DHOM_HELPY P56429 HELICOBACTER PYLORI 210 -11538733 7000689994 homoserine dehydrogenase (cl:homoserine dehydrogenase:homoserine dehydrogenase homology) (ec:1.1.1.3) (db:pir2.dat) F64622 F64622 Helicobacter pylori 210 -11538733 7500880270 hp0822 homoserine dehydrogenase metl (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:7108 percent identity: 37.74;) (le:9608) (re:10873) (di:direct) HPAE000593 AE000593 g2313952 Helicobacter pylori 210 -11538733 7502852582 hp0822 homoserine dehydrogenase metl (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:7108 percent identity: 37.74;) (le:9608) (re:10873) (di:direct) HPAE000593 AE000593 g2313952 Helicobacter pylori 26695 85962 -11538733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900748	16952	39108	648	215

Description

6500734876 dapa:hp1013 dihydrodipicolinate synthetase (gtcfc:5.2:5.8) (ec:4.2.1.52) (keggfc:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP1013 HP1013 Helicobacter pylori 210 -11538734 7000689890 dihydrodipicolinate synthetase (db:pir2.dat) E64646 E64646 Helicobacter pylori 210 -11538734 7500958688 hp1013 dihydrodipicolinate synthetase dapa (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:similar to egad:14906 percent identity: 39.51;) (le:9909) (re:10811) (di:direct) HPAE000609 AE000609 g2314156 Helicobacter pylori 210 -11538734 7502852583 hp1013 dihydrodipicolinate synthetase dapa (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:similar to egad:14906 percent identity: 39.51;) (le:9909) (re:10811) (di:direct) HPAE000609 AE000609 g2314156 Helicobacter pylori 26695 85962 -11538734

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900749	16953	39109	438	145

Description

6500734877 thrb:hp1050 homoserine kinase (gtcfc:5.2:5.3) (ec:2.7.1.39) (keggfc:5.3) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP1050 HP1050 Helicobacter pylori 210 -11538735 7000689995 homoserine kinase (db:pir2.dat) B64651 B64651 Helicobacter pylori 210 -11538735 7500958773 hp1050 homoserine kinase thrb (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to egad:8419 percent identity: 27.74;) (le:12193) (re:13074) (di:complement) HPAE000612 AE000612 g2314197 Helicobacter pylori 210 -11538735 7502852584 hp1050 homoserine kinase thrb (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to egad:8419 percent identity: 27.74;) (le:12193) (re:13074) (di:complement) HPAE000612 AE000612 g2314197 Helicobacter pylori 26695 85962 -11538735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900761	16954	39110	666	221

Description

6500734878 asd:hp1189 aspartate-semialdehyde dehydrogenase (gtcfc:5.2) (ec:1.2.1.11) (keggfc:5.3:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP1189 HP1189 Helicobacter pylori 210 -11538736 7000689646 aspartate-semialdehyde dehydrogenase (cl:aspartate-semialdehyde dehydrogenase) (ec:1.2.1.11) (db:pir2.dat) E64668 E64668 Helicobacter pylori 210 -11538736 7500953827 hp1189 aspartate-semialdehyde dehydrogenase asd (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to egad:15165 percent identity: 45.67;) (le:310) (re:1350) (di:complement) HPAE000625 AE000625 g2314350 Helicobacter pylori 210 -11538736 7502852585 hp1189 aspartate-semialdehyde dehydrogenase asd (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to egad:15165 percent identity: 45.67;) (le:310) (re:1350) (di:complement) HPAE000625 AE000625 g2314350 Helicobacter pylori 26695 85962 -11538736

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900764	16955	39111	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900784	16956	39112	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900793	16957	39113	351	116

Description

6500734879 lysc:hp1229 aspartokinase (gtcfc:5.2:5.3:5.8) (ec:2.7.2.4) (keggfc:5.3:5.8) (tigrfc:1.3) (db:gtc-helicobacter pylori) HP1229 HP1229 Helicobacter pylori 210 -11538737 7000689647 aspartokinase (cl:aspartate kinase:aspartate kinase homology) (db:pir2.dat) E64673 E64673 Helicobacter pylori 210 -11538737 7500958463 hp1229 aspartokinase lysc (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to egad:23981 percent identity: 48.01;) (le:3611) (re:4828) (di:direct) HPAE000628 AE000628 g2314392 Helicobacter pylori 210 -11538737 7502852586 hp1229 aspartokinase lysc (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to egad:23981 percent identity: 48.01;) (le:3611) (re:4828) (di:direct) HPAE000628 AE000628 g2314392 Helicobacter pylori 26695 85962 -11538737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900794	16958	39114	684	227

Description

6500734880 ilvc:hp0330 ketol-acid reductoisomerase (gtcfc:5.2:5.7:9.5) (ec:1.1.1.86) (keggfc:5.7:9.5) (tigrfc:1.5) (db:gtc-helicobacter pylori) HP0330 HP0330 Helicobacter pylori 210 -11538738 7000689029 ketol-acid reductoisomerase (cl:methanococcus ketol-acid reductoisomerase:ketol-acid reductoisomerase homology) (ec:1.1.1.86) (db:pir2.dat) B64561 B64561 Helicobacter pylori 210 -11538738 7500953816 hp0330 ketol-acid reductoisomerase ilvc (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:similar to egad:22947 percent identity: 48.15;) (le:237) (re:1229) (di:direct) HPAE000551 AE000551 g2313431 Helicobacter pylori 210 -11538738 7502852587 hp0330 ketol-acid reductoisomerase ilvc (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:similar to egad:22947 percent identity: 48.15;) (le:237) (re:1229) (di:direct) HPAE000551 AE000551 g2313431 Helicobacter pylori 26695 85962 -11538738

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900797	16959	39115	711	236

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900805	16960	39116	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900809	16961	39117	1221	406

Description

GTC ORF with score 186 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana lcada gene and partial lcadb and lg127/30gene.) (nt:protein sequence is in conflict with the conceptual) (le:90:482:734:952:1334) (re:260:628:840:1045:1475) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900811	16962	39118	282	93

Description

6500734881 ilve:hp1468 branched-chain-amino-acid aminotransferase (gtcfc:5.2:5.6:5.7:9.5) (ec:2.6.1.42) (keggfc:5.6:5.7:9.5) (tigrfc:1.5) (db:gtc-helicobacter pylori) HP1468 HP1468 Helicobacter pylori 210 -11538739 7500884051 ilve:hp1468 (sr:,campylobacter pylori) (ec:2.6.1.42) (de:branched-chain amino acid aminotransferase, (bcat)) (db:swissprot) ILVE_HELPY O26004 HELICOBACTER PYLORI 210 -11538739 7000689668 branched-chain-amino-acid aminotransferase (cl:branched-chain-amino-acid transaminase bat1) (db:pir2.dat) D64703 D64703 Helicobacter pylori 210 -11538739 7500884053 hp1468 branched-chain-amino-acid aminotransferase (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:28206 percent identity: 63.50;) (le:798) (re:1820) (di:complement) HPAE000647 AE000647 g2314646 Helicobacter pylori 210 -11538739 7502852588 hp1468 branched-chain-amino-acid aminotransferase (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:28206 percent identity: 63.50;) (le:798) (re:1820) (di:complement) HPAE000647 AE000647 g2314646 Helicobacter pylori 26695 85962 -11538739

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900822	16963	39119	774	257

Description

6500734882 phosphoglycerate dehydrogenase (gtcfc:5.3:5.5) (ec:1.1.1.95) (keggfc:5.3) (tigrfc:1.6) (db:gtc-helicobacter pylori) HP0096 HP0096 Helicobacter pylori 210 -11538740 7000690623 phosphoglycerate dehydrogenase (db:pir2.dat) H64531 H64531 Helicobacter pylori 210 -11538740 7500959402 hp0096 phosphoglycerate dehydrogenase (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:similar to egad:43637 percent identity: 31.03;) (le:3680) (re:4624) (di:direct) HPAE000531 AE000531 g2313177 Helicobacter pylori 210 -11538740 7502852589 hp0096 phosphoglycerate dehydrogenase (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:similar to egad:43637 percent identity: 31.03;) (le:3680) (re:4624) (di:direct) HPAE000531 AE000531 g2313177 Helicobacter pylori 26695 85962 -11538740

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900832	16964	39120	1257	418

Description

6500734883 thrs:hp0123 threonyl-trna synthetase (gtcfc:5.3:10.6) (ec:6.1.1.3) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0123 HP0123 Helicobacter pylori 210 -11538741 5500686027 thrs:hp0123 (sr:,campylobacter pylori) (ec:6.1.1.3) (de:(thrrs)) (db:swissprot) SYT_HELPY P56071 HELICOBACTER PYLORI 210 -11538741 7000686732 threonine--trna ligase (cl:threonine--trna ligase) (ec:6.1.1.3) (db:pir2.dat) C64535 C64535 Helicobacter pylori 210 -11538741 7500892606 hp0123 threonyl-trna synthetase thrs (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:similar to egad:9014 percent identity: 42.11;) (le:4262) (re:6100) (di:direct) HPAE000534 AE000534 g2313207 Helicobacter pylori 210 -11538741 7502852590 hp0123 threonyl-trna synthetase thrs (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:similar to egad:9014 percent identity: 42.11;) (le:4262) (re:6100) (di:direct) HPAE000534 AE000534 g2313207 Helicobacter pylori 26695 85962 -11538741

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900848	16965	39121	294	97

Description

6500734884 sera:hp0397 phosphoglycerate dehydrogenase (gtcfc:5.3:5.5) (ec:1.1.1.95) (keggfc:5.3) (tigrfc:1.6) (db:gtc-helicobacter pylori) HP0397 HP0397 Helicobacter pylori 210 -11538742 7000690622 phosphoglycerate dehydrogenase (cl:bacillus phosphoglycerate dehydrogenase) (db:pir2.dat) E64569 E64569 Helicobacter pylori 210 -11538742 7500959401 hp0397 phosphoglycerate dehydrogenase sera (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:13235 percent identity: 32.47;) (le:15790) (re:17364) (di:complement) HPAE000555 AE000555 g2313497 Helicobacter pylori 210 -11538742 7502852591 hp0397 phosphoglycerate dehydrogenase sera (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:13235 percent identity: 32.47;) (le:15790) (re:17364) (di:complement) HPAE000555 AE000555 g2313497 Helicobacter pylori 26695 85962 -11538742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900853	16966	39122	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900854	16967	39123	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900858	16968	39124	456	151

Description

6500734885 serb:hp0652 phosphoserine phosphatase (gtcfc:5.3:5.5) (ec:3.1.3.3) (keggfc:5.3) (tigrfc:1.6) (db:gtc-helicobacter pylori) HP0652 HP0652 Helicobacter pylori 210 -11538743 7000689118 phosphoserine phosphatase (cl:phosphoserine phosphatase) (ec:3.1.3.3) (db:pir2.dat) D64601 D64601 Helicobacter pylori 210 -11538743 7500954202 hp0652 phosphoserine phosphatase serb (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:8936 percent identity: 36.55;) (le:14484) (re:15107) (di:complement) HPAE000578 AE000578 g2313770 Helicobacter pylori 210 -11538743 7502852592 hp0652 phosphoserine phosphatase serb (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:8936 percent identity: 36.55;) (le:14484) (re:15107) (di:complement) HPAE000578 AE000578 g2313770 Helicobacter pylori 26695 85962 -11538743

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900859	16969	39125	897	298

Description

6500734886 glyq:hp0960 glycyl-trna synthetase:alpha subunit (gtcfc:5.3:10.6) (ec:6.1.1.14) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0960 HP0960 Helicobacter pylori 210 -11538744 7500892406 glyq:hp0960 (sr:,campylobacter pylori) (ec:6.1.1.14) (de:alpha chain) (glyrs)) (db:swissprot) SYGA_HELPY P56453 HELICOBACTER PYLORI 210 -11538744 7000689217 glycine--trna ligase:alpha chain (cl:glycine--trna ligase alpha chain) (ec:6.1.1.14) (db:pir2.dat) H64639 H64639 Helicobacter pylori 210 -11538744 7500892408 hp0960 glycyl-trna synthetase:alpha subunit glyq (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:29400 percent identity: 60.14;) (le:12203) (re:13114) (di:complement) HPAE000604 AE000604 g2314096 Helicobacter pylori 210 -11538744 7502852593 hp0960 glycyl-trna synthetase:alpha subunit glyq (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:29400 percent identity: 60.14;) (le:12203) (re:13114) (di:complement) HPAE000604 AE000604 g2314096 Helicobacter pylori 26695 85962 -11538744

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900861	16970	39126	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900865	16971	39127	1110	369

Description

GTC ORF with score 438 to: (de:(ygr202c) (pn:phosphorylcholine transferase:ct:cholinephosphate cytidylyltransferase) (gn:cct1:cct:g7729:pct1) (gtcfc:6.3:8.1) (ec:2.7.7.15) (ctpt_yeast) (keggfc:6.3:8.1) (sgdfc:1.6.1:9.4.0) (db:gtc-saccharomyces ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900874	16972	39128	654	217

Description

6500734887 glys:hp0972 glycyl-trna synthetase:beta subunit (gtcfc:5.3:10.6) (ec:6.1.1.14) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0972 HP0972 Helicobacter pylori 210 -11538745 7500892414 glys:hp0972 (sr:,campylobacter pylori) (ec:6.1.1.14) (de:beta chain) (glyrs)) (db:swissprot) SYGB_HELPY P56454 HELICOBACTER PYLORI 210 -11538745 7000689973 glycine--trna ligase:beta chain (ec:6.1.1.14) (db:pir2.dat) D64641 D64641 Helicobacter pylori 210 -11538745 7500892416 hp0972 glycyl-trna synthetase:beta subunit glys (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:similar to egad:29407 percent identity: 33.58;) (le:12169) (re:14274) (di:complement) HPAE000605 AE000605 g2314109 Helicobacter pylori 210 -11538745 7502852594 hp0972 glycyl-trna synthetase:beta subunit glys (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:similar to egad:29407 percent identity: 33.58;) (le:12169) (re:14274) (di:complement) HPAE000605 AE000605 g2314109 Helicobacter pylori 26695 85962 -11538745

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900878	16973	39129	1209	402

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900899	16974	39130	1074	357

Description

6500734888 sers:hp1480 seryl-trna synthetase (gtcfc:5.3:10.6) (ec:6.1.1.11) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP1480 HP1480 Helicobacter pylori 210 -11538746 7500892579 sers:hp1480 (sr:,campylobacter pylori) (ec:6.1.1.11) (de:seryl-trna synthetase, (serine--trna ligase) (serrs)) (db:swissprot) SYS_HELPY P56458 HELICOBACTER PYLORI 210 -11538746 7000690698 serine--trna ligase (cl:serine--trna ligase) (ec:6.1.1.11) (db:pir2.dat) H64704 H64704 Helicobacter pylori 210 -11538746 7500892581 hp1480 seryl-trna synthetase sers (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:8021 percent identity: 48.33;) (le:16236) (re:17483) (di:complement) HPAE000647 AE000647 g2314654 Helicobacter pylori 210 -11538746 7502852595 hp1480 seryl-trna synthetase sers (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:8021 percent identity: 48.33;) (le:16236) (re:17483) (di:complement) HPAE000647 AE000647 g2314654 Helicobacter pylori 26695 85962 -11538746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900901	16975	39131	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900906	16976	39132	534	177

Description

6500734889 serc:hp0736 phosphoserine aminotransferase (gtcfc:5.3:5.5) (keggfc:14.2) (tigrfc:1.6) (db:gtc-helicobacter pylori) HP0736 HP0736 Helicobacter pylori 210 -11538747 7502852596 serc:hp0736 (sr:,campylobacter pylori) (ec:2.6.1.52) (de:phosphoserine aminotransferase, (psat)) (db:swissprot) SERC_HELPY O25436 HELICOBACTER PYLORI 210 -11538747 7000690626 phosphoserine aminotransferase (db:pir2.dat) H64611 H64611 Helicobacter pylori 210 -11538747 7500959405 hp0736 phosphoserine aminotransferase serc (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:43580 percent identity: 30.73;) (le:8094) (re:9203) (di:complement) HPAE000586 AE000586 g2313858 Helicobacter pylori 210 -11538747 7502852597 hp0736 phosphoserine aminotransferase serc (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:43580 percent identity: 30.73;) (le:8094) (re:9203) (di:complement) HPAE000586 AE000586 g2313858 Helicobacter pylori 26695 85962 -11538747

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900929	16977	39133	888	296

Description

6500734890 mets:hp0417 methionyl-trna synthetase (gtcfc:5.4:6.4:10.6) (ec:6.1.1.10) (keggfc:5.4:6.4:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0417 HP0417 Helicobacter pylori 210 -11538748 5500686018 mets:hp0417 (sr:,campylobacter pylori) (ec:6.1.1.10) (de:(metrs)) (db:swissprot) SYM_HELPY P56127 HELICOBACTER PYLORI 210 -11538748 7000686724 methionine--trna ligase (cl:methionine--trna ligase) (ec:6.1.1.10) (db:pir2.dat) A64572 A64572 Helicobacter pylori 210 -11538748 7500892513 hp0417 methionyl-trna synthetase mets (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to egad:6356 percent identity: 42.38;) (le:9379) (re:11331) (di:direct) HPAE000557 AE000557 g2313521 Helicobacter pylori 210 -11538748 7502852598 hp0417 methionyl-trna synthetase mets (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to egad:6356 percent identity: 42.38;) (le:9379) (re:11331) (di:direct) HPAE000557 AE000557 g2313521 Helicobacter pylori 26695 85962 -11538748

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900957	16978	39134	735	244

Description

6500734891 fmt:hp1141 methionyl-trna formyltransferase (gtcfc:5.4:9.6:10.6) (ec:2.1.2.9) (keggfc:5.4:9.8:10.1) (tigrfc:12.7) (db:gtc-helicobacter pylori) (gtcfc:l-amino acid metabolism-methionine metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of ma... HP1141 HP1141 Helicobacter pylori 210 -11538749 7500881684 fmt:hp1141 (sr:,campylobacter pylori) (ec:2.1.2.9) (de:methionyl-trna formyltransferase,) (db:swissprot) FMT_HELPY P56461 HELICOBACTER PYLORI 210 -11538749 7000690516 methionyl-trna formyltransferase (cl:methionyl-trna formyltransferase:phosphoribosylglycinamide formyltransferase homology) (ec:2.1.2.9) (db:pir2.dat) E64662 E64662 Helicobacter pylori 210 -11538749 7500881686 hp1141 methionyl-trna formyltransferase fmt (db:genpept-bct1) (de:helicobacter pylori section 98 of 134 of the complete genome.) (nt:similar to egad:24704 percent identity: 37.46;) (le:2393) (re:3304) (di:complement) HPAE000620 AE000620 g2314297 Helicobacter pylori 210 -11538749 7502852599 hp1141 methionyl-trna formyltransferase fmt (db:genpept) (de:helicobacter pylori 26695 section 98 of 134 of the complete genome.) (nt:similar to egad:24704 percent identity: 37.46;) (le:2393) (re:3304) (di:complement) HPAE000620 AE000620 g2314297 Helicobacter pylori 26695 85962 -11538749

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900958	16979	39135	1437	478

Description

6500734892 cyss:hp0886 cysteinyl-trna synthetase:cysteine--trna ligase:cysrs (gtcfc:5.5:10.6) (ec:6.1.1.16) (keggfc:5.5:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0886 HP0886 Helicobacter pylori 210 -11538750 99998 cyss:hp0886 (sr:,campylobacter pylori) (ec:6.1.1.16) (de:(cysrs)) (db:swissprot) SYC_HELPY P41259 HELICOBACTER PYLORI 210 -11538750 7000686705 cysteine--trna ligase::cysteinyl-trna synthetase (cl:cysteine--trna ligase) (ec:6.1.1.16) (db:pir1.dat) F64630 F64630 Helicobacter pylori 210 -11538750 7500892338 hp0886 cysteinyl-trna synthetase cyss (db:genpept-bct1) (de:helicobacter pylori section 76 of 134 of the complete genome.) (nt:similar to egad:11755 percent identity: 97.34;) (le:4350) (re:5747) (di:direct) HPAE000598 AE000598 g2314022 Helicobacter pylori 210 -11538750 7502852600 hp0886 cysteinyl-trna synthetase cyss (db:genpept) (de:helicobacter pylori 26695 section 76 of 134 of the complete genome.) (nt:similar to egad:11755 percent identity: 97.34;) (le:4350) (re:5747) (di:direct) HPAE000598 AE000598 g2314022 Helicobacter pylori 26695 85962 -11538750

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900961	16980	39136	708	235

Description

6500734893 vals:hp1153 valyl-trna synthetase (gtcfc:5.7:10.6) (ec:6.1.1.9) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP1153 HP1153 Helicobacter pylori 210 -11538751 5500686031 vals:hp1153 (sr:,campylobacter pylori) (ec:6.1.1.9) (de:valyl-trna synthetase, (valine--trna ligase) (valrs)) (db:swissprot) SYV_HELPY P56000 HELICOBACTER PYLORI 210 -11538751 7000686735 valine--trna ligase (cl:valine--trna ligase) (ec:6.1.1.9) (db:pir2.dat) A64664 A64664 Helicobacter pylori 210 -11538751 7500892621 hp1153 valyl-trna synthetase vals (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:6368 percent identity: 43.73;) (le:5457) (re:8081) (di:complement) HPAE000621 AE000621 g2314306 Helicobacter pylori 210 -11538751 7502852601 hp1153 valyl-trna synthetase vals (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:6368 percent identity: 43.73;) (le:5457) (re:8081) (di:complement) HPAE000621 AE000621 g2314306 Helicobacter pylori 26695 85962 -11538751

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900969	16981	39137	1800	599

Description

6500734894 iles:hp1422 isoleucyl-trna synthetase (gtcfc:5.7:10.6) (ec:6.1.1.5) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP1422 HP1422 Helicobacter pylori 210 -11538752 7500892458 iles:hp1422 (sr:,campylobacter pylori) (ec:6.1.1.5) (de:(ilers)) (db:swissprot) SYI_HELPY P56456 HELICOBACTER PYLORI 210 -11538752 7000690495 isoleucine--trna ligase (cl:isoleucine--trna ligase) (ec:6.1.1.5) (db:pir2.dat) F64697 F64697 Helicobacter pylori 210 -11538752 7500892460 hp1422 isoleucyl-trna synthetase iles (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to egad:31040 percent identity: 49.73;) (le:7986) (re:10748) (di:complement) HPAE000642 AE000642 g2314596 Helicobacter pylori 210 -11538752 7502852602 hp1422 isoleucyl-trna synthetase iles (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to egad:31040 percent identity: 49.73;) (le:7986) (re:10748) (di:complement) HPAE000642 AE000642 g2314596 Helicobacter pylori 26695 85962 -11538752

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900973	16982	39138	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900978	16983	39139	657	218

Description

6500734895 leus:hp1547 leucyl-trna synthetase (gtcfc:5.7:10.6) (ec:6.1.1.4) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP1547 HP1547 Helicobacter pylori 210 -11538753 7500892496 leus:hp1547 (sr:,campylobacter pylori) (ec:6.1.1.4) (de:leucyl-trna synthetase, (leucine--trna ligase) (leurs)) (db:swissprot) SYL_HELPY P56457 HELICOBACTER PYLORI 210 -11538753 7000690498 leucine--trna ligase (cl:leucine--trna ligase) (ec:6.1.1.4) (db:pir2.dat) C64713 C64713 Helicobacter pylori 210 -11538753 7500892498 hp1547 leucyl-trna synthetase leus (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:29404 percent identity: 45.93;) (le:9730) (re:12150) (di:complement) HPAE000652 AE000652 g2314727 Helicobacter pylori 210 -11538753 7502852603 hp1547 leucyl-trna synthetase leus (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:29404 percent identity: 45.93;) (le:9730) (re:12150) (di:complement) HPAE000652 AE000652 g2314727 Helicobacter pylori 26695 85962 -11538753

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900979	16984	39140	444	147

Description

6500734896 lyss:hp0182 lysyl-trna synthetase (gtcfc:5.8:10.6) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0182 HP0182 Helicobacter pylori 210 -11538754 5500686016 lyss:hp0182 (sr:,campylobacter pylori) (ec:6.1.1.6) (de:lysyl-trna synthetase, (lysine--trna ligase) (lysrs)) (db:swissprot) SYK_HELPY P56126 HELICOBACTER PYLORI 210 -11538754 7000686720 lysine--trna ligase (cl:lysine--trna ligase) (ec:6.1.1.6) (db:pir2.dat) F64542 F64542 Helicobacter pylori 210 -11538754 7500892472 hp0182 lysyl-trna synthetase lyss (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:similar to egad:14748 percent identity: 58.63;) (le:7062) (re:8567) (di:direct) HPAE000538 AE000538 g2313270 Helicobacter pylori 210 -11538754 7502852604 hp0182 lysyl-trna synthetase lyss (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:similar to egad:14748 percent identity: 58.63;) (le:7062) (re:8567) (di:direct) HPAE000538 AE000538 g2313270 Helicobacter pylori 26695 85962 -11538754

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900982	16985	39141	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900987	16986	39142	537	178

Description

6500734897 mure:hp1494 udp-murnac-tripeptide synthetase (gtcfc:5.8:11.4) (ec:6.3.2.13) (keggfc:5.8:7.3) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1494 HP1494 Helicobacter pylori 210 -11538755 7000690782 udp-murnac-tripeptide synthetase (db:pir2.dat) F64706 F64706 Helicobacter pylori 210 -11538755 7500959545 hp1494 udp-murnac-tripeptide synthetase mure (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:28148 percent identity: 35.96;) (le:2718) (re:4061) (di:direct) HPAE000648 AE000648 g2314673 Helicobacter pylori 210 -11538755 7502852605 hp1494 udp-murnac-tripeptide synthetase mure (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:28148 percent identity: 35.96;) (le:2718) (re:4061) (di:direct) HPAE000648 AE000648 g2314673 Helicobacter pylori 26695 85962 -11538755

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900988	16987	39143	771	256

Description

6500734898 ymxg:hp0657 processing protease (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0657 HP0657 Helicobacter pylori 210 -11538756 7000690646 processing proteinase (ec:3.4.-.-) (db:pir2.dat) A64602 A64602 Helicobacter pylori 210 -11538756 7500959425 hp0657 processing protease ymxg (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:11963 percent identity: 24.20;) (le:5163) (re:6461) (di:direct) HPAE000579 AE000579 g2313782 Helicobacter pylori 210 -11538756 7502852606 hp0657 processing protease ymxg (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:11963 percent identity: 24.20;) (le:5163) (re:6461) (di:direct) HPAE000579 AE000579 g2313782 Helicobacter pylori 26695 85962 -11538756

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900989	16988	39144	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501900990	16989	39145	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901004	16990	39146	261	86

Description

6500734899 pqqe:hp1012 protease (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP1012 HP1012 Helicobacter pylori 210 -11538757 7000690656 proteinase (ec:3.4.-.-) (db:pir2.dat) D64646 D64646 Helicobacter pylori 210 -11538757 7500959431 hp1012 protease pqqe (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:similar to egad:40492 percent identity: 29.64;) (le:8560) (re:9894) (di:direct) HPAE000609 AE000609 g2314155 Helicobacter pylori 210 -11538757 7502852607 hp1012 protease pqqe (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:similar to egad:40492 percent identity: 29.64;) (le:8560) (re:9894) (di:direct) HPAE000609 AE000609 g2314155 Helicobacter pylori 26695 85962 -11538757

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901009	16991	39147	390	129

Description

6500734900 protease iv pspa:protease iv:pspa (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP1435 HP1435 Helicobacter pylori 210 -11538758 7000690658 proteinase iv (cl:proteinase iv mth806) (ec:3.4.-.-) (db:pir2.dat) C64699 C64699 Helicobacter pylori 210 -11538758 7500959433 hp1435 protease iv pspa (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to gp:1655731 percent identity: 41.70;) (le:969) (re:1847) (di:complement) HPAE000644 AE000644 g2314611 Helicobacter pylori 210 -11538758 7502852608 hp1435 protease iv pspa (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to gp:1655731 percent identity: 41.70;) (le:969) (re:1847) (di:complement) HPAE000644 AE000644 g2314611 Helicobacter pylori 26695 85962 -11538758

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901011	16992	39148	483	160

Description

6500734901 panc:hp0006 pantoate-beta-alanine ligase (gtcfc:6.1:9.5) (ec:6.3.2.1) (keggfc:6.1:9.5) (tigrfc:2.7) (db:gtc-helicobacter pylori) HP0006 HP0006 Helicobacter pylori 210 -11538759 5500685702 panc:hp0006 (sr:,campylobacter pylori) (ec:6.3.2.1) (de:(pantoate activating enzyme)) (db:swissprot) PANC_HELPY P56061 HELICOBACTER PYLORI 210 -11538759 7000686081 pantoate-beta-alanine ligase (cl:pantoate--beta-alanine ligase) (db:pir2.dat) F64520 F64520 Helicobacter pylori 210 -11538759 7500887646 hp0006 pantoate-beta-alanine ligase panc (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to egad:37748 percent identity: 44.24;) (le:3403) (re:4233) (di:direct) HPAE000523 AE000523 g2313083 Helicobacter pylori 210 -11538759 7502852609 hp0006 pantoate-beta-alanine ligase panc (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to egad:37748 percent identity: 44.24;) (le:3403) (re:4233) (di:direct) HPAE000523 AE000523 g2313083 Helicobacter pylori 26695 85962 -11538759

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901012	16993	39149	288	95

Description

6500734902 beta-alanine synthetase homolog (gtcfc:6.1) (keggfc:14.2) (tigrfc:8.1) (db:gtc-helicobacter pylori) HP0757 HP0757 Helicobacter pylori 210 -11538760 7000689657 beta-alanine synthetase homolog (cl:hypothetical protein ylr351c) (db:pir2.dat) E64614 E64614 Helicobacter pylori 210 -11538760 7500958471 hp0757 beta-alanine synthetase homolog (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:similar to gp:624085 percent identity: 40.00;) (le:1549) (re:2427) (di:direct) HPAE000588 AE000588 g2313883 Helicobacter pylori 210 -11538760 7502852610 hp0757 beta-alanine synthetase homolog (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:similar to gp:624085 percent identity: 40.00;) (le:1549) (re:2427) (di:direct) HPAE000588 AE000588 g2313883 Helicobacter pylori 26695 85962 -11538760

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901025	16994	39150	216	72

Description

6500734903 ddla:hp0738 d-alanine:d-alanine ligase a (gtcfc:6.15:8.1:11.4) (ec:6.3.2.4) (keggfc:6.8:7.3:8.1) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0738 HP0738 Helicobacter pylori 210 -11538761 5500685080 ddl:ddla:hp0738 (sr:,campylobacter pylori) (ec:6.3.2.4) (de:d-alanine--d-alanine ligase, (d-alanylalanine synthetase)) (db:swissprot) DDL_HELPY P56191 HELICOBACTER PYLORI 210 -11538761 7000684998 d-alanine:d-alanine ligase a (db:pir2.dat) B64612 B64612 Helicobacter pylori 210 -11538761 7500880110 hp0738 d-alanine:d-alanine ligase a ddla (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:14437 percent identity: 28.48;) (le:9904) (re:10947) (di:direct) HPAE000586 AE000586 g2313860 Helicobacter pylori 210 -11538761 7502852611 hp0738 d-alanine:d-alanine ligase a ddla (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:14437 percent identity: 28.48;) (le:9904) (re:10947) (di:direct) HPAE000586 AE000586 g2313860 Helicobacter pylori 26695 85962 -11538761

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901026	16995	39151	435	144

Description

6500734904 ggt:hp1118 gamma-glutamyltranspeptidase (gtcfc:6.16:6.4:6.5:8.2) (ec:2.3.2.2) (keggfc:6.4:6.5:6.9:8.6) (tigrfc:2.10) (db:gtc-helicobacter pylori) HP1118 HP1118 Helicobacter pylori 210 -11538762 7000689072 gamma-glutamyltranspeptidase (cl:gamma-glutamyltransferase) (db:pir2.dat) F64659 F64659 Helicobacter pylori 210 -11538762 7500954001 hp1118 gamma-glutamyltranspeptidase ggt (db:genpept-bct1) (de:helicobacter pylori section 96 of 134 of the complete genome.) (nt:similar to egad:15586 percent identity: 53.21;) (le:5087) (re:6790) (di:complement) HPAE000618 AE000618 g2314270 Helicobacter pylori 210 -11538762 7502852612 hp1118 gamma-glutamyltranspeptidase ggt (db:genpept) (de:helicobacter pylori 26695 section 96 of 134 of the complete genome.) (nt:similar to egad:15586 percent identity: 53.21;) (le:5087) (re:6790) (di:complement) HPAE000618 AE000618 g2314270 Helicobacter pylori 26695 85962 -11538762

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901038	16996	39152	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901066	16997	39153	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901074	16998	39154	366	121

Description

7500893087 trxa:hp0824 thioredoxin (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-helicobacter pylori) HP0824 HP0824 Helicobacter pylori 210 -11538763 7500893084 trxa:hp0824 (sr:,campylobacter pylori) (de:thioredoxin (trx)) (db:swissprot) THIO_HELPY P56430 HELICOBACTER PYLORI 210 -11538763 7000689013 thioredoxin (cl:thioredoxin:thioredoxin homology) (db:pir2.dat) H64622 H64622 Helicobacter pylori 210 -11538763 7500893086 hp0824 thioredoxin trxa (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:13080 percent identity: 51.49;) (le:75) (re:395) (di:direct) HPAE000594 AE000594 g2313958 Helicobacter pylori 210 -11538763 7502852613 trxa thioredoxin (db:genpept) (de:helicobacter pylori, strain j99 section 68 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0824) (le:77) (re:397) (di:direct) AE001507 AE001507 g4155328 Helicobacter pylori J99 85963 -11538763 6500734905 hp0824 thioredoxin trxa (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:13080 percent identity: 51.49;) (le:75) (re:395) (di:direct) HPAE000594 AE000594 g2313958 Helicobacter pylori 26695 85962 -11538763

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901078	16999	39155	519	172

Description

6500734906 trxb:hp1164 thioredoxin reductase (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-helicobacter pylori) HP1164 HP1164 Helicobacter pylori 210 -11538764 7000690731 thioredoxin reductase (db:pir2.dat) D64665 D64665 Helicobacter pylori 210 -11538764 7500959496 hp1164 thioredoxin reductase trxb (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:similar to gp:886900 percent identity: 28.52;) (le:2061) (re:3035) (di:direct) HPAE000622 AE000622 g2314321 Helicobacter pylori 210 -11538764 7502852614 hp1164 thioredoxin reductase trxb (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:similar to gp:886900 percent identity: 28.52;) (le:2061) (re:3035) (di:direct) HPAE000622 AE000622 g2314321 Helicobacter pylori 26695 85962 -11538764

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901086	17000	39156	840	279

Description

6500734907 thioredoxin (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-helicobacter pylori) HP1458 HP1458 Helicobacter pylori 210 -11538765 7000690729 thioredoxin (cl:thioredoxin:thioredoxin homology) (db:pir2.dat) B64702 B64702 Helicobacter pylori 210 -11538765 7500959495 hp1458 thioredoxin (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:similar to egad:25870 percent identity: 38.27;) (le:215) (re:529) (di:complement) HPAE000646 AE000646 g2314636 Helicobacter pylori 210 -11538765 7502852615 hp1458 thioredoxin (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:similar to egad:25870 percent identity: 38.27;) (le:215) (re:529) (di:complement) HPAE000646 AE000646 g2314636 Helicobacter pylori 26695 85962 -11538765

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901091	17001	39157	306	101

Description

6500734908 sela:hp1513 selenocystein synthase (gtcfc:6.4:10.6) (ec:2.9.1.1) (keggfc:6.4) (tigrfc:12.7) (db:gtc-helicobacter pylori) HP1513 HP1513 Helicobacter pylori 210 -11538766 7000690699 seryl-trna sec selenium transferase::sela protein:selenocysteine synthase (ec:2.9.1.1) (db:pir2.dat) A64709 A64709 Helicobacter pylori 210 -11538766 7500959466 hp1513 selenocystein synthase sela (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:similar to egad:10596 percent identity: 36.21;) (le:7079) (re:8239) (di:direct) HPAE000649 AE000649 g2314693 Helicobacter pylori 210 -11538766 7502852616 hp1513 selenocystein synthase sela (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:similar to egad:10596 percent identity: 36.21;) (le:7079) (re:8239) (di:direct) HPAE000649 AE000649 g2314693 Helicobacter pylori 26695 85962 -11538766

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901092	17002	39158	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901095	17003	39159	189	63

Description

6500734909 hyua:hp0695 hydantoin utilization protein a (gtcfc:13.10) (keggfc:14.2) (tigrfc:1.1) (db:gtc-helicobacter pylori) HP0695 HP0695 Helicobacter pylori 210 -11538767 7000689997 hydantoin utilization protein a (db:pir2.dat) G64606 G64606 Helicobacter pylori 210 -11538767 7500958775 hp0695 hydantoin utilization protein a hyua (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:similar to egad:7557 percent identity: 28.57;) (le:8561) (re:10702) (di:direct) HPAE000582 AE000582 g2313818 Helicobacter pylori 210 -11538767 7502852617 hp0695 hydantoin utilization protein a hyua (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:similar to egad:7557 percent identity: 28.57;) (le:8561) (re:10702) (di:direct) HPAE000582 AE000582 g2313818 Helicobacter pylori 26695 85962 -11538767

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901097	17004	39160	1008	335

Description

6500734910 murd:hp0494 udp-n-acetylmuramoylalanine-d-glutamate ligase (gtcfc:6.7:11.4) (ec:6.3.2.9) (keggfc:6.6:7.3) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0494 HP0494 Helicobacter pylori 210 -11538768 7000690787 udp-n-acetylmuramoylalanine-d-glutamate ligase (db:pir2.dat) F64581 F64581 Helicobacter pylori 210 -11538768 7500959549 hp0494 udp-n-acetylmuramoylalanine-d-glutamate ligase (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:28151 percent identity: 31.14;) (le:3837) (re:5105) (di:direct) HPAE000564 AE000564 g2313605 Helicobacter pylori 210 -11538768 7502852618 hp0494 udp-n-acetylmuramoylalanine-d-glutamate ligase (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:28151 percent identity: 31.14;) (le:3837) (re:5105) (di:direct) HPAE000564 AE000564 g2313605 Helicobacter pylori 26695 85962 -11538768

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901099	17005	39161	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901118	17006	39162	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901121	17007	39163	432	143

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901122	17008	39164	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901125	17009	39165	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901131	17010	39166	468	155

Description

6500734911 murc:hp0623 udp-n-acetylmuramate-alanine ligase (gtcfc:6.7:11.4) (ec:6.3.2.8) (keggfc:6.6:7.3) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0623 HP0623 Helicobacter pylori 210 -11538769 7500886104 murc:hp0623 (sr:,campylobacter pylori) (ec:6.3.2.8) (de:acetylmuranoyl-l-alanine synthetase)) (db:swissprot) MURC_HELPY O25340 HELICOBACTER PYLORI 210 -11538769 7000690786 udp-n-acetylmuramate-alanine ligase (db:pir2.dat) G64597 G64597 Helicobacter pylori 210 -11538769 7500886106 hp0623 udp-n-acetylmuramate-alanine ligase murc (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:similar to egad:28144 percent identity: 37.30;) (le:10569) (re:11918) (di:complement) HPAE000576 AE000576 g2313743 Helicobacter pylori 210 -11538769 7502852619 hp0623 udp-n-acetylmuramate-alanine ligase murc (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:similar to egad:28144 percent identity: 37.30;) (le:10569) (re:11918) (di:complement) HPAE000576 AE000576 g2313743 Helicobacter pylori 26695 85962 -11538769

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901134	17011	39167	276	91

Description

6500734912 lpxb:hp0867 lipid a disaccharide synthetase (gtcfc:7.1:11.3) (ec:2.4.1.182) (keggfc:4.4) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0867 HP0867 Helicobacter pylori 210 -11538770 7502852620 lpxb:hp0867 (sr:,campylobacter pylori) (ec:2.4.1.182) (de:lipid-a-disaccharide synthase,) (db:swissprot) LPXB_HELPY O25537 HELICOBACTER PYLORI 210 -11538770 7000690500 lipid a disaccharide synthetase (db:pir2.dat) C64628 C64628 Helicobacter pylori 210 -11538770 7500959291 hp0867 lipid a disaccharide synthetase lpxb (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:28081 percent identity: 31.97;) (le:18900) (re:19982) (di:complement) HPAE000596 AE000596 g2313995 Helicobacter pylori 210 -11538770 7502852621 hp0867 lipid a disaccharide synthetase lpxb (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:28081 percent identity: 31.97;) (le:18900) (re:19982) (di:complement) HPAE000596 AE000596 g2313995 Helicobacter pylori 26695 85962 -11538770

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901142	17012	39168	363	120

Description

6500734913 lpxa:hp1375 udp-n-acetylglucosamine acyltransferase (gtcfc:7.1:11.3) (ec:2.3.1.129) (keggfc:4.4) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1375 HP1375 Helicobacter pylori 210 -11538771 7000690784 udp-n-acetylglucosamine acyltransferase (cl:udp-n-acetylglucosamine acyltransferase) (db:pir2.dat) G64691 G64691 Helicobacter pylori 210 -11538771 7500959547 hp1375 udp-n-acetylglucosamine acyltransferase lpxa (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:24779 percent identity: 41.80;) (le:11813) (re:12625) (di:complement) HPAE000637 AE000637 g2314545 Helicobacter pylori 210 -11538771 7502852622 hp1375 udp-n-acetylglucosamine acyltransferase lpxa (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:24779 percent identity: 41.80;) (le:11813) (re:12625) (di:complement) HPAE000637 AE000637 g2314545 Helicobacter pylori 26695 85962 -11538771

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901143	17013	39169	426	141

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901144	17014	39170	954	317

Description

6500734914 murb:hp1418 udp-n-acetylenolpyruvoylglucosamine reductase (gtcfc:7.1:11.4) (ec:1.1.1.158) (keggfc:4.4) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1418 HP1418 Helicobacter pylori 210 -11538772 7000690783 udp-n-acetylenolpyruvoylglucosamine reductase (db:pir2.dat) B64697 B64697 Helicobacter pylori 210 -11538772 7500959546 hp1418 udp-n-acetylenolpyruvoylglucosamine reductase (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to egad:14467 percent identity: 32.69;) (le:4690) (re:5469) (di:complement) HPAE000642 AE000642 g2314592 Helicobacter pylori 210 -11538772 7502852623 hp1418 udp-n-acetylenolpyruvoylglucosamine reductase (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to egad:14467 percent identity: 32.69;) (le:4690) (re:5469) (di:complement) HPAE000642 AE000642 g2314592 Helicobacter pylori 26695 85962 -11538772

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901152	17015	39171	534	177

Description

6500734915 ispb:hp0240 octaprenyl-diphosphate synthase (gtcfc:7.1:9.12:11.3) (ec:2.5.1.-) (keggfc:7.2:9.13) (tigrfc:2.5) (db:gtc-helicobacter pylori) HP0240 HP0240 Helicobacter pylori 210 -11538773 7000690562 octaprenyl-diphosphate synthase (db:pir2.dat) H64549 H64549 Helicobacter pylori 210 -11538773 7500959347 hp0240 octaprenyl-diphosphate synthase ispb (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to egad:8604 percent identity: 31.62;) (le:12033) (re:12956) (di:complement) HPAE000543 AE000543 g2313331 Helicobacter pylori 210 -11538773 7502852624 hp0240 octaprenyl-diphosphate synthase ispb (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to egad:8604 percent identity: 31.62;) (le:12033) (re:12956) (di:complement) HPAE000543 AE000543 g2313331 Helicobacter pylori 26695 85962 -11538773

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901154	17016	39172	738	245

Description

6500734916 ubia:hp1360 4-hydroxybenzoate octaprenyltransferase (gtcfc:7.1:9.12:11.3) (ec:2.5.1.-) (keggfc:7.2:9.13) (tigrfc:2.5) (db:gtc-helicobacter pylori) HP1360 HP1360 Helicobacter pylori 210 -11538774 7000689593 4-hydroxybenzoate octaprenyltransferase (db:pir2.dat) H64689 H64689 Helicobacter pylori 210 -11538774 7500958414 hp1360 4-hydroxybenzoate octaprenyltransferase ubia (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:6499 percent identity: 26.58;) (le:13587) (re:14471) (di:complement) HPAE000636 AE000636 g2314526 Helicobacter pylori 210 -11538774 7502852625 hp1360 4-hydroxybenzoate octaprenyltransferase ubia (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:6499 percent identity: 26.58;) (le:13587) (re:14471) (di:complement) HPAE000636 AE000636 g2314526 Helicobacter pylori 26695 85962 -11538774

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901155	17017	39173	783	260

Description

6500734917 protein kinase c-like protein (gtcfc:8.5:9.4:13.2) (ec:2.7.1.-) (keggfc:8.5:9.4) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP0432 HP0432 Helicobacter pylori 210 -11538775 7000690651 protein kinase c:delta type (db:pir2.dat) H64573 H64573 Helicobacter pylori 210 -11538775 7500959426 hp0432 protein kinase c-like protein (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:similar to sp:p28867 percent identity: 30.00;) (le:2497) (re:3387) (di:direct) HPAE000559 AE000559 g2313539 Helicobacter pylori 210 -11538775 7502852626 hp0432 protein kinase c-like protein (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:similar to sp:p28867 percent identity: 30.00;) (le:2497) (re:3387) (di:direct) HPAE000559 AE000559 g2313539 Helicobacter pylori 26695 85962 -11538775

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901167	17018	39174	612	203

Description

6500734918 lgt:hp0955 prolipoprotein diacylglyceryl transferase (gtcfc:8.5:11.1) (ec:2.4.99.-) (keggfc:8.5) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0955 HP0955 Helicobacter pylori 210 -11538776 7500884985 lgt:hp0955 (sr:,campylobacter pylori) (ec:2.4.99.-) (de:prolipoprotein diacylglyceryl transferase,) (db:swissprot) LGT_HELPY O25609 HELICOBACTER PYLORI 210 -11538776 7000690649 prolipoprotein diacylglyceryl transferase (cl:prolipoprotein diacylglyceryl transferase) (db:pir2.dat) C64639 C64639 Helicobacter pylori 210 -11538776 7500884987 hp0955 prolipoprotein diacylglyceryl transferase lgt (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:10579 percent identity: 34.35;) (le:7925) (re:8779) (di:complement) HPAE000604 AE000604 g2314092 Helicobacter pylori 210 -11538776 7502852627 hp0955 prolipoprotein diacylglyceryl transferase lgt (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:10579 percent identity: 34.35;) (le:7925) (re:8779) (di:complement) HPAE000604 AE000604 g2314092 Helicobacter pylori 26695 85962 -11538776

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901170	17019	39175	1209	402

Description

6500734919 hemb:hp0163 delta-aminolevulinic acid dehydratase (gtcfc:9.10) (ec:4.2.1.24) (keggfc:9.10) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP0163 HP0163 Helicobacter pylori 210 -11538777 5500685330 hemb:hp0163 (sr:,campylobacter pylori) (ec:4.2.1.24) (de:synthase) (alad) (aladh)) (db:swissprot) HEM2_HELPY P56074 HELICOBACTER PYLORI 210 -11538777 7000685507 delta-aminolevulinic acid dehydratase (cl:porphobilinogen synthase) (db:pir2.dat) C64540 C64540 Helicobacter pylori 210 -11538777 7500883147 hp0163 delta-aminolevulinic acid dehydratase hemb (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to egad:21380 percent identity: 50.47;) (le:2651) (re:3622) (di:complement) HPAE000537 AE000537 g2313250 Helicobacter pylori 210 -11538777 7502852628 hp0163 delta-aminolevulinic acid dehydratase hemb (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to egad:21380 percent identity: 50.47;) (le:2651) (re:3622) (di:complement) HPAE000537 AE000537 g2313250 Helicobacter pylori 26695 85962 -11538777

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901174	17020	39176	738	245

Description

6500734920 hemc:hp0237 porphobilinogen deaminase (gtcfc:9.10) (ec:4.3.1.8) (keggfc:9.10) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP0237 HP0237 Helicobacter pylori 210 -11538778 5500685334 hemc:hp0237 (sr:,campylobacter pylori) (ec:4.3.1.8) (de:synthase) (hmbs) (pre-uroporphyrinogen synthase)) (db:swissprot) HEM3_HELPY P56140 HELICOBACTER PYLORI 210 -11538778 7000685508 hydroxymethylbilane synthase::porphobilinogen deaminase (cl:hydroxymethylbilane synthase) (ec:4.3.1.8) (db:pir2.dat) E64549 E64549 Helicobacter pylori 210 -11538778 7500883153 hp0237 porphobilinogen deaminase hemc (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to egad:15661 percent identity: 45.70;) (le:8016) (re:8936) (di:complement) HPAE000543 AE000543 g2313328 Helicobacter pylori 210 -11538778 7502852629 hp0237 porphobilinogen deaminase hemc (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to egad:15661 percent identity: 45.70;) (le:8016) (re:8936) (di:complement) HPAE000543 AE000543 g2313328 Helicobacter pylori 26695 85962 -11538778

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901175	17021	39177	315	104

Description

6500734921 heml:hp0306 glutamate-1-semialdehyde 2:1-aminomutase (gtcfc:9.10) (ec:5.4.3.8) (keggfc:9.10) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP0306 HP0306 Helicobacter pylori 210 -11538779 5500685307 heml:hp0306 (sr:,campylobacter pylori) (ec:5.4.3.8) (de:(glutamate-1-semialdehyde aminotransferase) (gsa-at)) (db:swissprot) GSA_HELPY P56115 HELICOBACTER PYLORI 210 -11538779 7000685460 glutamate-1-semialdehyde 2:1-aminomutase (db:pir2.dat) B64558 B64558 Helicobacter pylori 210 -11538779 7500882784 hp0306 glutamate-1-semialdehyde 2:1-aminomutase heml (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:similar to egad:19989 percent identity: 51.30;) (le:716) (re:2008) (di:direct) HPAE000549 AE000549 g2313404 Helicobacter pylori 210 -11538779 7502852630 hp0306 glutamate-1-semialdehyde 2:1-aminomutase heml (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:similar to egad:19989 percent identity: 51.30;) (le:716) (re:2008) (di:direct) HPAE000549 AE000549 g2313404 Helicobacter pylori 26695 85962 -11538779

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901179	17022	39178	405	134

Description

6500734922 hemh:hp0376 ferrochelatase (gtcfc:9.10) (ec:4.99.1.1) (keggfc:9.10) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP0376 HP0376 Helicobacter pylori 210 -11538780 5500685335 hemh:hp0376 (sr:,campylobacter pylori) (ec:4.99.1.1) (de:synthetase)) (db:swissprot) HEMZ_HELPY P56107 HELICOBACTER PYLORI 210 -11538780 7000685519 ferrochelatase (cl:ferrochelatase) (ec:4.99.1.1) (db:pir2.dat) H64566 H64566 Helicobacter pylori 210 -11538780 7500883209 hp0376 ferrochelatase hemh (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:similar to egad:1658 percent identity: 33.44;) (le:4117) (re:5121) (di:direct) HPAE000554 AE000554 g2313479 Helicobacter pylori 210 -11538780 7502852631 hp0376 ferrochelatase hemh (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:similar to egad:1658 percent identity: 33.44;) (le:4117) (re:5121) (di:direct) HPAE000554 AE000554 g2313479 Helicobacter pylori 26695 85962 -11538780

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901181	17023	39179	765	255

Description

GTC ORF with score 133 to: (de:(ydr264c) (pn:ankyrin repeat-containing protein akr1:ankyrin repeat-containing protein) (gn:d9954:akr1) (gtcfc:12.9) (ec:) (akr1_yeast) (keggfc:11.2) (sgdfc:3.3.0:10.1.6) (db:gtc-saccharomyces cerevisiae))

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901184	17024	39180	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901193	17025	39181	984	327

Description

6500734923 hemk:hp0381 protoporphyrinogen oxidase (gtcfc:9.10) (ec:1.3.3.4) (keggfc:9.10) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP0381 HP0381 Helicobacter pylori 210 -11538781 7000690659 protoporphyrinogen oxidase (db:pir2.dat) E64567 E64567 Helicobacter pylori 210 -11538781 7500959434 hp0381 protoporphyrinogen oxidase hemk (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:29991 percent identity: 35.87;) (le:63) (re:893) (di:complement) HPAE000555 AE000555 g2313486 Helicobacter pylori 210 -11538781 7502852632 hp0381 protoporphyrinogen oxidase hemk (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:29991 percent identity: 35.87;) (le:63) (re:893) (di:complement) HPAE000555 AE000555 g2313486 Helicobacter pylori 26695 85962 -11538781

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901194	17026	39182	231	76

Description

6500734924 heme:hp0604 uroporphyrinogen decarboxylase (gtcfc:9.10) (ec:4.1.1.37) (keggfc:9.10) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP0604 HP0604 Helicobacter pylori 210 -11538782 7500880099 heme:hp0604 (sr:,campylobacter pylori) (ec:4.1.1.37) (de:uroporphyrinogen decarboxylase, (upd)) (db:swissprot) DCUP_HELPY O25325 HELICOBACTER PYLORI 210 -11538782 7000690790 uroporphyrinogen decarboxylase (cl:uroporphyrinogen decarboxylase) (db:pir2.dat) D64595 D64595 Helicobacter pylori 210 -11538782 7500880101 hp0604 uroporphyrinogen decarboxylase heme (db:genpept-bct1) (de:helicobacter pylori section 52 of 134 of the complete genome.) (nt:similar to egad:21997 percent identity: 46.29;) (le:3098) (re:4120) (di:direct) HPAE000574 AE000574 g2313724 Helicobacter pylori 210 -11538782 7502852633 hp0604 uroporphyrinogen decarboxylase heme (db:genpept) (de:helicobacter pylori 26695 section 52 of 134 of the complete genome.) (nt:similar to egad:21997 percent identity: 46.29;) (le:3098) (re:4120) (di:direct) HPAE000574 AE000574 g2313724 Helicobacter pylori 26695 85962 -11538782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901199	17027	39183	1851	616

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901213	17028	39184	339	112

Description

6500734925 hemd:hp1224 uroporphyrinogen iii cosynthase (gtcfc:9.10) (ec:4.2.1.24) (keggfc:9.10) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP1224 HP1224 Helicobacter pylori 210 -11538783 7000690791 uroporphyrinogen iii cosynthase (db:pir2.dat) H64672 H64672 Helicobacter pylori 210 -11538783 7500959550 hp1224 uroporphyrinogen iii cosynthase hemd (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to egad:17338 percent identity: 27.55;) (le:398) (re:1078) (di:direct) HPAE000628 AE000628 g2314387 Helicobacter pylori 210 -11538783 7502852634 hp1224 uroporphyrinogen iii cosynthase hemd (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to egad:17338 percent identity: 27.55;) (le:398) (re:1078) (di:direct) HPAE000628 AE000628 g2314387 Helicobacter pylori 26695 85962 -11538783

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901224	17029	39185	711	236

Description

6500734926 hemn:hp0665 oxygen-independent coproporphyrinogen iii oxidase:oxygen-independent coproporphyrinogen iiioxidase (gtcfc:9.10) (ec:1.-.-.-) (keggfc:14.1) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP0665 HP0665 Helicobacter pylori 210 -11538784 7500883194 hemn:hp0665 (sr:,campylobacter pylori) (ec:1.-.-.-) (de:(coproporphyrinogenase) (coprogen oxidase)) (db:swissprot) HEMN_HELPY O25376 HELICOBACTER PYLORI 210 -11538784 7000690601 oxygen-independent coproporphyrinogen iii oxidase (cl:oxygen-independent coproporphyrinogen oxidase) (db:pir2.dat) A64603 A64603 Helicobacter pylori 210 -11538784 7500883196 hp0665 oxygen-independent coproporphyrinogen iii (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:9664 percent identity: 42.35;) (le:12951) (re:14324) (di:direct) HPAE000579 AE000579 g2313787 Helicobacter pylori 210 -11538784 7502852635 hp0665 oxygen-independent coproporphyrinogen iii (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:9664 percent identity: 42.35;) (le:12951) (re:14324) (di:direct) HPAE000579 AE000579 g2313787 Helicobacter pylori 26695 85962 -11538784

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901235	17030	39186	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901237	17031	39187	1386	461

Description

6500734927 hemn:hp1226 oxygen-independent coproporphyrinogen iii oxidase:oxygen-independent coproporphyrinogen iiioxidase (gtcfc:9.10) (ec:1.-.-.-) (keggfc:14.1) (tigrfc:2.4) (db:gtc-helicobacter pylori) HP1226 HP1226 Helicobacter pylori 210 -11538785 7000690602 oxygen-independent coproporphyrinogen iii oxidase (cl:oxygen-independent coproporphyrinogen oxidase) (db:pir2.dat) B64673 B64673 Helicobacter pylori 210 -11538785 7500953844 hp1226 oxygen-independent coproporphyrinogen iii (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to egad:29089 percent identity: 37.89;) (le:1569) (re:2627) (di:complement) HPAE000628 AE000628 g2314389 Helicobacter pylori 210 -11538785 7502852636 hp1226 oxygen-independent coproporphyrinogen iii (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to egad:29089 percent identity: 37.89;) (le:1569) (re:2627) (di:complement) HPAE000628 AE000628 g2314389 Helicobacter pylori 26695 85962 -11538785

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901242	17032	39188	312	103

Description

6500734928 thib:hp0843 thiamin phosphate pyrophosphorylase/hyroxyethylthiazole kinase (gtcfc:9.1) (ec:2.5.1.3) (keggfc:9.1) (tigrfc:2.11) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) HP0843 HP0843 Helicobacter pylori 210 -11538786 7000689081 probable thiamin-phosphate pyrophosphorylase (cl:thie protein:thiamin-phosphate pyrophosphorylase homology) (ec:2.5.1.3) (db:pir2.dat) C64625 C64625 Helicobacter pylori 210 -11538786 7500954047 hp0843 thiamin phosphate (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:similar to sp:p41835 percent identity: 35.67;) (le:7035) (re:7694) (di:complement) HPAE000595 AE000595 g2313974 Helicobacter pylori 210 -11538786 7502852637 hp0843 thiamin phosphate (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:similar to sp:p41835 percent identity: 35.67;) (le:7035) (re:7694) (di:complement) HPAE000595 AE000595 g2313974 Helicobacter pylori 26695 85962 -11538786

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901243	17033	39189	963	320

Description

6500734929 thim:hp0845 thiamin phosphate pyrophosphorylase/hyroxyethylthiazole kinase (gtcfc:9.1) (ec:2.5.1.3) (keggfc:9.1) (tigrfc:2.11) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) HP0845 HP0845 Helicobacter pylori 210 -11538787 7000689082 hydroxyethylthiazole kinase (cl:hydroxyethylthiazole kinase:hydroxyethylthiazole kinase homology) (ec:2.7.1.50) (db:pir2.dat) E64625 E64625 Helicobacter pylori 210 -11538787 7500954048 hp0845 thiamin phosphate (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:similar to sp:p41835 percent identity: 37.92;) (le:8493) (re:9314) (di:complement) HPAE000595 AE000595 g2313976 Helicobacter pylori 210 -11538787 7502852638 hp0845 thiamin phosphate (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:similar to sp:p41835 percent identity: 37.92;) (le:8493) (re:9314) (di:complement) HPAE000595 AE000595 g2313976 Helicobacter pylori 26695 85962 -11538787

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901245	17034	39190	501	166

Description

6500734930 thif:hp0814 thiamin biosynthesis protein (gtcfc:9.1) (keggfc:14.2) (tigrfc:2.11) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) HP0814 HP0814 Helicobacter pylori 210 -11538788 7000690725 thiamin biosynthesis protein (cl:molybdopterin biosynthesis protein moeb) (db:pir2.dat) F64621 F64621 Helicobacter pylori 210 -11538788 7500959491 hp0814 thiamin biosynthesis protein thif (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:8413 percent identity: 34.60;) (le:2018) (re:2785) (di:direct) HPAE000593 AE000593 g2313946 Helicobacter pylori 210 -11538788 7502852639 hp0814 thiamin biosynthesis protein thif (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:8413 percent identity: 34.60;) (le:2018) (re:2785) (di:direct) HPAE000593 AE000593 g2313946 Helicobacter pylori 26695 85962 -11538788

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901252	17035	39191	189	62

Description

6500734931 thi:hp0844 amine biosynthesis protein:thiamine biosynthesis protein (gtcfc:9.1) (keggfc:14.2) (tigrfc:2.11) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) HP0844 HP0844 Helicobacter pylori 210 -11538789 7000690726 thiamine biosynthesis protein (cl:phosphomethylpyrimidine phosphate kinase) (db:pir2.dat) D64625 D64625 Helicobacter pylori 210 -11538789 7500959492 hp0844 thiamine biosynthesis protein thi (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:similar to egad:11602 percent identity: 41.03;) (le:7687) (re:8499) (di:complement) HPAE000595 AE000595 g2313975 Helicobacter pylori 210 -11538789 7502852640 hp0844 thiamine biosynthesis protein thi (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:similar to egad:11602 percent identity: 41.03;) (le:7687) (re:8499) (di:complement) HPAE000595 AE000595 g2313975 Helicobacter pylori 26695 85962 -11538789

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901278	17036	39192	744	247

Description

6500734932 moea:hp0172 molybdopterin biosynthesis protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-helicobacter pylori) HP0172 HP0172 Helicobacter pylori 210 -11538790 7000690527 molybdopterin biosynthesis protein (db:pir2.dat) D64541 D64541 Helicobacter pylori 210 -11538790 7500959317 hp0172 molybdopterin biosynthesis protein moea (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to egad:14334 percent identity: 36.28;) (le:9936) (re:11111) (di:complement) HPAE000537 AE000537 g2313255 Helicobacter pylori 210 -11538790 7502852641 hp0172 molybdopterin biosynthesis protein moea (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to egad:14334 percent identity: 36.28;) (le:9936) (re:11111) (di:complement) HPAE000537 AE000537 g2313255 Helicobacter pylori 26695 85962 -11538790

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901279	17037	39193	852	283

Description

GTC ORF with score 814 to: (sr:yeast (s.cerevisiae) dna) (db:genpept-pln1) (de:yeast (s.cerevisiae) snf1 gene encoding a carbon catabolitederepressing protein kinase, complete cds.) (nt:snf1 protein kinase) (le:391) (re:2292) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901294	17038	39194	648	215

Description

6500734933 moeb:hp0755 molybdopterin biosynthesis protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-helicobacter pylori) HP0755 HP0755 Helicobacter pylori 210 -11538791 7000690526 molybdopterin biosynthesis protein (db:pir2.dat) C64614 C64614 Helicobacter pylori 210 -11538791 7500959316 hp0755 molybdopterin biosynthesis protein moeb (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:similar to egad:28772 percent identity: 32.23;) (le:765) (re:1397) (di:direct) HPAE000588 AE000588 g2313882 Helicobacter pylori 210 -11538791 7502852642 hp0755 molybdopterin biosynthesis protein moeb (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:similar to egad:28772 percent identity: 32.23;) (le:765) (re:1397) (di:direct) HPAE000588 AE000588 g2313882 Helicobacter pylori 26695 85962 -11538791

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901295	17039	39195	1089	362

Description

GTC ORF with score 1446 to: (sr:aspergillus niger transposon ant1 chlorate-resistant mutant 46) (db:genpept-pln1) (de:orf1 3' of ant1 5' insertion site {niad insertion site}(aspergillus niger, chlorate-resistant mutant 46, transposon ant1,transposon, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901305	17040	39196	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901332	17041	39197	1110	369

Description

6500734934 moaa:hp0768 molybdenum cofactor biosynthesis protein a (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-helicobacter pylori) HP0768 HP0768 Helicobacter pylori 210 -11538792 7500885713 moaa:hp0768 (sr:,campylobacter pylori) (de:molybdenum cofactor biosynthesis protein a) (db:swissprot) MOAA_HELPY P56414 HELICOBACTER PYLORI 210 -11538792 7000690525 molybdenum cofactor biosynthesis protein a (cl:haemophilus influenzae molybdenum cofactor biosynthesis protein a) (db:pir2.dat) H64615 H64615 Helicobacter pylori 210 -11538792 7500885715 hp0768 molybdenum cofactor biosynthesis protein a (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:similar to egad:28655 percent identity: 31.38;) (le:251) (re:1216) (di:complement) HPAE000589 AE000589 g2313896 Helicobacter pylori 210 -11538792 7502852643 hp0768 molybdenum cofactor biosynthesis protein a (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:similar to egad:28655 percent identity: 31.38;) (le:251) (re:1216) (di:complement) HPAE000589 AE000589 g2313896 Helicobacter pylori 26695 85962 -11538792

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901356	17042	39198	345	114

Description

6500734935 moba:hp0769 molybdopterin-guanine dinucleotide biosynthesis protein a:molybdopterin-guanine dinucleotide biosynthesisprotein a (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-helicobacter pylori) HP0769 HP0769 Helicobacter pylori 210 -11538793 7500885743 moba:hp0769 (sr:,campylobacter pylori) (de:fa)) (db:swissprot) MOBA_HELPY P56415 HELICOBACTER PYLORI 210 -11538793 7000690531 molybdopterin-guanine dinucleotide biosynthesis protein a (db:pir2.dat) A64616 A64616 Helicobacter pylori 210 -11538793 7500885745 hp0769 molybdopterin-guanine dinucleotide biosynthesis (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:similar to egad:29329 percent identity: 28.34;) (le:1304) (re:1909) (di:direct) HPAE000589 AE000589 g2313897 Helicobacter pylori 210 -11538793 7502852644 hp0769 molybdopterin-guanine dinucleotide biosynthesis (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:similar to egad:29329 percent identity: 28.34;) (le:1304) (re:1909) (di:direct) HPAE000589 AE000589 g2313897 Helicobacter pylori 26695 85962 -11538793

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901359	17043	39199	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901364	17044	39200	1275	424

Description

GTC ORF with score 466 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f12l6 genomic sequence,complete sequence.) (nt:unknown protein) (le:40434:40859:41173) (re:40781:41092:41253) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901371	17045	39201	186	61

Description

GTC ORF with score 90 to: (sr:fruit fly) (db:genpept-inv) (de:drosophila melanogaster ribosomal protein s6 gene and two potentialalternatively spliced proteins, complete cds.) (nt:putative) (le:850:1092:1811) (re:855:1297:2345) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901378	17046	39202	342	113

Description

6500734936 moac:hp0798 molybdenum cofactor biosynthesis protein c (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-helicobacter pylori) HP0798 HP0798 Helicobacter pylori 210 -11538794 4000708938 moac:hp0798 (sr:,campylobacter pylori) (de:molybdenum cofactor biosynthesis protein c) (db:swissprot) MOAC_HELPY Q48260 HELICOBACTER PYLORI 210 -11538794 7000685859 molybdenum cofactor biosynthesis protein c (cl:molybdenum cofactor biosynthesis protein c) (db:pir2.dat) F64619 F64619 Helicobacter pylori 210 -11538794 7500885726 hp0798 molybdenum cofactor biosynthesis protein c (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:34182 percent identity: 97.93;) (le:90) (re:566) (di:complement) HPAE000592 AE000592 g2313930 Helicobacter pylori 210 -11538794 7502852645 hp0798 molybdenum cofactor biosynthesis protein c (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:34182 percent identity: 97.93;) (le:90) (re:566) (di:complement) HPAE000592 AE000592 g2313930 Helicobacter pylori 26695 85962 -11538794

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901382	17047	39203	237	78

Description

6500734937 mog:hp0799 molybdopterin biosynthesis protein (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-helicobacter pylori) HP0799 HP0799 Helicobacter pylori 210 -11538795 7500885767 mog:hp0799 (sr:,campylobacter pylori) (de:molybdopterin biosynthesis mog protein) (db:swissprot) MOG_HELPY P56421 HELICOBACTER PYLORI 210 -11538795 7000690528 molybdopterin biosynthesis protein (db:pir2.dat) G64619 G64619 Helicobacter pylori 210 -11538795 7500885769 hp0799 molybdopterin biosynthesis protein mog (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:8773 percent identity: 50.85;) (le:575) (re:1105) (di:complement) HPAE000592 AE000592 g2313931 Helicobacter pylori 210 -11538795 7502852646 hp0799 molybdopterin biosynthesis protein mog (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:8773 percent identity: 50.85;) (le:575) (re:1105) (di:complement) HPAE000592 AE000592 g2313931 Helicobacter pylori 26695 85962 -11538795

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901392	17048	39204	741	246

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901421	17049	39205	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901426	17050	39206	1728	575

Description

6500734938 moae:hp0800 molybdopterin converting factor:subunit 2 (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-helicobacter pylori) HP0800 HP0800 Helicobacter pylori 210 -11538796 7500885732 moae:hp0800 (sr:,campylobacter pylori) (de:subunit)) (db:swissprot) MOAE_HELPY P56422 HELICOBACTER PYLORI 210 -11538796 7000690530 molybdopterin converting factor:subunit 2 (db:pir2.dat) H64619 H64619 Helicobacter pylori 210 -11538796 7500885734 hp0800 molybdopterin converting factor:subunit 2 (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to gp:1480153 percent identity: 31.13;) (le:1118) (re:1555) (di:complement) HPAE000592 AE000592 g2313932 Helicobacter pylori 210 -11538796 7502852647 hp0800 molybdopterin converting factor:subunit 2 (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to gp:1480153 percent identity: 31.13;) (le:1118) (re:1555) (di:complement) HPAE000592 AE000592 g2313932 Helicobacter pylori 26695 85962 -11538796

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901436	17051	39207	1617	538

Description

6500734939 moad:hp0801 molybdopterin converting factor:subunit 1 (gtcfc:9.11) (keggfc:14.2) (tigrfc:2.6) (db:gtc-helicobacter pylori) HP0801 HP0801 Helicobacter pylori 210 -11538797 7000690529 molybdopterin converting factor:subunit 1 (db:pir2.dat) A64620 A64620 Helicobacter pylori 210 -11538797 7500959318 hp0801 molybdopterin converting factor:subunit 1 (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:6975 percent identity: 31.08;) (le:1556) (re:1780) (di:complement) HPAE000592 AE000592 g2313939 Helicobacter pylori 210 -11538797 7502852648 hp0801 molybdopterin converting factor:subunit 1 (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:6975 percent identity: 31.08;) (le:1556) (re:1780) (di:complement) HPAE000592 AE000592 g2313939 Helicobacter pylori 26695 85962 -11538797

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901444	17052	39208	471	156

Description

6500734940 nifs:hp0220 synthesis of (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.1) (db:gtc-helicobacter pylori) HP0220 HP0220 Helicobacter pylori 210 -11538798 7000690722 synthesis of fe-s cluster) (cl:nitrogen fixation protein nifs) (db:pir2.dat) D64547 D64547 Helicobacter pylori 210 -11538798 7500959488 hp0220 synthesis of fe-s cluster (nifs)) (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:similar to egad:10138 percent identity: 48.02;) (le:747) (re:1910) (di:direct) HPAE000542 AE000542 g2313311 Helicobacter pylori 210 -11538798 7502852649 hp0220 synthesis of fe-s cluster (nifs)) (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:similar to egad:10138 percent identity: 48.02;) (le:747) (re:1910) (di:direct) HPAE000542 AE000542 g2313311 Helicobacter pylori 26695 85962 -11538798

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901446	17053	39209	246	81

Description

6500734941 ribe:hp0002 riboflavin synthase beta chain (gtcfc:9.2) (ec:2.5.1.9) (keggfc:9.2) (tigrfc:2.9) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HP0002 HP0002 Helicobacter pylori 210 -11538799 7000690689 ribe riboflavin synthase:beta chain:6:7-dimethyl-8-ribityllumazine synthase:lumazine synthase (ec:2.5.1.9) (db:pir2.dat) B64520 B64520 Helicobacter pylori 210 -11538799 7500959458 hp0002 riboflavin synthase beta chain ribe (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to egad:28309 percent identity: 52.45;) (le:635) (re:1105) (di:complement) HPAE000523 AE000523 g2313079 Helicobacter pylori 210 -11538799 7502852650 hp0002 riboflavin synthase beta chain ribe (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to egad:28309 percent identity: 52.45;) (le:635) (re:1105) (di:complement) HPAE000523 AE000523 g2313079 Helicobacter pylori 26695 85962 -11538799

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901447	17054	39210	582	193

Description

6500734942 riba:hp0802 gtp cyclohydrolase ii (gtcfc:9.2) (ec:3.5.4.25) (keggfc:9.2) (tigrfc:2.9) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HP0802 HP0802 Helicobacter pylori 210 -11538800 5500685265 riba:hp0802 (sr:,campylobacter pylori) (ec:3.5.4.25) (de:gtp cyclohydrolase ii,) (db:swissprot) GCH2_HELPY O08315 HELICOBACTER PYLORI 210 -11538800 7000685374 gtp cyclohydrolase ii (cl:escherichia coli cyclohydrolase ii:cyclohydrolase homology) (ec:3.5.4.25) (db:pir2.dat) B64620 B64620 Helicobacter pylori 210 -11538800 7500882254 hp0802 gtp cyclohydrolase ii riba (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:28849 percent identity: 47.18;) (le:1853) (re:2431) (di:complement) HPAE000592 AE000592 g2313933 Helicobacter pylori 210 -11538800 7502852651 hp0802 gtp cyclohydrolase ii riba (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:28849 percent identity: 47.18;) (le:1853) (re:2431) (di:complement) HPAE000592 AE000592 g2313933 Helicobacter pylori 26695 85962 -11538800

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901448	17055	39211	2226	742

Description

6500734943 riba:ribb:hp0804 gtp cyclohydrolase ii/3:4-dihydroxy-2-butanone 4-phosphate synthase:gtp cyclohydrolase ii/3:4-dihydroxy-2-butanone4-phosphate synthase:riba:ribb (gtcfc:9.2) (ec:3.5.4.25) (keggfc:9.2) (tigrfc:2.9) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HP0804 HP0804 Helicobacter pylori 210 -11538801 7000689163 gtp cyclohydrolase ii:3:4-dihydroxy-2-butanone 4-phosphate synthase (cl:riba bifunctional protein:3, 4-dihydroxy-2-butanone 4-phosphate synthase homology:cyclohydrolase homology) (ec:3.5.4.25:5.4.99.-) (db:pir2.dat) D64620 D64620 Helicobacter pylori 210 -11538801 7500954327 hp0804 gtp cyclohydrolase ii/3:4-dihydroxy-2-butanone (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:37790 percent identity: 44.02;) (le:3448) (re:4482) (di:complement) HPAE000592 AE000592 g2313934 Helicobacter pylori 210 -11538801 7502852652 hp0804 gtp cyclohydrolase ii/3:4-dihydroxy-2-butanone (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:37790 percent identity: 44.02;) (le:3448) (re:4482) (di:complement) HPAE000592 AE000592 g2313934 Helicobacter pylori 26695 85962 -11538801

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901459	17056	39212	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901461	17057	39213	270	89

Description

6500734944 ribc:hp1574 riboflavin synthase alpha subunit (gtcfc:9.2) (ec:2.5.1.9) (keggfc:9.2) (tigrfc:2.9) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HP1574 HP1574 Helicobacter pylori 210 -11538802 7000690690 riboflavin synthase alpha subunit (cl:riboflavin synthase alpha chain) (db:pir2.dat) F64716 F64716 Helicobacter pylori 210 -11538802 7500959459 hp1574 riboflavin synthase alpha subunit ribc (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:41143 percent identity: 32.80;) (le:913) (re:1533) (di:direct) HPAE000655 AE000655 g2314759 Helicobacter pylori 210 -11538802 7502852653 hp1574 riboflavin synthase alpha subunit ribc (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:41143 percent identity: 32.80;) (le:913) (re:1533) (di:direct) HPAE000655 AE000655 g2314759 Helicobacter pylori 26695 85962 -11538802

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901484	17058	39214	639	212

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901485	17059	39215	1116	371

Description

6500734945 ribc:hp1087 riboflavin biosynthesis regulatory protein (gtcfc:9.2) (keggfc:14.2) (tigrfc:2.9) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HP1087 HP1087 Helicobacter pylori 210 -11538803 7000690688 riboflavin biosynthesis regulatory protein (cl:conserved hypothetical protein hi0963) (db:pir2.dat) G64655 G64655 Helicobacter pylori 210 -11538803 7500959457 hp1087 riboflavin biosynthesis regulatory protein (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:similar to egad:37767 percent identity: 28.94;) (le:6895) (re:7737) (di:direct) HPAE000615 AE000615 g2314235 Helicobacter pylori 210 -11538803 7502852654 hp1087 riboflavin biosynthesis regulatory protein (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:similar to egad:37767 percent identity: 28.94;) (le:6895) (re:7737) (di:direct) HPAE000615 AE000615 g2314235 Helicobacter pylori 26695 85962 -11538803

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901487	17060	39216	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901493	17061	39217	696	231

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901497	17062	39218	1086	362

Description

GTC ORF with score 243 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c16c4.) (nt:spcc14g10.05, len:669, similarity:bos taurus,) (le:10794:11045:11673:12455) (re:11000:11609:12413:12951) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901498	17063	39219	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901514	17064	39220	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901518	17065	39221	705	234

Description

6500734946 ribg:hp1505 riboflavin biosynthesis protein (gtcfc:9.2) (keggfc:14.2) (tigrfc:2.9) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) HP1505 HP1505 Helicobacter pylori 210 -11538804 7000690687 riboflavin biosynthesis protein (db:pir2.dat) A64708 A64708 Helicobacter pylori 210 -11538804 7500959456 hp1505 riboflavin biosynthesis protein ribg (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:27967 percent identity: 33.10;) (le:13498) (re:14532) (di:complement) HPAE000648 AE000648 g2314679 Helicobacter pylori 210 -11538804 7502852655 hp1505 riboflavin biosynthesis protein ribg (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:27967 percent identity: 33.10;) (le:13498) (re:14532) (di:complement) HPAE000648 AE000648 g2314679 Helicobacter pylori 26695 85962 -11538804

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901519	17066	39222	627	208

Description

6500734947 pdxj:hp1582 pyridoxal phosphate biosynthetic protein j (gtcfc:9.3) (keggfc:14.2) (tigrfc:2.8) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6)) HP1582 HP1582 Helicobacter pylori 210 -11538805 7000690664 pyridoxal phosphate biosynthetic protein j (db:pir2.dat) F64717 F64717 Helicobacter pylori 210 -11538805 7500959437 hp1582 pyridoxal phosphate biosynthetic protein j (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:30156 percent identity: 42.55;) (le:6827) (re:7615) (di:direct) HPAE000655 AE000655 g2314765 Helicobacter pylori 210 -11538805 7502852656 hp1582 pyridoxal phosphate biosynthetic protein j (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:30156 percent identity: 42.55;) (le:6827) (re:7615) (di:direct) HPAE000655 AE000655 g2314765 Helicobacter pylori 26695 85962 -11538805

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901526	17067	39223	3942	1313

Description

6500734948 pdxa:hp1583 pyridoxal phosphate biosynthetic protein a (gtcfc:9.3) (keggfc:14.2) (tigrfc:2.8) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6)) HP1583 HP1583 Helicobacter pylori 210 -11538806 7000690663 pyridoxal phosphate biosynthetic protein a (cl:pdxa protein) (db:pir2.dat) G64717 G64717 Helicobacter pylori 210 -11538806 7500955456 hp1583 pyridoxal phosphate biosynthetic protein a (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:22942 percent identity: 34.17;) (le:7617) (re:8540) (di:direct) HPAE000655 AE000655 g2314766 Helicobacter pylori 210 -11538806 7502852657 hp1583 pyridoxal phosphate biosynthetic protein a (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:22942 percent identity: 34.17;) (le:7617) (re:8540) (di:direct) HPAE000655 AE000655 g2314766 Helicobacter pylori 26695 85962 -11538806

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901533	17068	39224	1200	399

Description

6500734949 nadc:hp1355 nicotinate-nucleotide pyrophosphorylase (gtcfc:9.4) (ec:2.4.2.19) (keggfc:9.4) (tigrfc:2.12) (db:gtc-helicobacter pylori) HP1355 HP1355 Helicobacter pylori 210 -11538807 7500886237 nadc:hp1355 (sr:,campylobacter pylori) (ec:2.4.2.19) (de:(decarboxylating)) (qaprtase)) (db:swissprot) NADC_HELPY O25909 HELICOBACTER PYLORI 210 -11538807 7000690557 nicotinate-nucleotide pyrophosphorylase (cl:nicotinate-nucleotide pyrophosphorylase (carboxylating)) (db:pir2.dat) C64689 C64689 Helicobacter pylori 210 -11538807 7500886239 hp1355 nicotinate-nucleotide pyrophosphorylase nadc (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:30416 percent identity: 36.33;) (le:9963) (re:10784) (di:complement) HPAE000636 AE000636 g2314523 Helicobacter pylori 210 -11538807 7502852658 hp1355 nicotinate-nucleotide pyrophosphorylase nadc (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:30416 percent identity: 36.33;) (le:9963) (re:10784) (di:complement) HPAE000636 AE000636 g2314523 Helicobacter pylori 26695 85962 -11538807

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901544	17069	39225	246	81

Description

6500734950 panb:hp1058 3-methyl-2-oxobutanoate hydroxymethyltransferase (gtcfc:9.5:9.6) (ec:2.1.2.11) (keggfc:9.5:9.8) (tigrfc:2.7) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-pantothenate and coa biosynthesis:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP1058 HP1058 Helicobacter pylori 210 -11538808 7000689592 3-methyl-2-oxobutanoate hydroxymethyltransferase (cl:3-methyl-2-oxobutanoate hydroxymethyltransferase) (db:pir2.dat) B64652 B64652 Helicobacter pylori 210 -11538808 7500958413 hp1058 3-methyl-2-oxobutanoate hydroxymethyltransferase (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:similar to egad:37747 percent identity: 43.73;) (le:5529) (re:6341) (di:direct) HPAE000613 AE000613 g2314202 Helicobacter pylori 210 -11538808 7502852659 hp1058 3-methyl-2-oxobutanoate hydroxymethyltransferase (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:similar to egad:37747 percent identity: 43.73;) (le:5529) (re:6341) (di:direct) HPAE000613 AE000613 g2314202 Helicobacter pylori 26695 85962 -11538808

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901556	17070	39226	1875	624

Description

6500734951 dfp:hp0841 pantothenate metabolism flavoprotein (gtcfc:9.5:2.8) (keggfc:14.2) (tigrfc:2.7) (db:gtc-helicobacter pylori) HP0841 HP0841 Helicobacter pylori 210 -11538809 7000690604 pantothenate metabolism flavoprotein (db:pir2.dat) A64625 A64625 Helicobacter pylori 210 -11538809 7500959384 hp0841 pantothenate metabolism flavoprotein dfp (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:similar to egad:27976 percent identity: 31.30;) (le:4996) (re:6273) (di:direct) HPAE000595 AE000595 g2313973 Helicobacter pylori 210 -11538809 7502852660 hp0841 pantothenate metabolism flavoprotein dfp (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:similar to egad:27976 percent identity: 31.30;) (le:4996) (re:6273) (di:direct) HPAE000595 AE000595 g2313973 Helicobacter pylori 26695 85962 -11538809

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901574	17071	39227	393	130

Description

GTC ORF with score 111 to: (de:(yfr047c) (pn:putative nicotinate-nucleotide pyrophosphorylase:carboxylating:quinolinate phosphoribosyltransferase:decarboxylating:qaprtase:similarity to human quinolinate phosphoribosyltransferase) (gtcfc:9.4) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901575	17072	39228	747	248

Description

6500734952 biod:hp0029 dethiobiotin synthetase (gtcfc:9.6) (ec:6.3.3.3) (keggfc:9.6) (tigrfc:2.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP0029 HP0029 Helicobacter pylori 210 -11538810 5000696085 biod:hp0029 (sr:,campylobacter pylori) (ec:6.3.3.3) (de:synthetase) (dtbs)) (db:swissprot) BIOD_HELPY O24872 HELICOBACTER PYLORI 210 -11538810 7000689887 dethiobiotin synthetase (cl:dethiobiotin synthase) (db:pir2.dat) E64523 E64523 Helicobacter pylori 210 -11538810 7500954497 hp0029 dethiobiotin synthetase biod (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to egad:43909 percent identity: 36.00;) (le:6282) (re:6938) (di:complement) HPAE000525 AE000525 g2313106 Helicobacter pylori 210 -11538810 7502852661 hp0029 dethiobiotin synthetase biod (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to egad:43909 percent identity: 36.00;) (le:6282) (re:6938) (di:complement) HPAE000525 AE000525 g2313106 Helicobacter pylori 26695 85962 -11538810

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901597	17073	39229	2535	844

Description

6500734953 biof:hp0598 8-amino-7-oxononanoate synthase (gtcfc:9.6) (ec:2.3.1.47) (keggfc:9.6) (tigrfc:2.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP0598 HP0598 Helicobacter pylori 210 -11538811 7500877832 biof:hp0598 (sr:,campylobacter pylori) (ec:2.3.1.47) (de:ligase)) (db:swissprot) BIOF_HELPY O25320 HELICOBACTER PYLORI 210 -11538811 7000689598 8-amino-7-oxononanoate synthase (db:pir2.dat) F64594 F64594 Helicobacter pylori 210 -11538811 7500877834 hp0598 8-amino-7-oxononanoate synthase biof (db:genpept-bct1) (de:helicobacter pylori section 51 of 134 of the complete genome.) (nt:similar to egad:28547 percent identity: 34.93;) (le:6641) (re:7762) (di:complement) HPAE000573 AE000573 g2313715 Helicobacter pylori 210 -11538811 7502852662 hp0598 8-amino-7-oxononanoate synthase biof (db:genpept) (de:helicobacter pylori 26695 section 51 of 134 of the complete genome.) (nt:similar to egad:28547 percent identity: 34.93;) (le:6641) (re:7762) (di:complement) HPAE000573 AE000573 g2313715 Helicobacter pylori 26695 85962 -11538811

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901609	17074	39230	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901617	17075	39231	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901618	17076	39232	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901625	17077	39233	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901659	17078	39234	1581	526

Description

6500734954 bioa:hp0976 adenosylmethionine-8-amino-7-oxononanoate aminotransferase:adenosylmethionine-8-amino-7-oxononanoateaminotransferase (gtcfc:9.6) (ec:2.6.1.62) (keggfc:9.6) (tigrfc:2.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP0976 HP0976 Helicobacter pylori 210 -11538812 7500877801 bioa:hp0976 (sr:,campylobacter pylori) (ec:2.6.1.62) (de:aminotransferase)) (db:swissprot) BIOA_HELPY O25627 HELICOBACTER PYLORI 210 -11538812 7000689619 adenosylmethionine-8-amino-7-oxononanoate aminotransferase (db:pir2.dat) H64641 H64641 Helicobacter pylori 210 -11538812 7500877803 hp0976 adenosylmethionine-8-amino-7-oxononanoate (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:similar to egad:24237 percent identity: 49.16;) (le:3051) (re:4361) (di:complement) HPAE000606 AE000606 g2314118 Helicobacter pylori 210 -11538812 7502852663 hp0976 adenosylmethionine-8-amino-7-oxononanoate (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:similar to egad:24237 percent identity: 49.16;) (le:3051) (re:4361) (di:complement) HPAE000606 AE000606 g2314118 Helicobacter pylori 26695 85962 -11538812

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901661	17079	39235	699	232

Description

6500734955 biob:hp1406 biotin synthetase (gtcfc:9.6) (ec:2.8.1.-) (keggfc:9.6) (tigrfc:2.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP1406 HP1406 Helicobacter pylori 210 -11538813 7500877812 biob:hp1406 (sr:,campylobacter pylori) (ec:2.8.1.6) (de:biotin synthase, (biotin synthetase)) (db:swissprot) BIOB_HELPY O25956 HELICOBACTER PYLORI 210 -11538813 7000689667 biotin synthetase (db:pir2.dat) F64695 F64695 Helicobacter pylori 210 -11538813 7500877814 hp1406 biotin synthetase biob (db:genpept-bct1) (de:helicobacter pylori section 118 of 134 of the complete genome.) (nt:similar to egad:24934 percent identity: 36.19;) (le:9987) (re:10835) (di:direct) HPAE000640 AE000640 g2314578 Helicobacter pylori 210 -11538813 7502852664 hp1406 biotin synthetase biob (db:genpept) (de:helicobacter pylori 26695 section 118 of 134 of the completegenome.) (nt:similar to egad:24934 percent identity: 36.19;) (le:9987) (re:10835) (di:direct) HPAE000640 AE000640 g2314578 Helicobacter pylori 26695 85962 -11538813

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901667	17080	39236	186	61

Description

6500734956 cada:hp0791 cadmium-transporting atpase:p-type (gtcfc:9.6:12.5) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP0791 HP0791 Helicobacter pylori 210 -11538814 1500685877 cada:hp0791 (sr:,campylobacter pylori) (ec:3.6.1.-) (de:probable heavy-metal cation-transporting atpase,) (db:swissprot) HMCT_HELPY Q59465 HELICOBACTER PYLORI 210 -11538814 7000685541 cadmium-transporting atpase:p-type (cl:atpase nucleotide-binding domain homology) (db:pir2.dat) G64618 G64618 Helicobacter pylori 210 -11538814 7500883419 hp0791 cadmium-transporting atpase:p-type cada (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:similar to egad:34144 percent identity: 97.52;) (le:3368) (re:5428) (di:complement) HPAE000591 AE000591 g2313920 Helicobacter pylori 210 -11538814 7502852665 hp0791 cadmium-transporting atpase:p-type cada (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:similar to egad:34144 percent identity: 97.52;) (le:3368) (re:5428) (di:complement) HPAE000591 AE000591 g2313920 Helicobacter pylori 26695 85962 -11538814

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901690	17081	39237	2778	925

Description

GTC ORF with score 256 to: (sr:saccharomyces cerevisiae (clone: plg1) (clone library: hieter yeas) (db:genpept-pln2) (de:saccharomyces cerevisiae nucleoporin (rat7/nup159) gene, completecds.) (nt:rat7p or nup159p) (le:313) (re:4695) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901700	17082	39238	636	211

Description

6500734957 rep:hp0911 helicase:single-stranded dna-dependent atpase:rep helicase:single-stranded dna-dependentatpase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HP0911 HP0911 Helicobacter pylori 210 -11538815 7000690679 rep helicase:single-stranded dna-dependent atpase (db:pir2.dat) G64633 G64633 Helicobacter pylori 210 -11538815 7500959449 hp0911 rep helicase:single-stranded dna-dependent (db:genpept-bct1) (de:helicobacter pylori section 78 of 134 of the complete genome.) (nt:similar to egad:29271 percent identity: 33.79;) (le:6306) (re:8333) (di:direct) HPAE000600 AE000600 g2314046 Helicobacter pylori 210 -11538815 7502852666 hp0911 rep helicase:single-stranded dna-dependent (db:genpept) (de:helicobacter pylori 26695 section 78 of 134 of the complete genome.) (nt:similar to egad:29271 percent identity: 33.79;) (le:6306) (re:8333) (di:direct) HPAE000600 AE000600 g2314046 Helicobacter pylori 26695 85962 -11538815

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901731	17083	39239	1158	385

Description

6500734958 fole:hp0928 gtp cyclohydrolase i (gtcfc:9.6) (ec:3.5.4.16) (keggfc:9.7) (tigrfc:2.3) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP0928 HP0928 Helicobacter pylori 210 -11538816 7500882244 fole:hp0928 (sr:,campylobacter pylori) (ec:3.5.4.16) (de:gtp cyclohydrolase i, (gtp-ch-i)) (db:swissprot) GCH1_HELPY P56462 HELICOBACTER PYLORI 210 -11538816 7000689162 gtp cyclohydrolase i (cl:gtp cyclohydrolase i) (ec:3.5.4.16) (db:pir2.dat) H64635 H64635 Helicobacter pylori 210 -11538816 7500882246 hp0928 gtp cyclohydrolase i fole (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:42665 percent identity: 50.87;) (le:11886) (re:12428) (di:direct) HPAE000602 AE000602 g2314065 Helicobacter pylori 210 -11538816 7502852667 hp0928 gtp cyclohydrolase i fole (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:42665 percent identity: 50.87;) (le:11886) (re:12428) (di:direct) HPAE000602 AE000602 g2314065 Helicobacter pylori 26695 85962 -11538816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901732	17084	39240	1044	347

Description

6500734959 folk:hp1036 7:8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (gtcfc:9.6) (ec:2.7.6.3) (keggfc:9.7) (tigrfc:2.3) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP1036 HP1036 Helicobacter pylori 210 -11538817 7000689596 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase::6-hydroxymethyl-7:8-dihydropterin pyrophosphokinase:7:8-dihydro-6-hydroxymethylpterin pyrophosphokinase (cl:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase homology) (ec:2.7.6.3) (db:pir2.dat) D64649 D64649 Helicobacter pylori 210 -11538817 7500958416 hp1036 7 (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to egad:18680 percent identity: 34.56;) (le:6885) (re:7376) (di:complement) HPAE000611 AE000611 g2314180 Helicobacter pylori 210 -11538817 7502852668 hp1036 7 (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to egad:18680 percent identity: 34.56;) (le:6885) (re:7376) (di:complement) HPAE000611 AE000611 g2314180 Helicobacter pylori 26695 85962 -11538817

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901739	17085	39241	1362	453

Description

6500734960 folp:hp1232 dihydropteroate synthase (gtcfc:9.6) (ec:2.5.1.15) (keggfc:9.7) (tigrfc:2.3) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP1232 HP1232 Helicobacter pylori 210 -11538818 7000689894 dihydropteroate synthase::dihydropteroate pyrophosphorylase (cl:dihydropteroate synthase homology) (ec:2.5.1.15) (db:pir2.dat) H64673 H64673 Helicobacter pylori 210 -11538818 7500958691 hp1232 dihydropteroate synthase folp (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to egad:28331 percent identity: 34.48;) (le:6017) (re:7159) (di:direct) HPAE000628 AE000628 g2314394 Helicobacter pylori 210 -11538818 7502852669 hp1232 dihydropteroate synthase folp (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to egad:28331 percent identity: 34.48;) (le:6017) (re:7159) (di:direct) HPAE000628 AE000628 g2314394 Helicobacter pylori 26695 85962 -11538818

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901744	17086	39242	879	292

Description

6500734961 dnab:hp1362 replicative dna helicase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HP1362 HP1362 Helicobacter pylori 210 -11538819 7500880405 dnab:hp1362 (sr:,campylobacter pylori) (ec:3.6.1.-) (de:replicative dna helicase,) (db:swissprot) DNAB_HELPY O25916 HELICOBACTER PYLORI 210 -11538819 7000690680 replicative dna helicase (db:pir2.dat) B64690 B64690 Helicobacter pylori 210 -11538819 7500880407 hp1362 replicative dna helicase dnab (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:21924 percent identity: 39.39;) (le:15810) (re:17276) (di:complement) HPAE000636 AE000636 g2314528 Helicobacter pylori 210 -11538819 7502852670 hp1362 replicative dna helicase dnab (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:21924 percent identity: 39.39;) (le:15810) (re:17276) (di:complement) HPAE000636 AE000636 g2314528 Helicobacter pylori 26695 85962 -11538819

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901750	17087	39243	873	290

Description

6500734962 uvrd:hp1478 dna helicase ii uvrd:dna helicase ii (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HP1478 HP1478 Helicobacter pylori 210 -11538820 7000689898 dna helicase ii (db:pir2.dat) F64704 F64704 Helicobacter pylori 210 -11538820 7500958695 hp1478 dna helicase ii uvrd (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:39913 percent identity: 35.34;) (le:11647) (re:13695) (di:complement) HPAE000647 AE000647 g2314653 Helicobacter pylori 210 -11538820 7502852671 hp1478 dna helicase ii uvrd (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:39913 percent identity: 35.34;) (le:11647) (re:13695) (di:complement) HPAE000647 AE000647 g2314653 Helicobacter pylori 26695 85962 -11538820

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901752	17088	39244	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901767	17089	39245	336	111

Description

6500734963 copa:hp1503 cation-transporting atpase:p-type (gtcfc:9.6:12.5) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1503 HP1503 Helicobacter pylori 210 -11538821 7000689699 cation-transporting atpase:p-type (cl:atpase nucleotide-binding domain homology) (db:pir2.dat) G64707 G64707 Helicobacter pylori 210 -11538821 7500958510 hp1503 cation-transporting atpase:p-type copa (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:5970 percent identity: 30.27;) (le:10408) (re:12774) (di:complement) HPAE000648 AE000648 g2314677 Helicobacter pylori 210 -11538821 7502852672 hp1503 cation-transporting atpase:p-type copa (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:5970 percent identity: 30.27;) (le:10408) (re:12774) (di:complement) HPAE000648 AE000648 g2314677 Helicobacter pylori 26695 85962 -11538821

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901768	17090	39246	411	136

Description

6500734964 recg:hp1523 dna recombinase recg:dna recombinase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) HP1523 HP1523 Helicobacter pylori 210 -11538822 7502852673 recg:hp1523 (sr:,campylobacter pylori) (ec:3.6.1.-) (de:atp-dependent dna helicase recg,) (db:swissprot) RECG_HELPY O26051 HELICOBACTER PYLORI 210 -11538822 7000689906 dna recombinase (cl:dead/h box helicase homology) (db:pir2.dat) C64710 C64710 Helicobacter pylori 210 -11538822 7500958702 hp1523 dna recombinase recg (db:genpept-bct1) (de:helicobacter pylori section 128 of 134 of the complete genome.) (nt:similar to egad:16079 percent identity: 32.67;) (le:7276) (re:9147) (di:complement) HPAE000650 AE000650 g2314702 Helicobacter pylori 210 -11538822 7502852674 hp1523 dna recombinase recg (db:genpept) (de:helicobacter pylori 26695 section 128 of 134 of the completegenome.) (nt:similar to egad:16079 percent identity: 32.67;) (le:7276) (re:9147) (di:complement) HPAE000650 AE000650 g2314702 Helicobacter pylori 26695 85962 -11538822

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901780	17091	39247	285	94

Description

6500734965 folc:hp1545 folylpolyglutamate synthase (gtcfc:9.6) (ec:6.3.2.17) (keggfc:9.7) (tigrfc:2.3) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP1545 HP1545 Helicobacter pylori 210 -11538823 7000689951 folylpolyglutamate synthase (db:pir2.dat) A64713 A64713 Helicobacter pylori 210 -11538823 7500958739 hp1545 folylpolyglutamate synthase folc (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:28270 percent identity: 35.17;) (le:8047) (re:9231) (di:complement) HPAE000652 AE000652 g2314726 Helicobacter pylori 210 -11538823 7502852675 hp1545 folylpolyglutamate synthase folc (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:28270 percent identity: 35.17;) (le:8047) (re:9231) (di:complement) HPAE000652 AE000652 g2314726 Helicobacter pylori 26695 85962 -11538823

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901781	17092	39248	306	101

Description

6500734966 bisc:hp0407 biotin sulfoxide reductase (gtcfc:9.6) (ec:1.-.-.-) (keggfc:14.1) (tigrfc:2.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP0407 HP0407 Helicobacter pylori 210 -11538824 7000689665 biotin sulfoxide reductase (cl:trimethylamine-n-oxide reductase) (ec:1.8.4.-) (db:pir2.dat) G64570 G64570 Helicobacter pylori 210 -11538824 7500958479 hp0407 biotin sulfoxide reductase bisc (db:genpept-bct1) (de:helicobacter pylori section 34 of 134 of the complete genome.) (nt:similar to egad:29279 percent identity: 42.75;) (le:7946) (re:10336) (di:direct) HPAE000556 AE000556 g2313512 Helicobacter pylori 210 -11538824 7502852676 hp0407 biotin sulfoxide reductase bisc (db:genpept) (de:helicobacter pylori 26695 section 34 of 134 of the complete genome.) (nt:similar to egad:29279 percent identity: 42.75;) (le:7946) (re:10336) (di:direct) HPAE000556 AE000556 g2313512 Helicobacter pylori 26695 85962 -11538824

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901787	17093	39249	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901794	17094	39250	1662	553

Description

6500734967 bira:hp1140 biotin operon repressor:biotin acetyl coenzyme a carboxylase synthetase (gtcfc:9.6) (ec:6.3.4.15) (keggfc:14.1) (tigrfc:2.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP1140 HP1140 Helicobacter pylori 210 -11538825 7000689664 biotin operon repressor/biotin acetyl coenzyme a carboxylase synthetase (db:pir2.dat) D64662 D64662 Helicobacter pylori 210 -11538825 7500958478 hp1140 biotin operon repressor/biotin acetyl coenzyme a (db:genpept-bct1) (de:helicobacter pylori section 98 of 134 of the complete genome.) (nt:similar to egad:7148 percent identity: 36.94;) (le:1758) (re:2396) (di:complement) HPAE000620 AE000620 g2314296 Helicobacter pylori 210 -11538825 7502852677 hp1140 biotin operon repressor/biotin acetyl coenzyme a (db:genpept) (de:helicobacter pylori 26695 section 98 of 134 of the complete genome.) (nt:similar to egad:7148 percent identity: 36.94;) (le:1758) (re:2396) (di:complement) HPAE000620 AE000620 g2314296 Helicobacter pylori 26695 85962 -11538825

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901798	17095	39251	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901799	17096	39252	1239	413

Description

6500734968 bioc:hp1254 biotin synthesis protein (gtcfc:9.6) (keggfc:14.2) (tigrfc:2.2) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP1254 HP1254 Helicobacter pylori 210 -11538826 7000689666 biotin synthesis protein (db:pir2.dat) F64676 F64676 Helicobacter pylori 210 -11538826 7500958480 hp1254 biotin synthesis protein bioc (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to egad:13763 percent identity: 32.12;) (le:9802) (re:10524) (di:complement) HPAE000630 AE000630 g2314418 Helicobacter pylori 210 -11538826 7502852678 hp1254 biotin synthesis protein bioc (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to egad:13763 percent identity: 32.12;) (le:9802) (re:10524) (di:complement) HPAE000630 AE000630 g2314418 Helicobacter pylori 26695 85962 -11538826

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901800	17097	39253	1164	387

Description

6500734969 pabc:hp0587 aminodeoxychorismate lyase (gtcfc:9.6) (keggfc:14.2) (tigrfc:2.3) (db:gtc-helicobacter pylori) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HP0587 HP0587 Helicobacter pylori 210 -11538827 7000689634 aminodeoxychorismate lyase (db:pir2.dat) C64593 C64593 Helicobacter pylori 210 -11538827 7500958452 hp0587 aminodeoxychorismate lyase pabc (db:genpept-bct1) (de:helicobacter pylori section 50 of 134 of the complete genome.) (nt:similar to egad:29093 percent identity: 32.43;) (le:3807) (re:4796) (di:direct) HPAE000572 AE000572 g2313705 Helicobacter pylori 210 -11538827 7502852679 hp0587 aminodeoxychorismate lyase pabc (db:genpept) (de:helicobacter pylori 26695 section 50 of 134 of the complete genome.) (nt:similar to egad:29093 percent identity: 32.43;) (le:3807) (re:4796) (di:direct) HPAE000572 AE000572 g2313705 Helicobacter pylori 26695 85962 -11538827

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901836	17098	39254	369	122

Description

6500734970 hup:hp0835 histone-like dna-binding protein hu (gtcfc:10.1) (keggfc:14.2) (tigrfc:12.4) (db:gtc-helicobacter pylori) HP0835 HP0835 Helicobacter pylori 210 -11538828 7502852680 hup:hp0835 (sr:,campylobacter pylori) (de:dna-binding protein hu) (db:swissprot) DBH_HELPY O25506 HELICOBACTER PYLORI 210 -11538828 7000689990 histone-like dna-binding protein hu (cl:bacterial dna-binding protein) (db:pir2.dat) C64624 C64624 Helicobacter pylori 210 -11538828 7500958771 hp0835 histone-like dna-binding protein hu hup (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:similar to egad:8515 percent identity: 44.57;) (le:101) (re:385) (di:direct) HPAE000595 AE000595 g2313970 Helicobacter pylori 210 -11538828 7502852681 hp0835 histone-like dna-binding protein hu hup (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:similar to egad:8515 percent identity: 44.57;) (le:101) (re:385) (di:direct) HPAE000595 AE000595 g2313970 Helicobacter pylori 26695 85962 -11538828

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901837	17099	39255	1458	485

Description

GTC ORF with score 108 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f53a3.) (nt:contains similarity to the e. coli umuc protein) (le:6499:6678:6873:7323) (re:6626:6824:7032:7527) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901839	17100	39256	1890	630

Description

6500734971 xsea:hp0259 exonuclease vii:large subunit (gtcfc:10.10) (ec:3.1.11.6) (keggfc:14.1) (tigrfc:10.1) (db:gtc-helicobacter pylori) HP0259 HP0259 Helicobacter pylori 210 -11538829 7000689914 exonuclease vii:large subunit (db:pir2.dat) C64552 C64552 Helicobacter pylori 210 -11538829 7500958709 hp0259 exonuclease vii:large subunit xsea (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to egad:29033 percent identity: 37.58;) (le:3451) (re:4713) (di:direct) HPAE000545 AE000545 g2313353 Helicobacter pylori 210 -11538829 7502852682 hp0259 exonuclease vii:large subunit xsea (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to egad:29033 percent identity: 37.58;) (le:3451) (re:4713) (di:direct) HPAE000545 AE000545 g2313353 Helicobacter pylori 26695 85962 -11538829

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901885	17101	39257	459	153

Description

6500734972 addb:hp0275 atp-dependent nuclease (gtcfc:10.10) (keggfc:14.2) (tigrfc:10.1) (db:gtc-helicobacter pylori) HP0275 HP0275 Helicobacter pylori 210 -11538830 7000689653 atp-dependent nuclease (db:pir2.dat) C64554 C64554 Helicobacter pylori 210 -11538830 7500958468 hp0275 atp-dependent nuclease addb (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:similar to egad:18428 percent identity: 27.24;) (le:4806) (re:6098) (di:direct) HPAE000546 AE000546 g2313366 Helicobacter pylori 210 -11538830 7502852683 hp0275 atp-dependent nuclease addb (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:similar to egad:18428 percent identity: 27.24;) (le:4806) (re:6098) (di:direct) HPAE000546 AE000546 g2313366 Helicobacter pylori 26695 85962 -11538830

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901886	17102	39258	1407	468

Description

GTC ORF with score 131 to: (db:genpept-inv) (de:caenorhabditis elegans unc-89 (unc-89) gene, complete cds.) (nt:giant ig superfamily member located in the middle) (le:4920:5656:5974:7518) (re:4969:5929:6110:7688) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901900	17103	39259	678	225

Description

6500734973 clpa:hp0033 atp-dependent clp protease (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0033 HP0033 Helicobacter pylori 210 -11538831 7000689652 atp-dependent clp proteinase (cl:atp-dependent clp proteinase chain a) (ec:3.4.21.92) (db:pir2.dat) A64524 A64524 Helicobacter pylori 210 -11538831 7500958467 hp0033 atp-dependent clp protease clpa (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to egad:17776 percent identity: 40.32;) (le:9551) (re:11776) (di:direct) HPAE000525 AE000525 g2313108 Helicobacter pylori 210 -11538831 7502852684 hp0033 atp-dependent clp protease clpa (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to egad:17776 percent identity: 40.32;) (le:9551) (re:11776) (di:direct) HPAE000525 AE000525 g2313108 Helicobacter pylori 26695 85962 -11538831

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901902	17104	39260	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901905	17105	39261	606	201

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901916	17106	39262	363	120

Description

6500734974 prtc:hp0169 collagenase prtc:collagenase (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0169 HP0169 Helicobacter pylori 210 -11538832 5500686285 hp0169 (sr:,campylobacter pylori) (ec:3.4.-.-) (de:putative protease hp0169 precursor,) (db:swissprot) Y169_HELPY P56113 HELICOBACTER PYLORI 210 -11538832 7000687071 collagenase prtc homolog (cl:collagenase prtc) (db:pir2.dat) A64541 A64541 Helicobacter pylori 210 -11538832 7500894813 hp0169 collagenase prtc (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to egad:29055 percent identity: 40.05;) (le:6677) (re:7945) (di:complement) HPAE000537 AE000537 g2313253 Helicobacter pylori 210 -11538832 7502852685 hp0169 collagenase prtc (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to egad:29055 percent identity: 40.05;) (le:6677) (re:7945) (di:complement) HPAE000537 AE000537 g2313253 Helicobacter pylori 26695 85962 -11538832

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901960	17107	39263	1989	662

Description

6500734975 sms:hp0223 atp-dependent protease (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0223 HP0223 Helicobacter pylori 210 -11538833 5500685804 rada:sms:hp0223 (sr:,campylobacter pylori) (de:dna repair protein rada homolog (dna repair protein sms homolog)) (db:swissprot) RADA_HELPY P56148 HELICOBACTER PYLORI 210 -11538833 7000686265 atp-dependent proteinase sms (cl:dna repair protein sms) (ec:3.4.21.-) (db:pir2.dat) G64547 G64547 Helicobacter pylori 210 -11538833 7500889338 hp0223 atp-dependent protease sms (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:similar to egad:28579 percent identity: 40.99;) (le:3381) (re:4751) (di:direct) HPAE000542 AE000542 g2313313 Helicobacter pylori 210 -11538833 7502852686 hp0223 atp-dependent protease sms (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:similar to egad:28579 percent identity: 40.99;) (le:3381) (re:4751) (di:direct) HPAE000542 AE000542 g2313313 Helicobacter pylori 26695 85962 -11538833

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901962	17108	39264	2949	982

Description

6500734976 clpb:hp0264 atp-dependent protease binding subunit:protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0264 HP0264 Helicobacter pylori 210 -11538834 117850 clpb:hp0264 (sr:,campylobacter pylori) (de:clpb protein) (db:swissprot) CLPB_HELPY P71404 HELICOBACTER PYLORI 210 -11538834 7000684839 atp-dependent clp proteinase:regulatory chain b (cl:atp-dependent clp proteinase chain a) (ec:3.4.21.-) (db:pir2.dat) H64552 H64552 Helicobacter pylori 210 -11538834 7500878854 hp0264 atp-dependent protease binding subunit clpb (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to gp:1563721 percent identity: 97.66;) (le:7997) (re:10567) (di:direct) HPAE000545 AE000545 g2313356 Helicobacter pylori 210 -11538834 7502852687 hp0264 atp-dependent protease binding subunit clpb (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to gp:1563721 percent identity: 97.66;) (le:7997) (re:10567) (di:direct) HPAE000545 AE000545 g2313356 Helicobacter pylori 26695 85962 -11538834

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901969	17109	39265	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901971	17110	39266	411	136

Description

GTC ORF with score 164 to: (sr:thale cress) (db:genpept-pln2) (de:genomic sequence for arabidopsis thaliana bac t25n20, completesequence.) (nt:unknown; similar to ests emb|z34019, emb|z27266,) (le:61600:62089:62588) (re:61745:62492:62763) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901979	17111	39267	549	182

Description

6500734977 yjr117w:hp0382 zinc-metallo protease (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0382 HP0382 Helicobacter pylori 210 -11538835 7000690799 zinc metalloproteinase (ec:3.4.24.-) (db:pir2.dat) F64567 F64567 Helicobacter pylori 210 -11538835 7500959557 hp0382 zinc-metallo protease yjr117w (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:53859 percent identity: 36.16;) (le:890) (re:2113) (di:complement) HPAE000555 AE000555 g2313487 Helicobacter pylori 210 -11538835 5000696109 hp0382 zinc-metallo protease yjr117w (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:53859 percent identity: 36.16;) (le:890) (re:2113) (di:complement) HPAE000555 AE000555 g2313487 Helicobacter pylori 26695 85962 -11538835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901986	17112	39268	549	182

Description

GTC ORF with score 322 to: (sr:thale cress) (db:genpept-pln2) (de:genomic sequence for arabidopsis thaliana bac t25n20, completesequence.) (nt:unknown; similar to ests emb|z34019, emb|z27266,) (le:61600:62089:62588) (re:61745:62492:62763) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901987	17113	39269	396	131

Description

7500937000 protein kinase c inhibitor (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0404 HP0404 Helicobacter pylori 210 -11538836 5500686604 hp0404 (sr:,campylobacter pylori) (de:hypothetical hit-like protein hp0404) (db:swissprot) YHIT_HELPY P56147 HELICOBACTER PYLORI 210 -11538836 7000688001 protein kinase c inhibitor homolog (cl:protein kinase c inhibitor:histidine triad homology) (db:pir2.dat) D64570 D64570 Helicobacter pylori 210 -11538836 7500936999 hp0404 protein kinase c inhibitor sp:p16436 (db:genpept-bct1) (de:helicobacter pylori section 34 of 134 of the complete genome.) (nt:similar to egad:27984 percent identity: 40.20;) (le:5571) (re:5885) (di:direct) HPAE000556 AE000556 g2313510 Helicobacter pylori 210 -11538836 7502852688 jhp0977 hit family protein (db:genpept) (de:helicobacter pylori, strain j99 section 88 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0404) (le:2040) (re:2354) (di:complement) AE001527 AE001527 g4155566 Helicobacter pylori J99 85963 -11538836 6500734978 hp0404 protein kinase c inhibitor sp:p16436 (db:genpept) (de:helicobacter pylori 26695 section 34 of 134 of the complete genome.) (nt:similar to egad:27984 percent identity: 40.20;) (le:5571) (re:5885) (di:direct) HPAE000556 AE000556 g2313510 Helicobacter pylori 26695 85962 -11538836

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901993	17114	39270	222	73

Description

6500734979 pepf:hp0470 oligoendopeptidase f (gtcfc:10.11) (ec:3.4.24.-) (keggfc:14.1) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0470 HP0470 Helicobacter pylori 210 -11538837 7000690563 oligoendopeptidase f (cl:oligoendopeptidase f) (db:pir2.dat) F64578 F64578 Helicobacter pylori 210 -11538837 7500955939 hp0470 oligoendopeptidase f pepf (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to gp:1800182 percent identity: 97.92;) (le:16816) (re:18552) (di:complement) HPAE000561 AE000561 g2313574 Helicobacter pylori 210 -11538837 7502852689 hp0470 oligoendopeptidase f pepf (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to gp:1800182 percent identity: 97.92;) (le:16816) (re:18552) (di:complement) HPAE000561 AE000561 g2313574 Helicobacter pylori 26695 85962 -11538837

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901994	17115	39271	933	310

Description

GTC ORF with score 581 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f09f7.) (nt:similar to enoyl-coa hydratases; highest similarity) (le:8908:9038:9483:10055) (re:8961:9430:9856:10275) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501901995	17116	39272	255	84

Description

6500734980 hslv:hp0515 heat shock protein hslv:heat shock protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0515 HP0515 Helicobacter pylori 210 -11538838 7000689981 heat shock protein (db:pir2.dat) C64584 C64584 Helicobacter pylori 210 -11538838 7500958762 hp0515 heat shock protein hslv (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to egad:29122 percent identity: 57.14;) (le:517) (re:1059) (di:direct) HPAE000566 AE000566 g2313630 Helicobacter pylori 210 -11538838 7502852690 hp0515 heat shock protein hslv (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to egad:29122 percent identity: 57.14;) (le:517) (re:1059) (di:direct) HPAE000566 AE000566 g2313630 Helicobacter pylori 26695 85962 -11538838

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902002	17117	39273	612	203

Description

6500734981 hslu:hp0516 orf1 heat shock protein hslu:heat shock protein orf1 (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0516 HP0516 Helicobacter pylori 210 -11538839 7000689350 heat shock protein (cl:heat shock protein hslu:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir2.dat) D64584 D64584 Helicobacter pylori 210 -11538839 7500955126 hp0516 heat shock protein hslu orf1 (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800152 percent identity: 98.42;) (le:1059) (re:2390) (di:direct) HPAE000566 AE000566 g2313631 Helicobacter pylori 210 -11538839 7502852691 hp0516 heat shock protein hslu orf1 (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800152 percent identity: 98.42;) (le:1059) (re:2390) (di:direct) HPAE000566 AE000566 g2313631 Helicobacter pylori 26695 85962 -11538839

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902006	17118	39274	411	137

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902012	17119	39275	735	244

Description

6500734982 pepa:hp0570 aminopeptidase a/i pepa:aminopeptidase a/i (gtcfc:10.11) (ec:3.4.11.1) (keggfc:14.1) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0570 HP0570 Helicobacter pylori 210 -11538840 7500876829 pepa:hp0570 (sr:,campylobacter pylori) (ec:3.4.11.1) (de:aminopeptidase a/i,) (db:swissprot) AMPA_HELPY O25294 HELICOBACTER PYLORI 210 -11538840 7000689635 aminopeptidase a/i (cl:cytosol aminopeptidase) (db:pir2.dat) B64591 B64591 Helicobacter pylori 210 -11538840 7500876831 hp0570 aminopeptidase a/i pepa (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:28683 percent identity: 38.48;) (le:1200) (re:2690) (di:complement) HPAE000571 AE000571 g2313690 Helicobacter pylori 210 -11538840 7502852692 hp0570 aminopeptidase a/i pepa (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:28683 percent identity: 38.48;) (le:1200) (re:2690) (di:complement) HPAE000571 AE000571 g2313690 Helicobacter pylori 26695 85962 -11538840

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902055	17120	39276	1386	461

Description

GTC ORF with score 150 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902070	17121	39277	570	189

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902072	17122	39278	2511	836

Description

GTC ORF with score 146 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902073	17123	39279	744	247

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902093	17124	39280	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902094	17125	39281	732	243

Description

6500734983 clpp:hp0794 atp-dependent clp protease proteolytic component (gtcfc:10.11) (ec:3.4.21.92) (keggfc:14.1) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP0794 HP0794 Helicobacter pylori 210 -11538841 5500685000 clpp:hp0794 (sr:,campylobacter pylori) (ec:3.4.21.92) (de:(endopeptidase clp)) (db:swissprot) CLPP_HELPY P56156 HELICOBACTER PYLORI 210 -11538841 7000684840 clpp atp-dependent clp proteinase:chain p (cl:atp-dependent clp proteinase chain p) (ec:3.4.21.-) (db:pir2.dat) B64619 B64619 Helicobacter pylori 210 -11538841 7500878872 hp0794 atp-dependent clp protease proteolytic component (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:similar to egad:29481 percent identity: 64.58;) (le:7508) (re:8098) (di:complement) HPAE000591 AE000591 g2313923 Helicobacter pylori 210 -11538841 7502852693 hp0794 atp-dependent clp protease proteolytic component (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:similar to egad:29481 percent identity: 64.58;) (le:7508) (re:8098) (di:complement) HPAE000591 AE000591 g2313923 Helicobacter pylori 26695 85962 -11538841

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902114	17126	39282	4131	1376

Description

6500734984 htra:hp1019 serine protease htra:serine protease (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP1019 HP1019 Helicobacter pylori 210 -11538842 7000690697 serine proteinase (ec:3.4.21.-) (db:pir2.dat) C64647 C64647 Helicobacter pylori 210 -11538842 7500959465 hp1019 serine protease htra (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:similar to egad:40391 percent identity: 52.86;) (le:2930) (re:4261) (di:direct) HPAE000610 AE000610 g2314163 Helicobacter pylori 210 -11538842 7502852694 hp1019 serine protease htra (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:similar to egad:40391 percent identity: 52.86;) (le:2930) (re:4261) (di:direct) HPAE000610 AE000610 g2314163 Helicobacter pylori 26695 85962 -11538842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902116	17127	39283	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902122	17128	39284	837	278

Description

6500734985 protease (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP1350 HP1350 Helicobacter pylori 210 -11538843 7000690657 proteinase (cl:carboxyl-terminal processing proteinase) (ec:3.4.-.-) (db:pir2.dat) F64688 F64688 Helicobacter pylori 210 -11538843 7500959432 hp1350 protease (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:41981 percent identity: 40.62;) (le:2652) (re:4031) (di:complement) HPAE000636 AE000636 g2314520 Helicobacter pylori 210 -11538843 7502852695 hp1350 protease (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:41981 percent identity: 40.62;) (le:2652) (re:4031) (di:complement) HPAE000636 AE000636 g2314520 Helicobacter pylori 26695 85962 -11538843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902123	17129	39285	630	209

Description

6500734986 clpx:hp1374 atp-dependent protease atpase subunit (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP1374 HP1374 Helicobacter pylori 210 -11538844 7000689654 clpx atp-dependent clp proteinase:regulatory chain x (ec:3.4.21.-) (db:pir2.dat) F64691 F64691 Helicobacter pylori 210 -11538844 7500958469 hp1374 atp-dependent protease atpase subunit clpx (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:21920 percent identity: 56.28;) (le:10471) (re:11811) (di:complement) HPAE000637 AE000637 g2314544 Helicobacter pylori 210 -11538844 7502852696 hp1374 atp-dependent protease atpase subunit clpx (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:21920 percent identity: 56.28;) (le:10471) (re:11811) (di:complement) HPAE000637 AE000637 g2314544 Helicobacter pylori 26695 85962 -11538844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902132	17130	39286	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902138	17131	39287	375	124

Description

6500734987 lon:hp1379 atp-dependent protease (gtcfc:10.11) (ec:3.4.21.53) (keggfc:14.1) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP1379 HP1379 Helicobacter pylori 210 -11538845 5500685525 lon:hp1379 (sr:,campylobacter pylori) (ec:3.4.21.53) (de:atp-dependent protease la,) (db:swissprot) LON_HELPY P55995 HELICOBACTER PYLORI 210 -11538845 7000685758 atp-dependent proteinase lon (ec:3.4.21.-) (db:pir2.dat) C64692 C64692 Helicobacter pylori 210 -11538845 7500885103 hp1379 atp-dependent protease lon (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:similar to egad:37242 percent identity: 43.94;) (le:1618) (re:4125) (di:direct) HPAE000638 AE000638 g2314549 Helicobacter pylori 210 -11538845 7502852697 hp1379 atp-dependent protease lon (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:similar to egad:37242 percent identity: 43.94;) (le:1618) (re:4125) (di:direct) HPAE000638 AE000638 g2314549 Helicobacter pylori 26695 85962 -11538845

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902150	17132	39288	312	103

Description

6500734988 pepq:hp1485 proline dipeptidase (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP1485 HP1485 Helicobacter pylori 210 -11538846 7000690647 conserved hypothetical protein:proline dipeptidase (cl:hypothetical protein hi0722) (db:pir2.dat) E64705 E64705 Helicobacter pylori 210 -11538846 7500955836 hp1485 proline dipeptidase pepq (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:29489 percent identity: 35.23;) (le:19779) (re:20351) (di:complement) HPAE000647 AE000647 g2314657 Helicobacter pylori 210 -11538846 7502852698 hp1485 proline dipeptidase pepq (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:29489 percent identity: 35.23;) (le:19779) (re:20351) (di:complement) HPAE000647 AE000647 g2314657 Helicobacter pylori 26695 85962 -11538846

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902155	17133	39289	1422	473

Description

6500734989 sialoglycoprotease gcp:sialoglycoprotease:gcp (gtcfc:10.11) (ec:3.4.24.57) (keggfc:14.1) (tigrfc:12.3) (db:gtc-helicobacter pylori) HP1584 HP1584 Helicobacter pylori 210 -11538847 5500685267 gcp:hp1584 (sr:,campylobacter pylori) (ec:3.4.24.57) (de:(glycoprotease)) (db:swissprot) GCP_HELPY P55996 HELICOBACTER PYLORI 210 -11538847 7000685376 sialoglycoproteinase gcp (cl:o-sialoglycoprotein endopeptidase) (ec:3.4.-.-) (db:pir2.dat) H64717 H64717 Helicobacter pylori 210 -11538847 7500882263 hp1584 sialoglycoprotease gcp (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:29166 percent identity: 35.74;) (le:8605) (re:9627) (di:direct) HPAE000655 AE000655 g2314767 Helicobacter pylori 210 -11538847 7502852699 hp1584 sialoglycoprotease gcp (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:29166 percent identity: 35.74;) (le:8605) (re:9627) (di:direct) HPAE000655 AE000655 g2314767 Helicobacter pylori 26695 85962 -11538847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902164	17134	39290	1401	466

Description

6500734990 nusb:hp0001 transcription termination factor nusb (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-helicobacter pylori) HP0001 HP0001 Helicobacter pylori 210 -11538848 7000690740 transcription termination factor nusb (cl:nusb protein) (db:pir2.dat) A64520 A64520 Helicobacter pylori 210 -11538848 7500959505 hp0001 transcription termination factor nusb nusb (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to egad:24212 percent identity: 30.23;) (le:217) (re:633) (di:complement) HPAE000523 AE000523 g2313078 Helicobacter pylori 210 -11538848 7502852700 hp0001 transcription termination factor nusb nusb (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to egad:24212 percent identity: 30.23;) (le:217) (re:633) (di:complement) HPAE000523 AE000523 g2313078 Helicobacter pylori 26695 85962 -11538848

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902166	17135	39291	507	168

Description

6500734991 rho:hp0550 transcription termination factor rho (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-helicobacter pylori) HP0550 HP0550 Helicobacter pylori 210 -11538849 7500889759 rho:hp0550 (sr:,campylobacter pylori) (de:transcription termination factor rho) (db:swissprot) RHO_HELPY P56466 HELICOBACTER PYLORI 210 -11538849 7000689413 transcription termination factor rho (cl:transcription termination factor rho) (db:pir2.dat) F64588 F64588 Helicobacter pylori 210 -11538849 7500889761 hp0550 transcription termination factor rho rho (db:genpept-bct1) (de:helicobacter pylori section 47 of 134 of the complete genome.) (nt:similar to egad:28936 percent identity: 56.59;) (le:5914) (re:7230) (di:complement) HPAE000569 AE000569 g2313666 Helicobacter pylori 210 -11538849 7502852701 hp0550 transcription termination factor rho rho (db:genpept) (de:helicobacter pylori 26695 section 47 of 134 of the complete genome.) (nt:similar to egad:28936 percent identity: 56.59;) (le:5914) (re:7230) (di:complement) HPAE000569 AE000569 g2313666 Helicobacter pylori 26695 85962 -11538849

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902176	17136	39292	426	141

Description

7500882724 grea:hp0866 transcription elongation factor grea (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-helicobacter pylori) HP0866 HP0866 Helicobacter pylori 210 -11538850 5500685298 grea:hp0866 (sr:,campylobacter pylori) (de:grea)) (db:swissprot) GREA_HELPY P55978 HELICOBACTER PYLORI 210 -11538850 7000685452 transcription elongation factor grea (cl:transcription elongation factor greb) (db:pir2.dat) B64628 B64628 Helicobacter pylori 210 -11538850 7500882723 hp0866 transcription elongation factor grea grea (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:9031 percent identity: 50.32;) (le:18365) (re:18859) (di:complement) HPAE000596 AE000596 g2313994 Helicobacter pylori 210 -11538850 7502852702 grea transcription elongation factor transcript (db:genpept) (de:helicobacter pylori, strain j99 section 70 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0866) (le:14762) (re:15256) (di:complement) AE001509 AE001509 g4155364 Helicobacter pylori J99 85963 -11538850 6500734992 hp0866 transcription elongation factor grea grea (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:9031 percent identity: 50.32;) (le:18365) (re:18859) (di:complement) HPAE000596 AE000596 g2313994 Helicobacter pylori 26695 85962 -11538850

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902184	17137	39293	858	285

Description

6500734993 nusg:hp1203 transcription termination factor nusg (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-helicobacter pylori) HP1203 HP1203 Helicobacter pylori 210 -11538851 5500685673 nusg:hp1203 (sr:,campylobacter pylori) (de:transcription antitermination protein nusg) (db:swissprot) NUSG_HELPY P55976 HELICOBACTER PYLORI 210 -11538851 7000686022 transcription termination factor nusg (cl:transcription antitermination factor nusg) (db:pir2.dat) C64670 C64670 Helicobacter pylori 210 -11538851 7500887018 hp1203 transcription termination factor nusg nusg (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to egad:9614 percent identity: 41.04;) (le:2360) (re:2890) (di:complement) HPAE000626 AE000626 g2314365 Helicobacter pylori 210 -11538851 7502852703 hp1203 transcription termination factor nusg nusg (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to egad:9614 percent identity: 41.04;) (le:2360) (re:2890) (di:complement) HPAE000626 AE000626 g2314365 Helicobacter pylori 26695 85962 -11538851

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902190	17138	39294	1068	355

Description

6500734994 nusa:hp1514 transcription termination factor nusa (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-helicobacter pylori) HP1514 HP1514 Helicobacter pylori 210 -11538852 5500685672 nusa:hp1514 (sr:,campylobacter pylori) (de:n-utilization substance protein a homolog) (db:swissprot) NUSA_HELPY P55977 HELICOBACTER PYLORI 210 -11538852 7000686019 transcription termination factor nusa (cl:transcription termination factor nusa homology) (db:pir2.dat) B64709 B64709 Helicobacter pylori 210 -11538852 7500887009 hp1514 transcription termination factor nusa nusa (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:similar to egad:32069 percent identity: 39.09;) (le:8341) (re:9528) (di:direct) HPAE000649 AE000649 g2314694 Helicobacter pylori 210 -11538852 7502852704 hp1514 transcription termination factor nusa nusa (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:similar to egad:32069 percent identity: 39.09;) (le:8341) (re:9528) (di:direct) HPAE000649 AE000649 g2314694 Helicobacter pylori 26695 85962 -11538852

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902192	17139	39295	4104	1367

Description

6500734995 rps20:hp0076 ribosomal protein s20 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0076 HP0076 Helicobacter pylori 210 -11538853 5500685927 rpst:hp0076 (sr:,campylobacter pylori) (de:30s ribosomal protein s20) (db:swissprot) RS20_HELPY P56027 HELICOBACTER PYLORI 210 -11538853 7000686500 ribosomal protein s20 (cl:escherichia coli ribosomal protein s20) (db:pir2.dat) D64529 D64529 Helicobacter pylori 210 -11538853 7500890989 hp0076 ribosomal protein s20 rps20 (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:similar to egad:31905 percent identity: 41.38;) (le:4796) (re:5065) (di:direct) HPAE000529 AE000529 g2313157 Helicobacter pylori 210 -11538853 7502852705 hp0076 ribosomal protein s20 rps20 (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:similar to egad:31905 percent identity: 41.38;) (le:4796) (re:5065) (di:direct) HPAE000529 AE000529 g2313157 Helicobacter pylori 26695 85962 -11538853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902225	17140	39296	462	153

Description

6500734996 rps9:hp0083 ribosomal protein s9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0083 HP0083 Helicobacter pylori 210 -11538854 5500685941 rpsi:hp0083 (sr:,campylobacter pylori) (de:30s ribosomal protein s9) (db:swissprot) RS9_HELPY P56016 HELICOBACTER PYLORI 210 -11538854 7000686520 ribosomal protein s9 (cl:escherichia coli ribosomal protein s9) (db:pir2.dat) C64530 C64530 Helicobacter pylori 210 -11538854 7500891124 hp0083 ribosomal protein s9 rps9 (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:similar to egad:12856 percent identity: 50.39;) (le:2588) (re:2977) (di:complement) HPAE000530 AE000530 g2313164 Helicobacter pylori 210 -11538854 7500891125 rpsi 30s ribosomal protein s9 (db:genpept) (de:helicobacter pylori, strain j99 section 8 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0083) (le:106) (re:495) (di:complement) AE001447 AE001447 g4154586 Helicobacter pylori J99 85963 -11538854 7502852706 hp0083 ribosomal protein s9 rps9 (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:similar to egad:12856 percent identity: 50.39;) (le:2588) (re:2977) (di:complement) HPAE000530 AE000530 g2313164 Helicobacter pylori 26695 85962 -11538854

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902233	17141	39297	2127	708

Description

6500734997 rpl13:hp0084 ribosomal protein l13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0084 HP0084 Helicobacter pylori 210 -11538855 5500685842 rplm:hp0084 (sr:,campylobacter pylori) (de:50s ribosomal protein l13) (db:swissprot) RL13_HELPY P56038 HELICOBACTER PYLORI 210 -11538855 7000686352 ribosomal protein l13 (cl:escherichia coli ribosomal protein l13) (db:pir2.dat) D64530 D64530 Helicobacter pylori 210 -11538855 7500889931 hp0084 ribosomal protein l13 rpl13 (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:similar to egad:7868 percent identity: 50.00;) (le:2974) (re:3399) (di:complement) HPAE000530 AE000530 g2313165 Helicobacter pylori 210 -11538855 7502852707 hp0084 ribosomal protein l13 rpl13 (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:similar to egad:7868 percent identity: 50.00;) (le:2974) (re:3399) (di:complement) HPAE000530 AE000530 g2313165 Helicobacter pylori 26695 85962 -11538855

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902240	17142	39298	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902242	17143	39299	426	141

Description

6500734998 rpl35:hp0125 ribosomal protein l35 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0125 HP0125 Helicobacter pylori 210 -11538856 5500685872 rpmi:hp0125 (sr:,campylobacter pylori) (de:50s ribosomal protein l35) (db:swissprot) RL35_HELPY P56057 HELICOBACTER PYLORI 210 -11538856 7000686397 ribosomal protein l35 (cl:escherichia coli ribosomal protein l35) (db:pir2.dat) E64535 E64535 Helicobacter pylori 210 -11538856 7500890235 hp0125 ribosomal protein l35 rpl35 (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:similar to egad:38528 percent identity: 50.82;) (le:6689) (re:6883) (di:direct) HPAE000534 AE000534 g2313210 Helicobacter pylori 210 -11538856 7500890236 rpmi 50s ribosomal protein l35 (db:genpept) (de:helicobacter pylori, strain j99 section 11 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0125) (le:9947) (re:10141) (di:direct) AE001450 AE001450 g4154623 Helicobacter pylori J99 85963 -11538856 7502852708 hp0125 ribosomal protein l35 rpl35 (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:similar to egad:38528 percent identity: 50.82;) (le:6689) (re:6883) (di:direct) HPAE000534 AE000534 g2313210 Helicobacter pylori 26695 85962 -11538856

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902244	17144	39300	420	139

Description

GTC ORF with score 111 to: (fn:binds to orip to permit replication of the) (db:genpept-vrl) (de:herpesvirus papio brrf2 homolog gene, partial cds, ebna1, bkrf2homolog and bkrf3 homolog genes, complete cds, and bkrf4 homologgene, partial cds.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902247	17145	39301	588	195

Description

6500734999 rpl20:hp0126 ribosomal protein l20 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0126 HP0126 Helicobacter pylori 210 -11538857 5500685852 rplt:hp0126 (sr:,campylobacter pylori) (de:50s ribosomal protein l20) (db:swissprot) RL20_HELPY P56045 HELICOBACTER PYLORI 210 -11538857 7000686364 ribosomal protein l20 (cl:escherichia coli ribosomal protein l20) (db:pir2.dat) F64535 F64535 Helicobacter pylori 210 -11538857 7500890043 hp0126 ribosomal protein l20 rpl20 (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:similar to egad:38529 percent identity: 54.78;) (le:6977) (re:7327) (di:direct) HPAE000534 AE000534 g2313209 Helicobacter pylori 210 -11538857 7502852709 hp0126 ribosomal protein l20 rpl20 (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:similar to egad:38529 percent identity: 54.78;) (le:6977) (re:7327) (di:direct) HPAE000534 AE000534 g2313209 Helicobacter pylori 26695 85962 -11538857

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902263	17146	39302	240	79

Description

6500735000 rpl32:hp0200 ribosomal protein l32 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0200 HP0200 Helicobacter pylori 210 -11538858 5500685867 rpmf:hp0200 (sr:,campylobacter pylori) (de:50s ribosomal protein l32) (db:swissprot) RL32_HELPY P56054 HELICOBACTER PYLORI 210 -11538858 7000686389 ribosomal protein l32 (db:pir2.dat) H64544 H64544 Helicobacter pylori 210 -11538858 7500890202 hp0200 ribosomal protein l32 rpl32 (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:similar to egad:5230 percent identity: 41.67;) (le:2098) (re:2244) (di:direct) HPAE000540 AE000540 g2313293 Helicobacter pylori 210 -11538858 7502852710 hp0200 ribosomal protein l32 rpl32 (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:similar to egad:5230 percent identity: 41.67;) (le:2098) (re:2244) (di:direct) HPAE000540 AE000540 g2313293 Helicobacter pylori 26695 85962 -11538858

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902267	17147	39303	507	168

Description

6500735001 rpl21:hp0296 ribosomal protein l21 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0296 HP0296 Helicobacter pylori 210 -11538859 5500685854 rplu:hp0296 (sr:,campylobacter pylori) (de:50s ribosomal protein l21) (db:swissprot) RL21_HELPY P56046 HELICOBACTER PYLORI 210 -11538859 7000686366 ribosomal protein l21 (cl:escherichia coli ribosomal protein l21) (db:pir2.dat) H64556 H64556 Helicobacter pylori 210 -11538859 7500890055 hp0296 ribosomal protein l21 rpl21 (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:23167 percent identity: 46.08;) (le:3977) (re:4291) (di:direct) HPAE000548 AE000548 g2313394 Helicobacter pylori 210 -11538859 7502852711 hp0296 ribosomal protein l21 rpl21 (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:23167 percent identity: 46.08;) (le:3977) (re:4291) (di:direct) HPAE000548 AE000548 g2313394 Helicobacter pylori 26695 85962 -11538859

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902272	17148	39304	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902276	17149	39305	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902293	17150	39306	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902315	17151	39307	510	169

Description

6500735002 rpl27:hp0297 ribosomal protein l27 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0297 HP0297 Helicobacter pylori 210 -11538860 5500685862 rpma:hp0297 (sr:,campylobacter pylori) (de:50s ribosomal protein l27) (db:swissprot) RL27_HELPY P56050 HELICOBACTER PYLORI 210 -11538860 7000686375 ribosomal protein l27 (cl:escherichia coli ribosomal protein l27:eubacterial ribosomal protein l27 homology) (db:pir2.dat) A64557 A64557 Helicobacter pylori 210 -11538860 7500890130 hp0297 ribosomal protein l27 rpl27 (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:29362 percent identity: 64.71;) (le:4306) (re:4572) (di:direct) HPAE000548 AE000548 g2313395 Helicobacter pylori 210 -11538860 7502852712 hp0297 ribosomal protein l27 rpl27 (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:29362 percent identity: 64.71;) (le:4306) (re:4572) (di:direct) HPAE000548 AE000548 g2313395 Helicobacter pylori 26695 85962 -11538860

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902335	17152	39308	2304	767

Description

GTC ORF with score 1229 to: (fn:hydrolysis of inositol phospholipids) (db:genpept-pln1) (de:botryotinia fuckeliana phosphoinositide-specific phospholipase c(bcplc1) gene, complete cds.) (nt:the designation of the start codon at 1483 is by) (le:1483) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902344	17153	39309	1422	474

Description

GTC ORF with score 968 to: (fn:hydrolysis of inositol phospholipids) (db:genpept-pln1) (de:botryotinia fuckeliana phosphoinositide-specific phospholipase c(bcplc1) gene, complete cds.) (nt:the designation of the start codon at 1483 is by) (le:1483) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902356	17154	39310	792	263

Description

GTC ORF with score 117 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana dna chromosome 4, essa i ap2 contig fragmentno. 2.) (nt:similar to hypothetical protein ynl231c,) (le:90970:91116:91393:91576) (re:91029:91292:91491:91821) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902373	17155	39311	201	66

Description

6500735003 rps1:hp0399 ribosomal protein s1 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0399 HP0399 Helicobacter pylori 210 -11538861 5500685926 rpsa:hp0399 (sr:,campylobacter pylori) (de:30s ribosomal protein s1) (db:swissprot) RS1_HELPY P56008 HELICOBACTER PYLORI 210 -11538861 7000686498 ribosomal protein s1 (db:pir2.dat) G64569 G64569 Helicobacter pylori 210 -11538861 7500890985 hp0399 ribosomal protein s1 rps1 (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:10276 percent identity: 30.48;) (le:17957) (re:19627) (di:complement) HPAE000555 AE000555 g2313498 Helicobacter pylori 210 -11538861 7502852713 hp0399 ribosomal protein s1 rps1 (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:10276 percent identity: 30.48;) (le:17957) (re:19627) (di:complement) HPAE000555 AE000555 g2313498 Helicobacter pylori 26695 85962 -11538861

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902379	17156	39312	387	128

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902386	17157	39313	960	319

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902398	17158	39314	501	167

Description

6500735004 rpl28:hp0491 ribosomal protein l28 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0491 HP0491 Helicobacter pylori 210 -11538862 5500685863 rpmb:hp0491 (sr:,campylobacter pylori) (de:50s ribosomal protein l28) (db:swissprot) RL28_HELPY P56051 HELICOBACTER PYLORI 210 -11538862 7000686377 ribosomal protein l28 (cl:escherichia coli ribosomal protein l28) (db:pir2.dat) C64581 C64581 Helicobacter pylori 210 -11538862 7500890138 hp0491 ribosomal protein l28 rpl28 (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:31639 percent identity: 41.67;) (le:1525) (re:1713) (di:complement) HPAE000564 AE000564 g2313612 Helicobacter pylori 210 -11538862 7500890139 rpmb 50s ribosomal protein l28 (db:genpept) (de:helicobacter pylori, strain j99 section 39 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0491) (le:9856) (re:10044) (di:complement) AE001478 AE001478 g4154978 Helicobacter pylori J99 85963 -11538862 7502852714 hp0491 ribosomal protein l28 rpl28 (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:31639 percent identity: 41.67;) (le:1525) (re:1713) (di:complement) HPAE000564 AE000564 g2313612 Helicobacter pylori 26695 85962 -11538862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902405	17159	39315	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902432	17160	39316	2040	679

Description

6500735005 rpl9:hp0514 ribosomal protein l9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0514 HP0514 Helicobacter pylori 210 -11538863 5500685880 rpli:hp0514 (sr:,campylobacter pylori) (de:50s ribosomal protein l9) (db:swissprot) RL9_HELPY P56035 HELICOBACTER PYLORI 210 -11538863 7000686411 ribosomal protein l9 (cl:escherichia coli ribosomal protein l9) (db:pir2.dat) B64584 B64584 Helicobacter pylori 210 -11538863 7500890364 hp0514 ribosomal protein l9 rpl9 (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to egad:17362 percent identity: 39.60;) (le:61) (re:513) (di:direct) HPAE000566 AE000566 g2313629 Helicobacter pylori 210 -11538863 7502852715 hp0514 ribosomal protein l9 rpl9 (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to egad:17362 percent identity: 39.60;) (le:61) (re:513) (di:direct) HPAE000566 AE000566 g2313629 Helicobacter pylori 26695 85962 -11538863

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902442	17161	39317	396	131

Description

6500735006 rpl31:hp0551 ribosomal protein l31 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0551 HP0551 Helicobacter pylori 210 -11538864 5500685866 rpme:hp0551 (sr:,campylobacter pylori) (de:50s ribosomal protein l31) (db:swissprot) RL31_HELPY P56053 HELICOBACTER PYLORI 210 -11538864 7000686381 ribosomal protein l31 (cl:escherichia coli ribosomal protein l31) (db:pir2.dat) G64588 G64588 Helicobacter pylori 210 -11538864 7500890189 hp0551 ribosomal protein l31 rpl31 (db:genpept-bct1) (de:helicobacter pylori section 47 of 134 of the complete genome.) (nt:similar to egad:15893 percent identity: 49.25;) (le:7494) (re:7697) (di:direct) HPAE000569 AE000569 g2313667 Helicobacter pylori 210 -11538864 7500890190 rpme 50s ribosomal protein l31 (db:genpept) (de:helicobacter pylori, strain j99 section 44 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0551) (le:7127) (re:7330) (di:direct) AE001483 AE001483 g4155038 Helicobacter pylori J99 85963 -11538864 7502852716 hp0551 ribosomal protein l31 rpl31 (db:genpept) (de:helicobacter pylori 26695 section 47 of 134 of the complete genome.) (nt:similar to egad:15893 percent identity: 49.25;) (le:7494) (re:7697) (di:direct) HPAE000569 AE000569 g2313667 Helicobacter pylori 26695 85962 -11538864

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902443	17162	39318	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902447	17163	39319	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902478	17164	39320	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902479	17165	39321	2574	857

Description

6500735007 rps21:hp0562 ribosomal protein s21 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP0562 HP0562 Helicobacter pylori 210 -11538865 5500685928 rpsu:hp0562 (sr:,campylobacter pylori) (de:30s ribosomal protein s21) (db:swissprot) RS21_HELPY P56028 HELICOBACTER PYLORI 210 -11538865 7000686501 ribosomal protein s21 (cl:escherichia coli ribosomal protein s21) (db:pir2.dat) B64590 B64590 Helicobacter pylori 210 -11538865 7500890996 hp0562 ribosomal protein s21 rps21 (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:similar to egad:31925 percent identity: 42.37;) (le:4732) (re:4944) (di:complement) HPAE000570 AE000570 g2313679 Helicobacter pylori 210 -11538865 7502852717 hp0562 ribosomal protein s21 rps21 (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:similar to egad:31925 percent identity: 42.37;) (le:4732) (re:4944) (di:complement) HPAE000570 AE000570 g2313679 Helicobacter pylori 26695 85962 -11538865

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902481	17166	39322	933	310

Description

6500735008 rps15:hp1040 ribosomal protein s15 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1040 HP1040 Helicobacter pylori 210 -11538866 5500685919 rpso:hp1040 (sr:,campylobacter pylori) (de:30s ribosomal protein s15) (db:swissprot) RS15_HELPY P56022 HELICOBACTER PYLORI 210 -11538866 7000686491 ribosomal protein s15 (cl:escherichia coli ribosomal protein s15:eubacterial ribosomal protein s15 homology) (db:pir2.dat) H64649 H64649 Helicobacter pylori 210 -11538866 7500890907 hp1040 ribosomal protein s15 rps15 (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to egad:31934 percent identity: 57.78;) (le:10412) (re:10684) (di:complement) HPAE000611 AE000611 g2314183 Helicobacter pylori 210 -11538866 7502852718 hp1040 ribosomal protein s15 rps15 (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to egad:31934 percent identity: 57.78;) (le:10412) (re:10684) (di:complement) HPAE000611 AE000611 g2314183 Helicobacter pylori 26695 85962 -11538866

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902482	17167	39323	438	145

Description

6500735009 rbfa:hp1047 ribosome-binding factor a (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1047 HP1047 Helicobacter pylori 210 -11538867 7000690692 ribosome-binding factor a (db:pir2.dat) G64650 G64650 Helicobacter pylori 210 -11538867 7500959460 hp1047 ribosome-binding factor a rbfa (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to egad:9902 percent identity: 26.32;) (le:8786) (re:9121) (di:complement) HPAE000612 AE000612 g2314194 Helicobacter pylori 210 -11538867 7502852719 hp1047 ribosome-binding factor a rbfa (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to egad:9902 percent identity: 26.32;) (le:8786) (re:9121) (di:complement) HPAE000612 AE000612 g2314194 Helicobacter pylori 26695 85962 -11538867

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902483	17168	39324	2787	928

Description

GTC ORF with score 1159 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 9931.) (nt:similar to rna helicases (swissprot accession) (le:21627) (re:25934) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902484	17169	39325	357	118

Description

6500735010 rpl19:hp1147 ribosomal protein l19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1147 HP1147 Helicobacter pylori 210 -11538868 5500685850 rpls:hp1147 (sr:,campylobacter pylori) (de:50s ribosomal protein l19) (db:swissprot) RL19_HELPY P56044 HELICOBACTER PYLORI 210 -11538868 7000686361 ribosomal protein l19 (cl:escherichia coli ribosomal protein l19) (db:pir2.dat) C64663 C64663 Helicobacter pylori 210 -11538868 7500890024 hp1147 ribosomal protein l19 rpl19 (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:28847 percent identity: 50.91;) (le:1805) (re:2161) (di:complement) HPAE000621 AE000621 g2314302 Helicobacter pylori 210 -11538868 7502852720 hp1147 ribosomal protein l19 rpl19 (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:28847 percent identity: 50.91;) (le:1805) (re:2161) (di:complement) HPAE000621 AE000621 g2314302 Helicobacter pylori 26695 85962 -11538868

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902492	17170	39326	489	163

Description

GTC ORF with score 102 to: (sr:drosophila melanogaster (strain iso-1) (library: gt11 embryoni) (db:genpept-inv) (de:drosophila melanogaster brahma protein mrna, complete cds.) (nt:homeotic gene regulator) (le:55) (re:4971) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902498	17171	39327	1017	338

Description

6500735011 rps16:hp1151 ribosomal protein s16 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1151 HP1151 Helicobacter pylori 210 -11538869 5500685920 rpsp:hp1151 (sr:,campylobacter pylori) (de:30s ribosomal protein s16) (db:swissprot) RS16_HELPY P56023 HELICOBACTER PYLORI 210 -11538869 7000686492 ribosomal protein s16 (cl:escherichia coli ribosomal protein s16) (db:pir2.dat) G64663 G64663 Helicobacter pylori 210 -11538869 7500890923 hp1151 ribosomal protein s16 rps16 (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:28841 percent identity: 46.75;) (le:3792) (re:4022) (di:complement) HPAE000621 AE000621 g2314310 Helicobacter pylori 210 -11538869 7502852721 hp1151 ribosomal protein s16 rps16 (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:28841 percent identity: 46.75;) (le:3792) (re:4022) (di:complement) HPAE000621 AE000621 g2314310 Helicobacter pylori 26695 85962 -11538869

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902503	17172	39328	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902504	17173	39329	750	249

Description

6500735012 rps7:hp1196 ribosomal protein s7 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1196 HP1196 Helicobacter pylori 210 -11538870 5500685938 rpsg:hp1196 (sr:,campylobacter pylori) (de:30s ribosomal protein s7) (db:swissprot) RS7_HELPY P56014 HELICOBACTER PYLORI 210 -11538870 7000686516 ribosomal protein s7 (cl:escherichia coli ribosomal protein s7) (db:pir2.dat) D64669 D64669 Helicobacter pylori 210 -11538870 7500891098 hp1196 ribosomal protein s7 rps7 (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to egad:11002 percent identity: 62.22;) (le:8089) (re:8556) (di:complement) HPAE000625 AE000625 g2314355 Helicobacter pylori 210 -11538870 7500891099 rpsg 30s ribosomal protein s7 (db:genpept) (de:helicobacter pylori, strain j99 section 100 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1196) (le:10570) (re:11037) (di:complement) AE001539 AE001539 g4155708 Helicobacter pylori J99 85963 -11538870 7502852722 hp1196 ribosomal protein s7 rps7 (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to egad:11002 percent identity: 62.22;) (le:8089) (re:8556) (di:complement) HPAE000625 AE000625 g2314355 Helicobacter pylori 26695 85962 -11538870

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902523	17174	39330	462	153

Description

6500735013 rps12:hp1197 ribosomal protein s12 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1197 HP1197 Helicobacter pylori 210 -11538871 5500685916 rpsl:hp1197 (sr:,campylobacter pylori) (de:30s ribosomal protein s12) (db:swissprot) RS12_HELPY P56019 HELICOBACTER PYLORI 210 -11538871 7000686486 ribosomal protein s12 (cl:escherichia coli ribosomal protein s12) (db:pir2.dat) E64669 E64669 Helicobacter pylori 210 -11538871 7500890869 hp1197 ribosomal protein s12 rps12 (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to egad:9001 percent identity: 79.03;) (le:8572) (re:8979) (di:complement) HPAE000625 AE000625 g2314356 Helicobacter pylori 210 -11538871 7502852723 rpsl 30s ribosomal protein s12 (db:genpept) (de:helicobacter pylori, strain j99 section 100 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1197) (le:11053) (re:11460) (di:complement) AE001539 AE001539 g4155709 Helicobacter pylori J99 85963 -11538871 7502852724 hp1197 ribosomal protein s12 rps12 (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to egad:9001 percent identity: 79.03;) (le:8572) (re:8979) (di:complement) HPAE000625 AE000625 g2314356 Helicobacter pylori 26695 85962 -11538871

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902524	17175	39331	453	150

Description

6500735014 rpl7:rpll:hp1199 ribosomal protein l7/l12:50s ribosomal protein l7/l12 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1199 HP1199 Helicobacter pylori 210 -11538872 500685267 rpll:hp1199 (sr:,campylobacter pylori) (de:50s ribosomal protein l7/l12) (db:swissprot) RL7_HELPY P55834 HELICOBACTER PYLORI 210 -11538872 7000686408 ribosomal protein l7/l12 (cl:escherichia coli ribosomal protein l12) (db:pir2.dat) G64669 G64669 Helicobacter pylori 210 -11538872 7500890356 hp1199 ribosomal protein l7/l12 rpl7/l12 (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to egad:10366 percent identity: 65.04;) (le:142) (re:519) (di:complement) HPAE000626 AE000626 g2314361 Helicobacter pylori 210 -11538872 7502852725 hp1199 ribosomal protein l7/l12 rpl7/l12 (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to egad:10366 percent identity: 65.04;) (le:142) (re:519) (di:complement) HPAE000626 AE000626 g2314361 Helicobacter pylori 26695 85962 -11538872

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902529	17176	39332	657	219

Description

6500735015 rpl10:hp1200 ribosomal protein l10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1200 HP1200 Helicobacter pylori 210 -11538873 5500685840 rplj:hp1200 (sr:,campylobacter pylori) (de:50s ribosomal protein l10) (db:swissprot) RL10_HELPY P56036 HELICOBACTER PYLORI 210 -11538873 7000686348 ribosomal protein l10 (cl:escherichia coli ribosomal protein l10) (db:pir2.dat) H64669 H64669 Helicobacter pylori 210 -11538873 7500889907 hp1200 ribosomal protein l10 rpl10 (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to egad:30973 percent identity: 30.38;) (le:565) (re:1059) (di:complement) HPAE000626 AE000626 g2314362 Helicobacter pylori 210 -11538873 7502852726 hp1200 ribosomal protein l10 rpl10 (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to egad:30973 percent identity: 30.38;) (le:565) (re:1059) (di:complement) HPAE000626 AE000626 g2314362 Helicobacter pylori 26695 85962 -11538873

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902537	17177	39333	525	174

Description

6500735016 rpl1:hp1201 ribosomal protein l1 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1201 HP1201 Helicobacter pylori 210 -11538874 5500685851 rpla:hp1201 (sr:,campylobacter pylori) (de:50s ribosomal protein l1) (db:swissprot) RL1_HELPY P56029 HELICOBACTER PYLORI 210 -11538874 7000686362 ribosomal protein l1 (cl:escherichia coli ribosomal protein l1) (db:pir2.dat) A64670 A64670 Helicobacter pylori 210 -11538874 7500890039 hp1201 ribosomal protein l1 rpl1 (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to egad:29142 percent identity: 51.98;) (le:1168) (re:1872) (di:complement) HPAE000626 AE000626 g2314363 Helicobacter pylori 210 -11538874 7502852727 hp1201 ribosomal protein l1 rpl1 (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to egad:29142 percent identity: 51.98;) (le:1168) (re:1872) (di:complement) HPAE000626 AE000626 g2314363 Helicobacter pylori 26695 85962 -11538874

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902556	17178	39334	309	102

Description

6500735017 rpl11:hp1202 ribosomal protein l11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1202 HP1202 Helicobacter pylori 210 -11538875 5500685841 rplk:hp1202 (sr:,campylobacter pylori) (de:50s ribosomal protein l11) (db:swissprot) RL11_HELPY P56037 HELICOBACTER PYLORI 210 -11538875 7000686350 ribosomal protein l11 (cl:escherichia coli ribosomal protein l11) (db:pir2.dat) B64670 B64670 Helicobacter pylori 210 -11538875 7500889914 hp1202 ribosomal protein l11 rpl11 (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to egad:5705 percent identity: 63.83;) (le:1917) (re:2342) (di:complement) HPAE000626 AE000626 g2314364 Helicobacter pylori 210 -11538875 7500889915 rplk 50s ribosomal protein l11 (db:genpept) (de:helicobacter pylori, strain j99 section 101 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1202) (le:10741) (re:11166) (di:complement) AE001540 AE001540 g4155722 Helicobacter pylori J99 85963 -11538875 7502852728 hp1202 ribosomal protein l11 rpl11 (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to egad:5705 percent identity: 63.83;) (le:1917) (re:2342) (di:complement) HPAE000626 AE000626 g2314364 Helicobacter pylori 26695 85962 -11538875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902567	17179	39335	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902568	17180	39336	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902579	17181	39337	510	169

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902581	17182	39338	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902584	17183	39339	309	102

Description

GTC ORF with score 137 to: (sr:aspergillus niger transposon ant1 chlorate-resistant mutant 46) (db:genpept-pln1) (de:orf1 3' of ant1 5' insertion site {niad insertion site}(aspergillus niger, chlorate-resistant mutant 46, transposon ant1,transposon, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902586	17184	39340	228	75

Description

GTC ORF with score 309 to: (sr:aspergillus niger transposon ant1 chlorate-resistant mutant 46) (db:genpept-pln1) (de:orf1 3' of ant1 5' insertion site {niad insertion site}(aspergillus niger, chlorate-resistant mutant 46, transposon ant1,transposon, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902593	17185	39341	378	125

Description

6500735018 rpl33:hp1204 ribosomal protein l33 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1204 HP1204 Helicobacter pylori 210 -11538876 5500685868 rpmg:hp1204 (sr:,campylobacter pylori) (de:50s ribosomal protein l33) (db:swissprot) RL33_HELPY P56055 HELICOBACTER PYLORI 210 -11538876 7000686391 ribosomal protein l33 (cl:escherichia coli ribosomal protein l33) (db:pir2.dat) D64670 D64670 Helicobacter pylori 210 -11538876 7500890211 hp1204 ribosomal protein l33 rpl33 (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to egad:9493 percent identity: 55.10;) (le:3354) (re:3512) (di:complement) HPAE000626 AE000626 g2314371 Helicobacter pylori 210 -11538876 7500890212 rpmg 50s ribosomal protein l33 (db:genpept) (de:helicobacter pylori, strain j99 section 102 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1204) (le:257) (re:415) (di:complement) AE001541 AE001541 g4155730 Helicobacter pylori J99 85963 -11538876 7502852729 hp1204 ribosomal protein l33 rpl33 (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to egad:9493 percent identity: 55.10;) (le:3354) (re:3512) (di:complement) HPAE000626 AE000626 g2314371 Helicobacter pylori 26695 85962 -11538876

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902611	17186	39342	1380	459

Description

6500735019 rps18:hp1244 ribosomal protein s18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1244 HP1244 Helicobacter pylori 210 -11538877 5500685923 rpsr:hp1244 (sr:,campylobacter pylori) (de:30s ribosomal protein s18) (db:swissprot) RS18_HELPY P56025 HELICOBACTER PYLORI 210 -11538877 7000686494 ribosomal protein s18 (cl:escherichia coli ribosomal protein s18) (db:pir2.dat) D64675 D64675 Helicobacter pylori 210 -11538877 7500890951 hp1244 ribosomal protein s18 rps18 (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to egad:5059 percent identity: 55.22;) (le:180) (re:437) (di:complement) HPAE000630 AE000630 g2314410 Helicobacter pylori 210 -11538877 7500890952 rpsr 30s ribosomal protein s18 (db:genpept) (de:helicobacter pylori, strain j99 section 105 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1244) (le:3675) (re:3932) (di:complement) AE001544 AE001544 g4155773 Helicobacter pylori J99 85963 -11538877 7502852730 hp1244 ribosomal protein s18 rps18 (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to egad:5059 percent identity: 55.22;) (le:180) (re:437) (di:complement) HPAE000630 AE000630 g2314410 Helicobacter pylori 26695 85962 -11538877

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902613	17187	39343	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902614	17188	39344	315	104

Description

6500735020 rps6:hp1246 ribosomal protein s6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1246 HP1246 Helicobacter pylori 210 -11538878 5500685936 rpsf:hp1246 (sr:,campylobacter pylori) (de:30s ribosomal protein s6) (db:swissprot) RS6_HELPY P56013 HELICOBACTER PYLORI 210 -11538878 7000686514 ribosomal protein s6 (cl:escherichia coli ribosomal protein s6) (db:pir2.dat) F64675 F64675 Helicobacter pylori 210 -11538878 7500891086 hp1246 ribosomal protein s6 rps6 (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to egad:9292 percent identity: 32.09;) (le:1009) (re:1437) (di:complement) HPAE000630 AE000630 g2314412 Helicobacter pylori 210 -11538878 7502852731 hp1246 ribosomal protein s6 rps6 (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to egad:9292 percent identity: 32.09;) (le:1009) (re:1437) (di:complement) HPAE000630 AE000630 g2314412 Helicobacter pylori 26695 85962 -11538878

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902623	17189	39345	549	182

Description

6500735021 rpl17:hp1292 ribosomal protein l17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1292 HP1292 Helicobacter pylori 210 -11538879 5500685848 rplq:hp1292 (sr:,campylobacter pylori) (de:50s ribosomal protein l17) (db:swissprot) RL17_HELPY P56042 HELICOBACTER PYLORI 210 -11538879 7000686359 ribosomal protein l17 (cl:escherichia coli ribosomal protein l17) (db:pir2.dat) D64681 D64681 Helicobacter pylori 210 -11538879 7500889993 hp1292 ribosomal protein l17 rpl17 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:29288 percent identity: 48.28;) (le:5780) (re:6130) (di:complement) HPAE000633 AE000633 g2314458 Helicobacter pylori 210 -11538879 7502852732 hp1292 ribosomal protein l17 rpl17 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:29288 percent identity: 48.28;) (le:5780) (re:6130) (di:complement) HPAE000633 AE000633 g2314458 Helicobacter pylori 26695 85962 -11538879

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902630	17190	39346	840	279

Description

GTC ORF with score 863 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmids 9379, 9581, andlambda clone 4678.) (nt:similar to putative regulatory subunit of 26s) (le:26050) (re:28743) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902631	17191	39347	237	78

Description

6500735022 rps4:hp1294 ribosomal protein s4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1294 HP1294 Helicobacter pylori 210 -11538880 5500685934 rpsd:hp1294 (sr:,campylobacter pylori) (de:30s ribosomal protein s4) (db:swissprot) RS4_HELPY P56011 HELICOBACTER PYLORI 210 -11538880 7000686508 ribosomal protein s4 (cl:escherichia coli ribosomal protein s4) (db:pir2.dat) F64681 F64681 Helicobacter pylori 210 -11538880 7500891051 hp1294 ribosomal protein s4 rps4 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:29286 percent identity: 51.21;) (le:7176) (re:7802) (di:complement) HPAE000633 AE000633 g2314460 Helicobacter pylori 210 -11538880 7502852733 hp1294 ribosomal protein s4 rps4 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:29286 percent identity: 51.21;) (le:7176) (re:7802) (di:complement) HPAE000633 AE000633 g2314460 Helicobacter pylori 26695 85962 -11538880

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902633	17192	39348	621	206

Description

GTC ORF with score 115 to: (fn:helicase, helicase-primase complex) (db:genpept-vrl) (de:human herpesvirus 6 serotype b putative major immediate-earlygenes.) (nt:similar to hhv6a u86, region ie-b) (le:16386) (re:19235) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902649	17193	39349	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902653	17194	39350	4200	1400

Description

GTC ORF with score 636 to: (fn:required for ime1 and ume6 dependent activation) (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae protein kinase rim15p (rim15) gene,complete cds.) (nt:protein kinase; previously sequenced as orf yfl033c)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902674	17195	39351	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902677	17196	39352	411	136

Description

6500735023 rps11:hp1295 ribosomal protein s11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1295 HP1295 Helicobacter pylori 210 -11538881 5500685915 rpsk:hp1295 (sr:,campylobacter pylori) (de:30s ribosomal protein s11) (db:swissprot) RS11_HELPY P56018 HELICOBACTER PYLORI 210 -11538881 7000686484 ribosomal protein s11 (cl:escherichia coli ribosomal protein s11) (db:pir2.dat) G64681 G64681 Helicobacter pylori 210 -11538881 7500890856 hp1295 ribosomal protein s11 rps11 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:5161 percent identity: 56.15;) (le:7812) (re:8207) (di:complement) HPAE000633 AE000633 g2314461 Helicobacter pylori 210 -11538881 7502852734 hp1295 ribosomal protein s11 rps11 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:5161 percent identity: 56.15;) (le:7812) (re:8207) (di:complement) HPAE000633 AE000633 g2314461 Helicobacter pylori 26695 85962 -11538881

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902685	17197	39353	678	225

Description

6500735024 rps13:hp1296 ribosomal protein s13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1296 HP1296 Helicobacter pylori 210 -11538882 5500685917 rpsm:hp1296 (sr:,campylobacter pylori) (de:30s ribosomal protein s13) (db:swissprot) RS13_HELPY P56020 HELICOBACTER PYLORI 210 -11538882 7000686488 ribosomal protein s13 (cl:escherichia coli ribosomal protein s13) (db:pir2.dat) H64681 H64681 Helicobacter pylori 210 -11538882 7500890883 hp1296 ribosomal protein s13 rps13 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:13524 percent identity: 55.83;) (le:8230) (re:8592) (di:complement) HPAE000633 AE000633 g2314462 Helicobacter pylori 210 -11538882 7502852735 hp1296 ribosomal protein s13 rps13 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:13524 percent identity: 55.83;) (le:8230) (re:8592) (di:complement) HPAE000633 AE000633 g2314462 Helicobacter pylori 26695 85962 -11538882

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902687	17198	39354	1596	531

Description

6500735025 rpl36:hp1297 ribosomal protein l36 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1297 HP1297 Helicobacter pylori 210 -11538883 5500685874 rpmj:hp1297 (sr:,campylobacter pylori) (de:50s ribosomal protein l36) (db:swissprot) RL36_HELPY P56058 HELICOBACTER PYLORI 210 -11538883 7000686399 ribosomal protein l36 (cl:escherichia coli ribosomal protein l36) (db:pir2.dat) A64682 A64682 Helicobacter pylori 210 -11538883 7500890244 hp1297 ribosomal protein l36 rpl36 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:7945 percent identity: 81.58;) (le:8596) (re:8709) (di:complement) HPAE000633 AE000633 g2314486 Helicobacter pylori 210 -11538883 7502852736 hp1297 ribosomal protein l36 rpl36 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:7945 percent identity: 81.58;) (le:8596) (re:8709) (di:complement) HPAE000633 AE000633 g2314486 Helicobacter pylori 26695 85962 -11538883

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902702	17199	39355	522	173

Description

6500735026 rpl15:hp1301 ribosomal protein l15 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1301 HP1301 Helicobacter pylori 210 -11538884 5500685846 rplo:hp1301 (sr:,campylobacter pylori) (de:50s ribosomal protein l15) (db:swissprot) RL15_HELPY P56040 HELICOBACTER PYLORI 210 -11538884 7000686356 ribosomal protein l15 (db:pir2.dat) E64682 E64682 Helicobacter pylori 210 -11538884 7500889967 hp1301 ribosomal protein l15 rpl15 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:29419 percent identity: 42.54;) (le:11072) (re:11479) (di:complement) HPAE000633 AE000633 g2314465 Helicobacter pylori 210 -11538884 7502852737 hp1301 ribosomal protein l15 rpl15 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:29419 percent identity: 42.54;) (le:11072) (re:11479) (di:complement) HPAE000633 AE000633 g2314465 Helicobacter pylori 26695 85962 -11538884

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902717	17200	39356	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902731	17201	39357	702	233

Description

GTC ORF with score 124 to: (sr:human) (db:genpept) (de:human dna sequence from clone 283e3 on chromosome 1p36.21-36.33.contains the alternatively spliced gene for matrixmetalloproteinase in the female reproductive tract mifr1, -2,mmp21/22a, -b and -c, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902742	17202	39358	1536	511

Description

6500735027 rps5:hp1302 ribosomal protein s5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1302 HP1302 Helicobacter pylori 210 -11538885 5500685935 rpse:hp1302 (sr:,campylobacter pylori) (de:30s ribosomal protein s5) (db:swissprot) RS5_HELPY P56012 HELICOBACTER PYLORI 210 -11538885 7000686511 ribosomal protein s5 (cl:escherichia coli ribosomal protein s5) (db:pir2.dat) F64682 F64682 Helicobacter pylori 210 -11538885 7500891061 hp1302 ribosomal protein s5 rps5 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:20146 percent identity: 65.49;) (le:11493) (re:11954) (di:complement) HPAE000633 AE000633 g2314466 Helicobacter pylori 210 -11538885 7500891062 rpse 30s ribosomal protein s5 (db:genpept) (de:helicobacter pylori, strain j99 section 108 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1302) (le:9180) (re:9641) (di:complement) AE001547 AE001547 g4155832 Helicobacter pylori J99 85963 -11538885 7502852738 hp1302 ribosomal protein s5 rps5 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:20146 percent identity: 65.49;) (le:11493) (re:11954) (di:complement) HPAE000633 AE000633 g2314466 Helicobacter pylori 26695 85962 -11538885

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902743	17203	39359	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902746	17204	39360	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902747	17205	39361	606	201

Description

6500735028 rpl18:hp1303 ribosomal protein l18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1303 HP1303 Helicobacter pylori 210 -11538886 5500685849 rplr:hp1303 (sr:,campylobacter pylori) (de:50s ribosomal protein l18) (db:swissprot) RL18_HELPY P56043 HELICOBACTER PYLORI 210 -11538886 7000686360 ribosomal protein l18 (cl:escherichia coli ribosomal protein l18) (db:pir2.dat) G64682 G64682 Helicobacter pylori 210 -11538886 7500890001 hp1303 ribosomal protein l18 rpl18 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:15826 percent identity: 45.54;) (le:11951) (re:12310) (di:complement) HPAE000633 AE000633 g2314467 Helicobacter pylori 210 -11538886 7502852739 hp1303 ribosomal protein l18 rpl18 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:15826 percent identity: 45.54;) (le:11951) (re:12310) (di:complement) HPAE000633 AE000633 g2314467 Helicobacter pylori 26695 85962 -11538886

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902752	17206	39362	228	75

Description

6500735029 rpl6:hp1304 ribosomal protein l6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1304 HP1304 Helicobacter pylori 210 -11538887 5500685879 rplf:hp1304 (sr:,campylobacter pylori) (de:50s ribosomal protein l6) (db:swissprot) RL6_HELPY P56034 HELICOBACTER PYLORI 210 -11538887 7000686407 ribosomal protein l6 (cl:escherichia coli ribosomal protein l6) (db:pir2.dat) H64682 H64682 Helicobacter pylori 210 -11538887 7500890342 hp1304 ribosomal protein l6 rpl6 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:10003 percent identity: 44.44;) (le:12321) (re:12857) (di:complement) HPAE000633 AE000633 g2314468 Helicobacter pylori 210 -11538887 7502852740 hp1304 ribosomal protein l6 rpl6 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:10003 percent identity: 44.44;) (le:12321) (re:12857) (di:complement) HPAE000633 AE000633 g2314468 Helicobacter pylori 26695 85962 -11538887

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902766	17207	39363	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902768	17208	39364	561	186

Description

6500735030 rps8:hp1305 ribosomal protein s8 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1305 HP1305 Helicobacter pylori 210 -11538888 5500685939 rpsh:hp1305 (sr:,campylobacter pylori) (de:30s ribosomal protein s8) (db:swissprot) RS8_HELPY P56015 HELICOBACTER PYLORI 210 -11538888 7000686519 ribosomal protein s8 (cl:escherichia coli ribosomal protein s8) (db:pir2.dat) A64683 A64683 Helicobacter pylori 210 -11538888 7500891111 hp1305 ribosomal protein s8 rps8 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:10594 percent identity: 45.04;) (le:12868) (re:13263) (di:complement) HPAE000633 AE000633 g2314469 Helicobacter pylori 210 -11538888 7500891112 rpsh putative 30s ribosomal protein s8 (db:genpept) (de:helicobacter pylori, strain j99 section 108 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1305) (le:10556) (re:10951) (di:complement) AE001547 AE001547 g4155835 Helicobacter pylori J99 85963 -11538888 7502852741 hp1305 ribosomal protein s8 rps8 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:10594 percent identity: 45.04;) (le:12868) (re:13263) (di:complement) HPAE000633 AE000633 g2314469 Helicobacter pylori 26695 85962 -11538888

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902821	17209	39365	1266	421

Description

6500735031 rps14:hp1306 ribosomal protein s14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1306 HP1306 Helicobacter pylori 210 -11538889 5500685918 rpsn:hp1306 (sr:,campylobacter pylori) (de:30s ribosomal protein s14) (db:swissprot) RS14_HELPY P56021 HELICOBACTER PYLORI 210 -11538889 7000686490 ribosomal protein s14 (cl:escherichia coli ribosomal protein s14) (db:pir2.dat) B64683 B64683 Helicobacter pylori 210 -11538889 7500890893 hp1306 ribosomal protein s14 rps14 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:32892 percent identity: 68.33;) (le:13273) (re:13458) (di:complement) HPAE000633 AE000633 g2314484 Helicobacter pylori 210 -11538889 7502852742 hp1306 ribosomal protein s14 rps14 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:32892 percent identity: 68.33;) (le:13273) (re:13458) (di:complement) HPAE000633 AE000633 g2314484 Helicobacter pylori 26695 85962 -11538889

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902822	17210	39366	582	193

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902823	17211	39367	2460	819

Description

6500735032 rpl5:hp1307 ribosomal protein l5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1307 HP1307 Helicobacter pylori 210 -11538890 5500685878 rple:hp1307 (sr:,campylobacter pylori) (de:50s ribosomal protein l5) (db:swissprot) RL5_HELPY P56033 HELICOBACTER PYLORI 210 -11538890 7000686406 ribosomal protein l5 (cl:escherichia coli ribosomal protein l5) (db:pir2.dat) C64683 C64683 Helicobacter pylori 210 -11538890 7500890327 hp1307 ribosomal protein l5 rpl5 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:8725 percent identity: 53.07;) (le:13468) (re:14013) (di:complement) HPAE000633 AE000633 g2314470 Helicobacter pylori 210 -11538890 7502852743 hp1307 ribosomal protein l5 rpl5 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:8725 percent identity: 53.07;) (le:13468) (re:14013) (di:complement) HPAE000633 AE000633 g2314470 Helicobacter pylori 26695 85962 -11538890

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902825	17212	39368	480	159

Description

6500735033 rpl24:hp1308 ribosomal protein l24 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1308 HP1308 Helicobacter pylori 210 -11538891 5500685858 rplx:hp1308 (sr:,campylobacter pylori) (de:50s ribosomal protein l24) (db:swissprot) RL24_HELPY P56049 HELICOBACTER PYLORI 210 -11538891 7000686372 ribosomal protein l24 (cl:escherichia coli ribosomal protein l24) (db:pir2.dat) D64683 D64683 Helicobacter pylori 210 -11538891 7500890104 hp1308 ribosomal protein l24 rpl24 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:6848 percent identity: 52.24;) (le:14026) (re:14247) (di:complement) HPAE000633 AE000633 g2314471 Helicobacter pylori 210 -11538891 7502852744 hp1308 ribosomal protein l24 rpl24 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:6848 percent identity: 52.24;) (le:14026) (re:14247) (di:complement) HPAE000633 AE000633 g2314471 Helicobacter pylori 26695 85962 -11538891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902826	17213	39369	606	201

Description

6500735034 rpl14:hp1309 ribosomal protein l14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1309 HP1309 Helicobacter pylori 210 -11538892 5500685844 rpln:hp1309 (sr:,campylobacter pylori) (de:50s ribosomal protein l14) (db:swissprot) RL14_HELPY P56039 HELICOBACTER PYLORI 210 -11538892 7000686355 ribosomal protein l14 (cl:escherichia coli ribosomal protein l14) (db:pir2.dat) E64683 E64683 Helicobacter pylori 210 -11538892 7500889943 hp1309 ribosomal protein l14 rpl14 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:7021 percent identity: 65.85;) (le:14247) (re:14615) (di:complement) HPAE000633 AE000633 g2314472 Helicobacter pylori 210 -11538892 7502852745 hp1309 ribosomal protein l14 rpl14 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:7021 percent identity: 65.85;) (le:14247) (re:14615) (di:complement) HPAE000633 AE000633 g2314472 Helicobacter pylori 26695 85962 -11538892

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902827	17214	39370	237	78

Description

6500735035 rps17:hp1310 ribosomal protein s17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1310 HP1310 Helicobacter pylori 210 -11538893 5500685922 rpsq:hp1310 (sr:,campylobacter pylori) (de:30s ribosomal protein s17) (db:swissprot) RS17_HELPY P56024 HELICOBACTER PYLORI 210 -11538893 7000686493 ribosomal protein s17 (cl:escherichia coli ribosomal protein s17) (db:pir2.dat) F64683 F64683 Helicobacter pylori 210 -11538893 7500890934 hp1310 ribosomal protein s17 rps17 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:27953 percent identity: 55.41;) (le:14618) (re:14878) (di:complement) HPAE000633 AE000633 g2314473 Helicobacter pylori 210 -11538893 7500890935 rpsq 30s ribosomal protein s17 (db:genpept) (de:helicobacter pylori, strain j99 section 108 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1310) (le:12307) (re:12567) (di:complement) AE001547 AE001547 g4155822 Helicobacter pylori J99 85963 -11538893 7502852746 hp1310 ribosomal protein s17 rps17 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:27953 percent identity: 55.41;) (le:14618) (re:14878) (di:complement) HPAE000633 AE000633 g2314473 Helicobacter pylori 26695 85962 -11538893

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902840	17215	39371	270	89

Description

6500735036 rpl29:hp1311 ribosomal protein l29 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1311 HP1311 Helicobacter pylori 210 -11538894 5500685864 rpmc:hp1311 (sr:,campylobacter pylori) (de:50s ribosomal protein l29) (db:swissprot) RL29_HELPY P56052 HELICOBACTER PYLORI 210 -11538894 7000686378 ribosomal protein l29 (cl:escherichia coli ribosomal protein l29) (db:pir2.dat) G64683 G64683 Helicobacter pylori 210 -11538894 7500890146 hp1311 ribosomal protein l29 rpl29 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:7124 percent identity: 45.61;) (le:14891) (re:15091) (di:complement) HPAE000633 AE000633 g2314485 Helicobacter pylori 210 -11538894 7502852747 hp1311 ribosomal protein l29 rpl29 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:7124 percent identity: 45.61;) (le:14891) (re:15091) (di:complement) HPAE000633 AE000633 g2314485 Helicobacter pylori 26695 85962 -11538894

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902851	17216	39372	288	95

Description

6500735037 rpl16:hp1312 ribosomal protein l16 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1312 HP1312 Helicobacter pylori 210 -11538895 5500685847 rplp:hp1312 (sr:,campylobacter pylori) (de:50s ribosomal protein l16) (db:swissprot) RL16_HELPY P56041 HELICOBACTER PYLORI 210 -11538895 7000686358 ribosomal protein l16 (cl:escherichia coli ribosomal protein l16) (db:pir2.dat) H64683 H64683 Helicobacter pylori 210 -11538895 7500889979 hp1312 ribosomal protein l16 rpl16 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:8200 percent identity: 62.41;) (le:15078) (re:15503) (di:complement) HPAE000633 AE000633 g2314474 Helicobacter pylori 210 -11538895 7502852748 hp1312 ribosomal protein l16 rpl16 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:8200 percent identity: 62.41;) (le:15078) (re:15503) (di:complement) HPAE000633 AE000633 g2314474 Helicobacter pylori 26695 85962 -11538895

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902852	17217	39373	612	203

Description

6500735038 rps3:hp1313 ribosomal protein s3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1313 HP1313 Helicobacter pylori 210 -11538896 5500685933 rpsc:hp1313 (sr:,campylobacter pylori) (de:30s ribosomal protein s3) (db:swissprot) RS3_HELPY P56010 HELICOBACTER PYLORI 210 -11538896 7000686507 ribosomal protein s3 (cl:escherichia coli ribosomal protein s3) (db:pir2.dat) A64684 A64684 Helicobacter pylori 210 -11538896 7500891044 hp1313 ribosomal protein s3 rps3 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:27950 percent identity: 56.65;) (le:15506) (re:16210) (di:complement) HPAE000633 AE000633 g2314475 Helicobacter pylori 210 -11538896 7502852749 hp1313 ribosomal protein s3 rps3 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:27950 percent identity: 56.65;) (le:15506) (re:16210) (di:complement) HPAE000633 AE000633 g2314475 Helicobacter pylori 26695 85962 -11538896

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902857	17218	39374	1368	455

Description

6500735039 rpl22:hp1314 ribosomal protein l22 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1314 HP1314 Helicobacter pylori 210 -11538897 5500685855 rplv:hp1314 (sr:,campylobacter pylori) (de:50s ribosomal protein l22) (db:swissprot) RL22_HELPY P56047 HELICOBACTER PYLORI 210 -11538897 7000686368 ribosomal protein l22 (cl:escherichia coli ribosomal protein l22) (db:pir2.dat) B64684 B64684 Helicobacter pylori 210 -11538897 7500890067 hp1314 ribosomal protein l22 rpl22 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:33078 percent identity: 44.86;) (le:16214) (re:16582) (di:complement) HPAE000633 AE000633 g2314476 Helicobacter pylori 210 -11538897 7502852750 hp1314 ribosomal protein l22 rpl22 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:33078 percent identity: 44.86;) (le:16214) (re:16582) (di:complement) HPAE000633 AE000633 g2314476 Helicobacter pylori 26695 85962 -11538897

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902859	17219	39375	393	130

Description

6500735040 rps19:hp1315 ribosomal protein s19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1315 HP1315 Helicobacter pylori 210 -11538898 5500685925 rpss:hp1315 (sr:,campylobacter pylori) (de:30s ribosomal protein s19) (db:swissprot) RS19_HELPY P56026 HELICOBACTER PYLORI 210 -11538898 7000686495 ribosomal protein s19 (cl:escherichia coli ribosomal protein s19) (db:pir2.dat) C64684 C64684 Helicobacter pylori 210 -11538898 7500890965 hp1315 ribosomal protein s19 rps19 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:19290 percent identity: 61.11;) (le:16592) (re:16873) (di:complement) HPAE000633 AE000633 g2314477 Helicobacter pylori 210 -11538898 7502852751 hp1315 ribosomal protein s19 rps19 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:19290 percent identity: 61.11;) (le:16592) (re:16873) (di:complement) HPAE000633 AE000633 g2314477 Helicobacter pylori 26695 85962 -11538898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902866	17220	39376	576	191

Description

6500735041 rpl2:hp1316 ribosomal protein l2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1316 HP1316 Helicobacter pylori 210 -11538899 5500685865 rplb:hp1316 (sr:,campylobacter pylori) (de:50s ribosomal protein l2) (db:swissprot) RL2_HELPY P56030 HELICOBACTER PYLORI 210 -11538899 7000686380 ribosomal protein l2 (cl:escherichia coli ribosomal protein l2) (db:pir2.dat) D64684 D64684 Helicobacter pylori 210 -11538899 7500890165 hp1316 ribosomal protein l2 rpl2 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:5072 percent identity: 58.91;) (le:16884) (re:17714) (di:complement) HPAE000633 AE000633 g2314478 Helicobacter pylori 210 -11538899 7502852752 hp1316 ribosomal protein l2 rpl2 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:5072 percent identity: 58.91;) (le:16884) (re:17714) (di:complement) HPAE000633 AE000633 g2314478 Helicobacter pylori 26695 85962 -11538899

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902894	17221	39377	1104	367

Description

6500735042 rpl23:hp1317 ribosomal protein l23 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1317 HP1317 Helicobacter pylori 210 -11538900 5500685857 rplw:hp1317 (sr:,campylobacter pylori) (de:50s ribosomal protein l23) (db:swissprot) RL23_HELPY P56048 HELICOBACTER PYLORI 210 -11538900 7000686371 ribosomal protein l23 (cl:escherichia coli ribosomal protein l23) (db:pir1.dat) E64684 E64684 Helicobacter pylori 210 -11538900 7500890089 hp1317 ribosomal protein l23 rpl23 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:7036 percent identity: 31.71;) (le:17731) (re:18012) (di:complement) HPAE000633 AE000633 g2314479 Helicobacter pylori 210 -11538900 7500890090 rplw 50s ribosomal protein l23 (db:genpept) (de:helicobacter pylori, strain j99 section 108 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1317) (le:15421) (re:15702) (di:complement) AE001547 AE001547 g4155814 Helicobacter pylori J99 85963 -11538900 7502852753 hp1317 ribosomal protein l23 rpl23 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:7036 percent identity: 31.71;) (le:17731) (re:18012) (di:complement) HPAE000633 AE000633 g2314479 Helicobacter pylori 26695 85962 -11538900

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902897	17222	39378	231	76

Description

6500735043 rpl4:hp1318 ribosomal protein l4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1318 HP1318 Helicobacter pylori 210 -11538901 5500685877 rpld:hp1318 (sr:,campylobacter pylori) (de:50s ribosomal protein l4) (db:swissprot) RL4_HELPY P56032 HELICOBACTER PYLORI 210 -11538901 7000686405 ribosomal protein l4 (db:pir2.dat) F64684 F64684 Helicobacter pylori 210 -11538901 7500890311 hp1318 ribosomal protein l4 rpl4 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:31926 percent identity: 40.56;) (le:18016) (re:18663) (di:complement) HPAE000633 AE000633 g2314480 Helicobacter pylori 210 -11538901 7502852754 hp1318 ribosomal protein l4 rpl4 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:31926 percent identity: 40.56;) (le:18016) (re:18663) (di:complement) HPAE000633 AE000633 g2314480 Helicobacter pylori 26695 85962 -11538901

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902904	17223	39379	345	114

Description

6500735044 rpl3:hp1319 ribosomal protein l3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1319 HP1319 Helicobacter pylori 210 -11538902 5500685876 rplc:hp1319 (sr:,campylobacter pylori) (de:50s ribosomal protein l3) (db:swissprot) RL3_HELPY P56031 HELICOBACTER PYLORI 210 -11538902 7000686401 ribosomal protein l3 (db:pir2.dat) G64684 G64684 Helicobacter pylori 210 -11538902 7500890271 hp1319 ribosomal protein l3 rpl3 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:41008 percent identity: 41.80;) (le:18698) (re:19273) (di:complement) HPAE000633 AE000633 g2314481 Helicobacter pylori 210 -11538902 7502852755 hp1319 ribosomal protein l3 rpl3 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:41008 percent identity: 41.80;) (le:18698) (re:19273) (di:complement) HPAE000633 AE000633 g2314481 Helicobacter pylori 26695 85962 -11538902

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902907	17224	39380	588	195

Description

6500735045 rps10:hp1320 ribosomal protein s10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1320 HP1320 Helicobacter pylori 210 -11538903 5500685914 rpsj:hp1320 (sr:,campylobacter pylori) (de:30s ribosomal protein s10) (db:swissprot) RS10_HELPY P56017 HELICOBACTER PYLORI 210 -11538903 7000686483 ribosomal protein s10 (cl:escherichia coli ribosomal protein s10) (db:pir2.dat) H64684 H64684 Helicobacter pylori 210 -11538903 7500890843 hp1320 ribosomal protein s10 rps10 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:27943 percent identity: 58.16;) (le:19310) (re:19624) (di:complement) HPAE000633 AE000633 g2314482 Helicobacter pylori 210 -11538903 7500890844 rpsj 30s ribosomal protein s10 (db:genpept) (de:helicobacter pylori, strain j99 section 108 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1320) (le:17000) (re:17314) (di:complement) AE001547 AE001547 g4155817 Helicobacter pylori J99 85963 -11538903 7502852756 hp1320 ribosomal protein s10 rps10 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:27943 percent identity: 58.16;) (le:19310) (re:19624) (di:complement) HPAE000633 AE000633 g2314482 Helicobacter pylori 26695 85962 -11538903

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902908	17225	39381	909	302

Description

GTC ORF with score 1503 to: (sr:aspergillus fumigatus strain=siu001) (db:genpept-pln1) (de:aspergillus fumigatus class iii chitin synthase g (chsg) gene,complete cds.) (le:751:900:1451:1864:2784) (re:834:1374:1812:2710:3613) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902912	17226	39382	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902925	17227	39383	870	289

Description

6500735046 rpl34:hp1447 ribosomal protein l34 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1447 HP1447 Helicobacter pylori 210 -11538904 5500685869 rpmh:hp1447 (sr:,campylobacter pylori) (de:50s ribosomal protein l34) (db:swissprot) RL34_HELPY P56056 HELICOBACTER PYLORI 210 -11538904 7000686394 ribosomal protein l34 (cl:escherichia coli ribosomal protein l34) (db:pir2.dat) G64700 G64700 Helicobacter pylori 210 -11538904 7500890223 hp1447 ribosomal protein l34 rpl34 (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:similar to egad:17150 percent identity: 70.45;) (le:66) (re:200) (di:direct) HPAE000645 AE000645 g2314630 Helicobacter pylori 210 -11538904 7500890224 rpmh 50s ribosomal protein l34 (db:genpept) (de:helicobacter pylori, strain j99 section 118 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1447) (le:67) (re:201) (di:direct) AE001557 AE001557 g4155963 Helicobacter pylori J99 85963 -11538904 7502852757 hp1447 ribosomal protein l34 rpl34 (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:similar to egad:17150 percent identity: 70.45;) (le:66) (re:200) (di:direct) HPAE000645 AE000645 g2314630 Helicobacter pylori 26695 85962 -11538904

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902926	17228	39384	819	272

Description

6500735047 rps2:hp1554 ribosomal protein s2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.6) (db:gtc-helicobacter pylori) HP1554 HP1554 Helicobacter pylori 210 -11538905 5500685932 rpsb:hp1554 (sr:,campylobacter pylori) (de:30s ribosomal protein s2) (db:swissprot) RS2_HELPY P56009 HELICOBACTER PYLORI 210 -11538905 7000686505 ribosomal protein s2 (cl:escherichia coli ribosomal protein s2) (db:pir2.dat) B64714 B64714 Helicobacter pylori 210 -11538905 7500891025 hp1554 ribosomal protein s2 rps2 (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:13773 percent identity: 49.58;) (le:4919) (re:5713) (di:direct) HPAE000653 AE000653 g2314737 Helicobacter pylori 210 -11538905 7502852758 hp1554 ribosomal protein s2 rps2 (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:13773 percent identity: 49.58;) (le:4919) (re:5713) (di:direct) HPAE000653 AE000653 g2314737 Helicobacter pylori 26695 85962 -11538905

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902927	17229	39385	879	292

Description

6500735048 gltx:hp0643 glutamyl-trna synthetase (gtcfc:10.6) (keggfc:14.2) (tigrfc:12.2) (db:gtc-helicobacter pylori) HP0643 HP0643 Helicobacter pylori 210 -11538906 7000689965 glutamate--trna ligase (cl:glutamate--trna ligase:glutamine--trna ligase homology) (ec:6.1.1.17) (db:pir2.dat) C64600 C64600 Helicobacter pylori 210 -11538906 7500954487 hp0643 glutamyl-trna synthetase gltx (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:15121 percent identity: 39.81;) (le:5098) (re:6417) (di:direct) HPAE000578 AE000578 g2313763 Helicobacter pylori 210 -11538906 7502852759 hp0643 glutamyl-trna synthetase gltx (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:15121 percent identity: 39.81;) (le:5098) (re:6417) (di:direct) HPAE000578 AE000578 g2313763 Helicobacter pylori 26695 85962 -11538906

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902937	17230	39386	669	222

Description

6500735049 tgt:hp0281 trna-guanine transglycosylase (gtcfc:10.6) (ec:2.4.2.29) (keggfc:14.1) (tigrfc:12.7) (db:gtc-helicobacter pylori) HP0281 HP0281 Helicobacter pylori 210 -11538907 5500686058 tgt:hp0281 (sr:,campylobacter pylori) (ec:2.4.2.29) (de:transglycosylase) (guanine insertion enzyme)) (db:swissprot) TGT_HELPY O08314 HELICOBACTER PYLORI 210 -11538907 7000686780 trna-guanine transglycosylase (cl:queuine trna-ribosyltransferase) (db:pir2.dat) A64555 A64555 Helicobacter pylori 210 -11538907 7500893012 hp0281 trna-guanine transglycosylase tgt (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:similar to egad:16012 percent identity: 45.63;) (le:80) (re:1195) (di:complement) HPAE000547 AE000547 g2313378 Helicobacter pylori 210 -11538907 7502852760 hp0281 trna-guanine transglycosylase tgt (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:similar to egad:16012 percent identity: 45.63;) (le:80) (re:1195) (di:complement) HPAE000547 AE000547 g2313378 Helicobacter pylori 26695 85962 -11538907

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902955	17231	39387	768	256

Description

6500735050 hist:hp0361 pseudouridylate synthase i (gtcfc:10.6) (ec:4.2.1.70) (keggfc:14.1) (tigrfc:12.7) (db:gtc-helicobacter pylori) HP0361 HP0361 Helicobacter pylori 210 -11538908 5500686082 trua:hist:hp0361 (sr:,campylobacter pylori) (ec:4.2.1.70) (de:i) (pseudouridine synthase i) (uracil hydrolyase)) (db:swissprot) TRUA_HELPY P56144 HELICOBACTER PYLORI 210 -11538908 7000686834 pseudouridylate synthase i (db:pir2.dat) A64565 A64565 Helicobacter pylori 210 -11538908 7500893517 hp0361 pseudouridylate synthase i hist (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:similar to egad:31395 percent identity: 32.20;) (le:1560) (re:2288) (di:complement) HPAE000553 AE000553 g2313463 Helicobacter pylori 210 -11538908 7502852761 hp0361 pseudouridylate synthase i hist (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:similar to egad:31395 percent identity: 32.20;) (le:1560) (re:2288) (di:complement) HPAE000553 AE000553 g2313463 Helicobacter pylori 26695 85962 -11538908

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902960	17232	39388	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902966	17233	39389	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902973	17234	39390	1209	402

Description

GTC ORF with score 1279 to: (sr:aspergillus parasiticus (individual_isolate su1) cdna to mrna) (db:genpept-pln2) (de:aspergillus parasiticus polygalacturonase (peca) mrna, completecds.) (nt:conserved aa domain 589..945.) (le:61) (re:1152) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902980	17235	39391	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501902989	17236	39392	270	89

Description

6500735051 quea:hp1062 trna ribosyltransferase-isomerase:s-adenosylmethionine:trnaribosyltransferase-isomerase (gtcfc:10.6) (ec:5.-.-.-) (keggfc:14.1) (tigrfc:12.7) (db:gtc-helicobacter pylori) HP1062 HP1062 Helicobacter pylori 210 -11538909 7502852762 quea:hp1062 (sr:,campylobacter pylori) (ec:5.-.-.-) (de:(queuosine biosynthesis protein quea)) (db:swissprot) QUEA_HELPY O25702 HELICOBACTER PYLORI 210 -11538909 7000690694 s-adenosylmethionine:trna ribosyltransferase-isomerase::queuosine biosynthesis-related protein quea (cl:s-adenosylmethionine:trna ribosyltransferase-isomerase) (ec:5.-.-.-) (db:pir2.dat) F64652 F64652 Helicobacter pylori 210 -11538909 7500959462 hp1062 s-adenosylmethionine:trna (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:similar to egad:28891 percent identity: 39.30;) (le:8656) (re:9693) (di:direct) HPAE000613 AE000613 g2314205 Helicobacter pylori 210 -11538909 7502852763 hp1062 s-adenosylmethionine:trna (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:similar to egad:28891 percent identity: 39.30;) (le:8656) (re:9693) (di:direct) HPAE000613 AE000613 g2314205 Helicobacter pylori 26695 85962 -11538909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903001	17237	39393	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903005	17238	39394	318	105

Description

GTC ORF with score 233 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome ii cosmid c31f10.) (nt:spbc31f10.16, unknown, len:679aa, similar eg. to) (le:31104:31185:31367:33132) (re:31135:31311:33076:33302) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903010	17239	39395	225	74

Description

GTC ORF with score 116 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome ii cosmid c31f10.) (nt:spbc31f10.16, unknown, len:679aa, similar eg. to) (le:31104:31185:31367:33132) (re:31135:31311:33076:33302) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903011	17240	39396	1023	340

Description

GTC ORF with score 546 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome ii cosmid c31f10.) (nt:spbc31f10.16, unknown, len:679aa, similar eg. to) (le:31104:31185:31367:33132) (re:31135:31311:33076:33302) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903012	17241	39397	339	112

Description

GTC ORF with score 295 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome ii cosmid c31f10.) (nt:spbc31f10.16, unknown, len:679aa, similar eg. to) (le:31104:31185:31367:33132) (re:31135:31311:33076:33302) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903018	17242	39398	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903027	17243	39399	429	143

Description

6500735052 trmd:hp1148 trna guanine-n1-methyltransferase:trna:guanine-n1-methyltransferase (gtcfc:10.6) (ec:2.1.1.31) (keggfc:14.1) (tigrfc:12.7) (db:gtc-helicobacter pylori) HP1148 HP1148 Helicobacter pylori 210 -11538910 7502852764 trmd:hp1148 (sr:,campylobacter pylori) (ec:2.1.1.31) (de:methyltransferase) (trna (gm37) methyltransferase)) (db:swissprot) TRMD_HELPY O25766 HELICOBACTER PYLORI 210 -11538910 7000690749 trna (cl:trna (guanine-n1) methyltransferase) (db:pir2.dat) D64663 D64663 Helicobacter pylori 210 -11538910 7500959515 hp1148 trna guanine-n1 -methyltransferase trmd (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:31193 percent identity: 39.11;) (le:2183) (re:2872) (di:complement) HPAE000621 AE000621 g2314303 Helicobacter pylori 210 -11538910 7502852765 hp1148 trna guanine-n1 -methyltransferase trmd (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:31193 percent identity: 39.11;) (le:2183) (re:2872) (di:complement) HPAE000621 AE000621 g2314303 Helicobacter pylori 26695 85962 -11538910

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903035	17244	39400	795	264

Description

6500735053 miaa:hp1415 trna delta2-isopentenylpyrophospha transferase:trna delta:2-isopentenylpyrophosphatetransferase (gtcfc:10.6) (ec:2.5.1.8) (keggfc:14.1) (tigrfc:12.7) (db:gtc-helicobacter pylori) HP1415 HP1415 Helicobacter pylori 210 -11538911 7000690750 trna delta 2 -isopentenylpyrophosphate transferase (cl:delta(2)-isopentenylpyrophosphate transferase) (db:pir2.dat) G64696 G64696 Helicobacter pylori 210 -11538911 7500959516 hp1415 trna delta 2 -isopentenylpyrophosphate (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to egad:9574 percent identity: 30.67;) (le:1042) (re:1842) (di:direct) HPAE000642 AE000642 g2314590 Helicobacter pylori 210 -11538911 7502852766 hp1415 trna delta 2 -isopentenylpyrophosphate (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to egad:9574 percent identity: 30.67;) (le:1042) (re:1842) (di:direct) HPAE000642 AE000642 g2314590 Helicobacter pylori 26695 85962 -11538911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903040	17245	39401	453	150

Description

6500735054 rnpa:hp1448 ribonuclease p:protein component (gtcfc:10.6) (ec:3.1.26.5) (keggfc:14.1) (tigrfc:12.7) (db:gtc-helicobacter pylori) HP1448 HP1448 Helicobacter pylori 210 -11538912 5500685890 rnpa:hp1448 (sr:,campylobacter pylori) (ec:3.1.26.5) (de:ribonuclease p protein component, (protein c5) (rnase p)) (db:swissprot) RNPA_HELPY P55997 HELICOBACTER PYLORI 210 -11538912 7000686428 ribonuclease p:protein component (db:pir2.dat) H64700 H64700 Helicobacter pylori 210 -11538912 7500890465 hp1448 ribonuclease p:protein component rnpa (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:similar to egad:24720 percent identity: 29.31;) (le:160) (re:645) (di:direct) HPAE000645 AE000645 g2314624 Helicobacter pylori 210 -11538912 7502852767 hp1448 ribonuclease p:protein component rnpa (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:similar to egad:24720 percent identity: 29.31;) (le:160) (re:645) (di:direct) HPAE000645 AE000645 g2314624 Helicobacter pylori 26695 85962 -11538912

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903047	17246	39402	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903048	17247	39403	390	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903065	17248	39404	681	226

Description

6500735055 pth:hp1497 peptidyl-trna hydrolase (gtcfc:10.6) (ec:3.1.1.29) (keggfc:14.1) (tigrfc:12.7) (db:gtc-helicobacter pylori) HP1497 HP1497 Helicobacter pylori 210 -11538913 5500685780 pth:hp1497 (sr:,campylobacter pylori) (ec:3.1.1.29) (de:peptidyl-trna hydrolase, (pth)) (db:swissprot) PTH_HELPY P56077 HELICOBACTER PYLORI 210 -11538913 7000686217 peptidyl-trna hydrolase (db:pir2.dat) A64707 A64707 Helicobacter pylori 210 -11538913 7500888967 hp1497 peptidyl-trna hydrolase pth (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:29020 percent identity: 46.56;) (le:5616) (re:6176) (di:direct) HPAE000648 AE000648 g2314676 Helicobacter pylori 210 -11538913 7502852768 hp1497 peptidyl-trna hydrolase pth (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:29020 percent identity: 46.56;) (le:5616) (re:6176) (di:direct) HPAE000648 AE000648 g2314676 Helicobacter pylori 26695 85962 -11538913

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903069	17249	39405	834	277

Description

6500735056 translation initiation inhibitor:putative (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.1) (db:gtc-helicobacter pylori) HP0944 HP0944 Helicobacter pylori 210 -11538914 7502852769 hp0944 (sr:,campylobacter pylori) (de:hypothetical protein hp0944) (db:swissprot) Y944_HELPY O25598 HELICOBACTER PYLORI 210 -11538914 7000689510 probable translation initiation inhibitor (cl:hypothetical protein hi0719) (db:pir2.dat) H64637 H64637 Helicobacter pylori 210 -11538914 7500955817 hp0944 translation initiation inhibitor:putative (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:similar to sp:p52759 percent identity: 45.60;) (le:8679) (re:9056) (di:complement) HPAE000603 AE000603 g2314082 Helicobacter pylori 210 -11538914 7502852770 hp0944 translation initiation inhibitor:putative (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:similar to sp:p52759 percent identity: 45.60;) (le:8679) (re:9056) (di:complement) HPAE000603 AE000603 g2314082 Helicobacter pylori 26695 85962 -11538914

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903081	17250	39406	2160	719

Description

6500735057 pcm:hp0363 l-isoaspartyl-protein carboxyl methyltransferase (gtcfc:10.7) (ec:2.1.1.77) (keggfc:14.1) (tigrfc:12.5) (db:gtc-helicobacter pylori) HP0363 HP0363 Helicobacter pylori 210 -11538915 5500685740 pcm:hp0363 (sr:,campylobacter pylori) (ec:2.1.1.77) (de:methyltransferase) (l-isoaspartyl protein carboxyl methyltransferase)) (db:swissprot) PIMT_HELPY P56133 HELICOBACTER PYLORI 210 -11538915 7000686143 l-isoaspartyl-protein carboxyl methyltransferase (cl:escherichia coli protein-l-isoaspartate (d-aspartate) o-methyltransferase type ii:bioc homology) (db:pir2.dat) C64565 C64565 Helicobacter pylori 210 -11538915 7500888093 hp0363 l-isoaspartyl-protein carboxyl methyltransferase (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:similar to egad:23058 percent identity: 43.01;) (le:3337) (re:3966) (di:complement) HPAE000553 AE000553 g2313465 Helicobacter pylori 210 -11538915 7502852771 hp0363 l-isoaspartyl-protein carboxyl methyltransferase (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:similar to egad:23058 percent identity: 43.01;) (le:3337) (re:3966) (di:complement) HPAE000553 AE000553 g2313465 Helicobacter pylori 26695 85962 -11538915

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903084	17251	39407	276	91

Description

6500735058 slyd:hp1123 peptidyl-prolyl cis-trans isomerase:fkbp-type rotamase:peptidyl-prolyl cis-trans isomerase:fkbp-typerotamase (gtcfc:10.7) (ec:5.2.1.8) (keggfc:14.1) (tigrfc:12.5) (db:gtc-helicobacter pylori) HP1123 HP1123 Helicobacter pylori 210 -11538916 7000690615 peptidyl-prolyl cis-trans isomerase:fkbp-type rotamase (db:pir2.dat) C64660 C64660 Helicobacter pylori 210 -11538916 7500959394 hp1123 peptidyl-prolyl cis-trans isomerase:fkbp-type (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:17346 percent identity: 40.35;) (le:616) (re:1173) (di:complement) HPAE000619 AE000619 g2314277 Helicobacter pylori 210 -11538916 7502852772 hp1123 peptidyl-prolyl cis-trans isomerase:fkbp-type (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:17346 percent identity: 40.35;) (le:616) (re:1173) (di:complement) HPAE000619 AE000619 g2314277 Helicobacter pylori 26695 85962 -11538916

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903102	17252	39408	1965	654

Description

6500735059 map:hp1299 methionine amino peptidase (gtcfc:10.7) (ec:3.4.11.18) (keggfc:14.1) (tigrfc:12.5) (db:gtc-helicobacter pylori) HP1299 HP1299 Helicobacter pylori 210 -11538917 5500684867 map:hp1299 (sr:,campylobacter pylori) (ec:3.4.11.18) (de:methionine aminopeptidase, (map) (peptidase m)) (db:swissprot) AMPM_HELPY P56102 HELICOBACTER PYLORI 210 -11538917 7000684575 methionine amino peptidase (cl:escherichia coli methionyl aminopeptidase) (db:pir2.dat) C64682 C64682 Helicobacter pylori 210 -11538917 7500876848 hp1299 methionine amino peptidase map (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:15503 percent identity: 43.03;) (le:9006) (re:9767) (di:complement) HPAE000633 AE000633 g2314463 Helicobacter pylori 210 -11538917 7502852773 hp1299 methionine amino peptidase map (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:15503 percent identity: 43.03;) (le:9006) (re:9767) (di:complement) HPAE000633 AE000633 g2314463 Helicobacter pylori 26695 85962 -11538917

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903127	17253	39409	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903134	17254	39410	3267	1088

Description

6500735060 ppi:hp1441 peptidyl-prolyl cis-trans isomerase b:cyclosporin-type rotamase:peptidyl-prolyl cis-trans isomerase b:cyclosporin-type rotamase (gtcfc:10.7) (ec:5.2.1.8) (keggfc:14.1) (tigrfc:12.5) (db:gtc-helicobacter pylori) HP1441 HP1441 Helicobacter pylori 210 -11538918 7000689195 peptidylprolyl isomerase:b:cyclosporin-type rotamase (cl:peptidylprolyl isomerase) (ec:5.2.1.8) (db:pir2.dat) A64700 A64700 Helicobacter pylori 210 -11538918 7500954446 hp1441 peptidyl-prolyl cis-trans isomerase b (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to egad:10504 percent identity: 58.09;) (le:8011) (re:8502) (di:direct) HPAE000644 AE000644 g2314613 Helicobacter pylori 210 -11538918 7502852774 hp1441 peptidyl-prolyl cis-trans isomerase b (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to egad:10504 percent identity: 58.09;) (le:8011) (re:8502) (di:direct) HPAE000644 AE000644 g2314613 Helicobacter pylori 26695 85962 -11538918

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903146	17255	39411	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903154	17256	39412	387	128

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903155	17257	39413	459	152

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903156	17258	39414	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903167	17259	39415	480	159

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903168	17260	39416	474	157

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903176	17261	39417	324	107

Description

6500735061 prfa:hp0077 peptide chain release factor rf-1 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP0077 HP0077 Helicobacter pylori 210 -11538919 5500685822 prfa:hp0077 (sr:,campylobacter pylori) (de:peptide chain release factor 1 (rf-1)) (db:swissprot) RF1_HELPY P55998 HELICOBACTER PYLORI 210 -11538919 7000686308 prfa translation releasing factor rf-1:peptide chain release factor rf-1 (cl:translation releasing factor) (db:pir2.dat) E64529 E64529 Helicobacter pylori 210 -11538919 7500889656 hp0077 peptide chain release factor rf-1 prfa (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:similar to egad:16992 percent identity: 52.59;) (le:5189) (re:6247) (di:direct) HPAE000529 AE000529 g2313158 Helicobacter pylori 210 -11538919 7502852775 hp0077 peptide chain release factor rf-1 prfa (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:similar to egad:16992 percent identity: 52.59;) (le:5189) (re:6247) (di:direct) HPAE000529 AE000529 g2313158 Helicobacter pylori 26695 85962 -11538919

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903185	17262	39418	810	269

Description

6500735062 infc:hp0124 translation initiation factor if-3 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP0124 HP0124 Helicobacter pylori 210 -11538920 5500685418 infc:hp0124 (sr:,campylobacter pylori) (de:translation initiation factor if-3) (db:swissprot) IF3_HELPY P55973 HELICOBACTER PYLORI 210 -11538920 7000685611 translation initiation factor if-3 (cl:translation initiation factor if-3) (db:pir2.dat) D64535 D64535 Helicobacter pylori 210 -11538920 7500883917 hp0124 translation initiation factor if-3 infc (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:similar to egad:12047 percent identity: 43.37;) (le:6097) (re:6708) (di:direct) HPAE000534 AE000534 g2313208 Helicobacter pylori 210 -11538920 7502852776 hp0124 translation initiation factor if-3 infc (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:similar to egad:12047 percent identity: 43.37;) (le:6097) (re:6708) (di:direct) HPAE000534 AE000534 g2313208 Helicobacter pylori 26695 85962 -11538920

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903188	17263	39419	1398	465

Description

6500735063 prfb:hp0171 peptide chain release factor rf-2 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP0171 HP0171 Helicobacter pylori 210 -11538921 5500685826 prfb:hp0171 (sr:,campylobacter pylori) (de:peptide chain release factor 2 (rf-2)) (db:swissprot) RF2_HELPY P55999 HELICOBACTER PYLORI 210 -11538921 7000686310 translation releasing factor rf-2 (cl:translation releasing factor) (db:pir2.dat) C64541 C64541 Helicobacter pylori 210 -11538921 7500889661 hp0171 peptide chain release factor rf-2 prfb (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to egad:14763 percent identity: 49.58;) (le:8784) (re:9875) (di:complement) HPAE000537 AE000537 g2313254 Helicobacter pylori 210 -11538921 7502852777 hp0171 peptide chain release factor rf-2 prfb (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to egad:14763 percent identity: 49.58;) (le:8784) (re:9875) (di:complement) HPAE000537 AE000537 g2313254 Helicobacter pylori 26695 85962 -11538921

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903201	17264	39420	759	252

Description

6500735064 efp:hp0177 translation elongation factor ef-p (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP0177 HP0177 Helicobacter pylori 210 -11538922 5500685152 efp:hp0177 (sr:,campylobacter pylori) (de:elongation factor p (ef-p)) (db:swissprot) EFP_HELPY P56004 HELICOBACTER PYLORI 210 -11538922 7000685142 translation elongation factor ef-p (cl:translation elongation factor ef-p) (db:pir2.dat) A64542 A64542 Helicobacter pylori 210 -11538922 7500880940 hp0177 translation elongation factor ef-p efp (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:similar to egad:13781 percent identity: 45.05;) (le:2107) (re:2670) (di:direct) HPAE000538 AE000538 g2313266 Helicobacter pylori 210 -11538922 7502852778 hp0177 translation elongation factor ef-p efp (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:similar to egad:13781 percent identity: 45.05;) (le:2107) (re:2670) (di:direct) HPAE000538 AE000538 g2313266 Helicobacter pylori 26695 85962 -11538922

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903262	17265	39421	312	103

Description

GTC ORF with score 227 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome i bac t14n5 genomic sequence,complete sequence.) (nt:putative amp-binding protein; highly similar to) (le:46479) (re:48116) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903272	17266	39422	759	252

Description

6500735065 dead:hp0247 atp-dependent rna helicase:dead-box family (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP0247 HP0247 Helicobacter pylori 210 -11538923 7000689655 atp-dependent rna helicase:dead-box family (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) G64550 G64550 Helicobacter pylori 210 -11538923 7500954373 hp0247 atp-dependent rna helicase:dead-box family (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:similar to egad:28878 percent identity: 37.71;) (le:2806) (re:4284) (di:direct) HPAE000544 AE000544 g2313340 Helicobacter pylori 210 -11538923 7502852779 hp0247 atp-dependent rna helicase:dead-box family (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:similar to egad:28878 percent identity: 37.71;) (le:2806) (re:4284) (di:direct) HPAE000544 AE000544 g2313340 Helicobacter pylori 26695 85962 -11538923

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903273	17267	39423	462	153

Description

6500735066 infb:hp1048 translation initiation factor if-2 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP1048 HP1048 Helicobacter pylori 210 -11538924 5500685417 infb:hp1048 (sr:,campylobacter pylori) (de:translation initiation factor if-2) (db:swissprot) IF2_HELPY P55972 HELICOBACTER PYLORI 210 -11538924 7000685610 translation initiation factor if-2 (cl:translation elongation factor tu homology) (db:pir2.dat) H64650 H64650 Helicobacter pylori 210 -11538924 7500883890 hp1048 translation initiation factor if-2 infb (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to egad:9805 percent identity: 45.44;) (le:9121) (re:11955) (di:complement) HPAE000612 AE000612 g2314195 Helicobacter pylori 210 -11538924 7502852780 hp1048 translation initiation factor if-2 infb (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to egad:9805 percent identity: 45.44;) (le:9121) (re:11955) (di:complement) HPAE000612 AE000612 g2314195 Helicobacter pylori 26695 85962 -11538924

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903274	17268	39424	717	238

Description

6500735067 fusa:hp1195 translation elongation factor ef-g (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP1195 HP1195 Helicobacter pylori 210 -11538925 7000689411 translation elongation factor ef-g (cl:translation elongation factor g:translation elongation factor tu homology) (db:pir2.dat) C64669 C64669 Helicobacter pylori 210 -11538925 7500955430 hp1195 translation elongation factor ef-g fusa (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to egad:13592 percent identity: 67.48;) (le:5999) (re:8077) (di:complement) HPAE000625 AE000625 g2314354 Helicobacter pylori 210 -11538925 7502852781 hp1195 translation elongation factor ef-g fusa (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to egad:13592 percent identity: 67.48;) (le:5999) (re:8077) (di:complement) HPAE000625 AE000625 g2314354 Helicobacter pylori 26695 85962 -11538925

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903275	17269	39425	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903277	17270	39426	861	286

Description

6500735068 tufb:hp1205 translation elongation factor ef-tu (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP1205 HP1205 Helicobacter pylori 210 -11538926 5500685156 tuf:hp1205 (sr:,campylobacter pylori) (de:elongation factor tu (ef-tu)) (db:swissprot) EFTU_HELPY P56003 HELICOBACTER PYLORI 210 -11538926 7000685145 translation elongation factor ef-tu (cl:translation elongation factor tu:translation elongation factor tu homology) (db:pir2.dat) E64670 E64670 Helicobacter pylori 210 -11538926 7500880958 hp1205 translation elongation factor ef-tu tufb (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to egad:30858 percent identity: 89.50;) (le:3548) (re:4747) (di:complement) HPAE000626 AE000626 g2314366 Helicobacter pylori 210 -11538926 7502852782 hp1205 translation elongation factor ef-tu tufb (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to egad:30858 percent identity: 89.50;) (le:3548) (re:4747) (di:complement) HPAE000626 AE000626 g2314366 Helicobacter pylori 26695 85962 -11538926

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903279	17271	39427	342	113

Description

6500735069 frr:hp1256 ribosome releasing factor (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP1256 HP1256 Helicobacter pylori 210 -11538927 7500890812 frr:hp1256 (sr:,campylobacter pylori) (de:ribosome recycling factor (ribosome releasing factor) (rrf)) (db:swissprot) RRF_HELPY P56398 HELICOBACTER PYLORI 210 -11538927 7000690691 frr:rrf ribosome releasing factor:ribosome recycling factor:translation releasing factor (cl:ribosome releasing factor) (db:pir1.dat) H64676 H64676 Helicobacter pylori 210 -11538927 7500890814 hp1256 ribosome releasing factor frr (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:29283 percent identity: 43.72;) (le:694) (re:1251) (di:direct) HPAE000631 AE000631 g2314423 Helicobacter pylori 210 -11538927 7502852783 hp1256 ribosome releasing factor frr (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:29283 percent identity: 43.72;) (le:694) (re:1251) (di:direct) HPAE000631 AE000631 g2314423 Helicobacter pylori 26695 85962 -11538927

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903287	17272	39428	579	192

Description

7500955440 infa:hp1298 translation initiation factor ef-1 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP1298 HP1298 Helicobacter pylori 210 -11538928 7000689412 infa translation initiation factor if-1 (cl:translation initiation factor if-1) (db:pir2.dat) B64682 B64682 Helicobacter pylori 210 -11538928 7500955439 hp1298 translation initiation factor ef-1 infa (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:13092 percent identity: 65.28;) (le:8788) (re:9006) (di:complement) HPAE000633 AE000633 g2314483 Helicobacter pylori 210 -11538928 7502852784 infa translation initiation factor if-1 (db:genpept) (de:helicobacter pylori, strain j99 section 108 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1298) (le:6485) (re:6703) (di:complement) AE001547 AE001547 g4155828 Helicobacter pylori J99 85963 -11538928 6500735070 hp1298 translation initiation factor ef-1 infa (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:13092 percent identity: 65.28;) (le:8788) (re:9006) (di:complement) HPAE000633 AE000633 g2314483 Helicobacter pylori 26695 85962 -11538928

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903298	17273	39429	408	135

Description

6500735071 tsf:hp1555 translation elongation factor ef-ts (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.8) (db:gtc-helicobacter pylori) HP1555 HP1555 Helicobacter pylori 210 -11538929 5500685155 tsf:hp1555 (sr:,campylobacter pylori) (de:elongation factor ts (ef-ts)) (db:swissprot) EFTS_HELPY P55975 HELICOBACTER PYLORI 210 -11538929 7000685143 translation elongation factor ef-ts (db:pir2.dat) C64714 C64714 Helicobacter pylori 210 -11538929 7500880945 hp1555 translation elongation factor ef-ts tsf (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:14701 percent identity: 43.14;) (le:5713) (re:6780) (di:direct) HPAE000653 AE000653 g2314738 Helicobacter pylori 210 -11538929 7502852785 hp1555 translation elongation factor ef-ts tsf (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:14701 percent identity: 43.14;) (le:5713) (re:6780) (di:direct) HPAE000653 AE000653 g2314738 Helicobacter pylori 26695 85962 -11538929

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903299	17274	39430	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903304	17275	39431	894	297

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903309	17276	39432	837	278

Description

6500735072 dnag:hp0012 dna primase dnag:dna primase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0012 HP0012 Helicobacter pylori 210 -11538930 5500685753 dnag:hp0012 (sr:,campylobacter pylori) (ec:2.7.7.-) (de:dna primase,) (db:swissprot) PRIM_HELPY P56064 HELICOBACTER PYLORI 210 -11538930 7000686175 dna primase (db:pir2.dat) D64521 D64521 Helicobacter pylori 210 -11538930 7500888463 hp0012 dna primase dnag (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to egad:29168 percent identity: 36.57;) (le:9911) (re:11590) (di:direct) HPAE000523 AE000523 g2313086 Helicobacter pylori 210 -11538930 7502852786 hp0012 dna primase dnag (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to egad:29168 percent identity: 36.57;) (le:9911) (re:11590) (di:direct) HPAE000523 AE000523 g2313086 Helicobacter pylori 26695 85962 -11538930

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903316	17277	39433	522	174

Description

6500735073 dpna:hp0050 adenine specific dna methyltransferase (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0050 HP0050 Helicobacter pylori 210 -11538931 7000689612 adenine specific dna methyltransferase (cl:site-specific dna-methyltransferase (adenine-specific) hpai) (db:pir2.dat) B64526 B64526 Helicobacter pylori 210 -11538931 7500958431 hp0050 adenine specific dna methyltransferase dpna (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:similar to egad:7667 percent identity: 37.39;) (le:11691) (re:12389) (di:complement) HPAE000526 AE000526 g2313123 Helicobacter pylori 210 -11538931 7502852787 hp0050 adenine specific dna methyltransferase dpna (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:similar to egad:7667 percent identity: 37.39;) (le:11691) (re:12389) (di:complement) HPAE000526 AE000526 g2313123 Helicobacter pylori 26695 85962 -11538931

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903321	17278	39434	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903350	17279	39435	1068	355

Description

6500735074 ddem:hp0051 cytosine specific dna methyltransferase (gtcfc:10.8) (ec:2.1.1.73) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0051 HP0051 Helicobacter pylori 210 -11538932 7000689882 cytosine specific dna methyltransferase (cl:dna methyltransferase (cytosine-specific)) (db:pir2.dat) C64526 C64526 Helicobacter pylori 210 -11538932 7500953979 hp0051 cytosine specific dna methyltransferase ddem (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:similar to egad:8482 percent identity: 38.97;) (le:12386) (re:13453) (di:complement) HPAE000526 AE000526 g2313124 Helicobacter pylori 210 -11538932 7502852788 hp0051 cytosine specific dna methyltransferase ddem (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:similar to egad:8482 percent identity: 38.97;) (le:12386) (re:13453) (di:complement) HPAE000526 AE000526 g2313124 Helicobacter pylori 26695 85962 -11538932

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903373	17280	39436	507	168

Description

6500735075 adenine/cytosine dna methyltransferase (gtcfc:10.8) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0054 HP0054 Helicobacter pylori 210 -11538933 7000689618 adenine/cytosine dna methyltransferase (db:pir2.dat) F64526 F64526 Helicobacter pylori 210 -11538933 7500958438 hp0054 adenine/cytosine dna methyltransferase (db:genpept-bct1) (de:helicobacter pylori section 5 of 134 of the complete genome.) (nt:similar to egad:15667 percent identity: 32.12;) (le:2561) (re:5032) (di:complement) HPAE000527 AE000527 g2313132 Helicobacter pylori 210 -11538933 7502852789 hp0054 adenine/cytosine dna methyltransferase (db:genpept) (de:helicobacter pylori 26695 section 5 of 134 of the complete genome.) (nt:similar to egad:15667 percent identity: 32.12;) (le:2561) (re:5032) (di:complement) HPAE000527 AE000527 g2313132 Helicobacter pylori 26695 85962 -11538933

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903379	17281	39437	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903404	17282	39438	2598	865

Description

GTC ORF with score 376 to: (sr:streptomyces thermoviolaceus (strain:opc-520) dna) (db:genpept-bct2) (ec:3.2.1.30) (de:streptomyces thermoviolaceus naga gene forbeta-n-acetylglucosaminidase, complete cds.) (le:400) (re:2298) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903431	17283	39439	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903433	17284	39440	573	191

Description

6500735076 hsdr:hp0091 type ii restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0091 HP0091 Helicobacter pylori 210 -11538934 7000690762 type ii restriction enzyme r protein (db:pir2.dat) C64531 C64531 Helicobacter pylori 210 -11538934 7500959528 hp0091 type ii restriction enzyme r protein hsdr (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:similar to egad:16732 percent identity: 50.74;) (le:394) (re:1227) (di:direct) HPAE000531 AE000531 g2313174 Helicobacter pylori 210 -11538934 7502852790 hp0091 type ii restriction enzyme r protein hsdr (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:similar to egad:16732 percent identity: 50.74;) (le:394) (re:1227) (di:direct) HPAE000531 AE000531 g2313174 Helicobacter pylori 26695 85962 -11538934

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903434	17285	39441	2931	976

Description

6500735077 hsdm:hp0092 type ii restriction enzyme m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0092 HP0092 Helicobacter pylori 210 -11538935 7000689062 type ii restriction enzyme m protein (cl:site-specific dna-methyltransferase (adenine-specific) hpai) (db:pir2.dat) D64531 D64531 Helicobacter pylori 210 -11538935 7500953976 hp0092 type ii restriction enzyme m protein hsdm (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:similar to egad:19903 percent identity: 55.30;) (le:1221) (re:2054) (di:direct) HPAE000531 AE000531 g2313175 Helicobacter pylori 210 -11538935 7502852791 hp0092 type ii restriction enzyme m protein hsdm (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:similar to egad:19903 percent identity: 55.30;) (le:1221) (re:2054) (di:direct) HPAE000531 AE000531 g2313175 Helicobacter pylori 26695 85962 -11538935

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903464	17286	39442	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903470	17287	39443	240	79

Description

6500735078 topa:hp0116 dna topoisomerase i (gtcfc:10.8) (ec:5.99.1.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0116 HP0116 Helicobacter pylori 210 -11538936 5500686071 topa:hp0116 (sr:,campylobacter pylori) (ec:5.99.1.2) (de:(untwisting enzyme) (swivelase)) (db:swissprot) TOP1_HELPY P55991 HELICOBACTER PYLORI 210 -11538936 7000686811 dna topoisomerase i (cl:dna topoisomerase i) (db:pir2.dat) D64534 D64534 Helicobacter pylori 210 -11538936 7500893257 hp0116 dna topoisomerase i topa (db:genpept-bct1) (de:helicobacter pylori section 11 of 134 of the complete genome.) (nt:similar to egad:20536 percent identity: 45.05;) (le:4872) (re:7082) (di:direct) HPAE000533 AE000533 g2313198 Helicobacter pylori 210 -11538936 7502852792 hp0116 dna topoisomerase i topa (db:genpept) (de:helicobacter pylori 26695 section 11 of 134 of the complete genome.) (nt:similar to egad:20536 percent identity: 45.05;) (le:4872) (re:7082) (di:direct) HPAE000533 AE000533 g2313198 Helicobacter pylori 26695 85962 -11538936

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903471	17288	39444	606	201

Description

6500735079 muty:hp0142 a/g-specific adenine glycosylase (gtcfc:10.8) (ec:3.2.2.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0142 HP0142 Helicobacter pylori 210 -11538937 7000689599 a/g-specific adenine glycosylase (db:pir2.dat) F64537 F64537 Helicobacter pylori 210 -11538937 7500958418 hp0142 a/g-specific adenine glycosylase muty (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:similar to egad:19423 percent identity: 38.19;) (le:12087) (re:13073) (di:complement) HPAE000535 AE000535 g2313226 Helicobacter pylori 210 -11538937 7502852793 hp0142 a/g-specific adenine glycosylase muty (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:similar to egad:19423 percent identity: 38.19;) (le:12087) (re:13073) (di:complement) HPAE000535 AE000535 g2313226 Helicobacter pylori 26695 85962 -11538937

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903501	17289	39445	678	225

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903507	17290	39446	1005	334

Description

6500735080 reca:hp0153 recombinase reca:protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0153 HP0153 Helicobacter pylori 210 -11538938 93744 reca:hp0153 (sr:,campylobacter pylori) (de:reca protein) (db:swissprot) RECA_HELPY P42445 HELICOBACTER PYLORI 210 -11538938 7500889541 hp0153 recombinase reca (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to egad:30827 percent identity: 99.14;) (le:6709) (re:7752) (di:direct) HPAE000536 AE000536 g2313235 Helicobacter pylori 210 -11538938 7502852794 hp0153 recombinase reca (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to egad:30827 percent identity: 99.14;) (le:6709) (re:7752) (di:direct) HPAE000536 AE000536 g2313235 Helicobacter pylori 26695 85962 -11538938

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903510	17291	39447	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903512	17292	39448	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903534	17293	39449	420	139

Description

6500735081 gida:hp0213 glucose inhibited division protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0213 HP0213 Helicobacter pylori 210 -11538939 5500685276 gida:hp0213 (sr:,campylobacter pylori) (de:glucose inhibited division protein a) (db:swissprot) GIDA_HELPY P56138 HELICOBACTER PYLORI 210 -11538939 7000685388 glucose inhibited division protein (cl:gida protein) (db:pir2.dat) E64546 E64546 Helicobacter pylori 210 -11538939 7500882339 hp0213 glucose inhibited division protein gida (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:similar to egad:29206 percent identity: 48.46;) (le:5621) (re:7486) (di:complement) HPAE000541 AE000541 g2313303 Helicobacter pylori 210 -11538939 7502852795 hp0213 glucose inhibited division protein gida (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:similar to egad:29206 percent identity: 48.46;) (le:5621) (re:7486) (di:complement) HPAE000541 AE000541 g2313303 Helicobacter pylori 26695 85962 -11538939

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903541	17294	39450	258	85

Description

6500735082 mod:hp0260 adenine specific dna methyltransferase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0260 HP0260 Helicobacter pylori 210 -11538940 7000689614 adenine specific dna methyltransferase (db:pir2.dat) D64552 D64552 Helicobacter pylori 210 -11538940 7500958434 hp0260 adenine specific dna methyltransferase mod (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to egad:7342 percent identity: 33.85;) (le:4749) (re:5903) (di:complement) HPAE000545 AE000545 g2313354 Helicobacter pylori 210 -11538940 7502852796 hp0260 adenine specific dna methyltransferase mod (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to egad:7342 percent identity: 33.85;) (le:4749) (re:5903) (di:complement) HPAE000545 AE000545 g2313354 Helicobacter pylori 26695 85962 -11538940

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903542	17295	39451	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903544	17296	39452	414	137

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903566	17297	39453	612	203

Description

GTC ORF with score 123 to: (sr:chlamydomonas reinhardtii (strain cc-621) vegetative cdna to mrna) (db:genpept-pln1) (de:chlamydomonas reinhardtii structural wall protein (vsp1) mrna,complete cds.) (le:273) (re:1175) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903568	17298	39454	231	76

Description

6500735083 hpaim:hp0263 adenine specific dna methyltransferase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0263 HP0263 Helicobacter pylori 210 -11538941 7000689617 adenine specific dna methyltransferase (cl:site-specific dna-methyltransferase (adenine-specific) hpai) (db:pir2.dat) G64552 G64552 Helicobacter pylori 210 -11538941 7500958437 hp0263 adenine specific dna methyltransferase hpaim (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to egad:14169 percent identity: 33.94;) (le:7166) (re:7924) (di:direct) HPAE000545 AE000545 g2313355 Helicobacter pylori 210 -11538941 7502852797 hp0263 adenine specific dna methyltransferase hpaim (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to egad:14169 percent identity: 33.94;) (le:7166) (re:7924) (di:direct) HPAE000545 AE000545 g2313355 Helicobacter pylori 26695 85962 -11538941

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903580	17299	39455	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903591	17300	39456	204	67

Description

6500735084 nuc:hp0323 membrane bound endolease:membrane bound endonuclease (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0323 HP0323 Helicobacter pylori 210 -11538942 7000690512 membrane bound endonuclease (db:pir2.dat) C64560 C64560 Helicobacter pylori 210 -11538942 7500959305 hp0323 membrane bound endonuclease nuc (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:16462 percent identity: 31.13;) (le:5206) (re:5748) (di:direct) HPAE000550 AE000550 g2313422 Helicobacter pylori 210 -11538942 7502852798 hp0323 membrane bound endonuclease nuc (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:16462 percent identity: 31.13;) (le:5206) (re:5748) (di:direct) HPAE000550 AE000550 g2313422 Helicobacter pylori 26695 85962 -11538942

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903592	17301	39457	471	156

Description

6500735085 recj:hp0348 single-stranded-dna-specific exonuclease (gtcfc:10.8) (ec:3.1.-.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0348 HP0348 Helicobacter pylori 210 -11538943 7000690708 single-stranded-dna-specific exonuclease (db:pir2.dat) D64563 D64563 Helicobacter pylori 210 -11538943 7500959475 hp0348 single-stranded-dna-specific exonuclease recj (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:similar to egad:24228 percent identity: 33.56;) (le:9574) (re:11124) (di:complement) HPAE000551 AE000551 g2313437 Helicobacter pylori 210 -11538943 7502852799 hp0348 single-stranded-dna-specific exonuclease recj (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:similar to egad:24228 percent identity: 33.56;) (le:9574) (re:11124) (di:complement) HPAE000551 AE000551 g2313437 Helicobacter pylori 26695 85962 -11538943

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903599	17302	39458	264	87

Description

6500735086 pria:hp0387 primosomal protein replication factor (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0387 HP0387 Helicobacter pylori 210 -11538944 7500888452 pria:hp0387 (sr:,campylobacter pylori) (de:primosomal protein n' (replication factor y)) (db:swissprot) PRIA_HELPY O25149 HELICOBACTER PYLORI 210 -11538944 7000690639 primosomal protein replication factor (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) C64568 C64568 Helicobacter pylori 210 -11538944 7500888454 hp0387 primosomal protein replication factor pria (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:28978 percent identity: 36.28;) (le:4279) (re:6138) (di:direct) HPAE000555 AE000555 g2313488 Helicobacter pylori 210 -11538944 7502852800 hp0387 primosomal protein replication factor pria (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:28978 percent identity: 36.28;) (le:4279) (re:6138) (di:direct) HPAE000555 AE000555 g2313488 Helicobacter pylori 26695 85962 -11538944

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903601	17303	39459	354	117

Description

6500735087 topa:hp0440 dna topoisomerase i (gtcfc:10.8) (ec:5.99.1.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0440 HP0440 Helicobacter pylori 210 -11538945 7000689908 dna topoisomerase i (db:pir2.dat) H64574 H64574 Helicobacter pylori 210 -11538945 7500958704 hp0440 dna topoisomerase i topa (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:similar to egad:28359 percent identity: 31.75;) (le:8990) (re:11023) (di:complement) HPAE000559 AE000559 g2313542 Helicobacter pylori 210 -11538945 7502852801 hp0440 dna topoisomerase i topa (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:similar to egad:28359 percent identity: 31.75;) (le:8990) (re:11023) (di:complement) HPAE000559 AE000559 g2313542 Helicobacter pylori 26695 85962 -11538945

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903603	17304	39460	285	94

Description

6500735088 hsds:hp0462 type i restriction enzyme s protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0462 HP0462 Helicobacter pylori 210 -11538946 7000690760 type i restriction enzyme s protein (db:pir2.dat) F64577 F64577 Helicobacter pylori 210 -11538946 7500959526 hp0462 type i restriction enzyme s protein hsds (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to egad:44312 percent identity: 37.04;) (le:5903) (re:7000) (di:complement) HPAE000561 AE000561 g2313566 Helicobacter pylori 210 -11538946 7502852802 hp0462 type i restriction enzyme s protein hsds (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to egad:44312 percent identity: 37.04;) (le:5903) (re:7000) (di:complement) HPAE000561 AE000561 g2313566 Helicobacter pylori 26695 85962 -11538946

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903604	17305	39461	255	84

Description

6500735089 hsdm:hp0463 type i restriction enzyme m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0463 HP0463 Helicobacter pylori 210 -11538947 7000690755 type i restriction enzyme m protein (db:pir2.dat) G64577 G64577 Helicobacter pylori 210 -11538947 7500959521 hp0463 type i restriction enzyme m protein hsdm (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to egad:7636 percent identity: 29.43;) (le:7160) (re:8623) (di:complement) HPAE000561 AE000561 g2313567 Helicobacter pylori 210 -11538947 7502852803 hp0463 type i restriction enzyme m protein hsdm (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to egad:7636 percent identity: 29.43;) (le:7160) (re:8623) (di:complement) HPAE000561 AE000561 g2313567 Helicobacter pylori 26695 85962 -11538947

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903609	17306	39462	594	197

Description

6500735090 hsdr:hp0464 type i restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0464 HP0464 Helicobacter pylori 210 -11538948 7000690758 type i restriction enzyme r protein (db:pir2.dat) H64577 H64577 Helicobacter pylori 210 -11538948 7500959524 hp0464 type i restriction enzyme r protein hsdr (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:contingency gene.; similar to egad:43825 percent) (le:8616) (re:11783) (di:complement) HPAE000561 AE000561 g2313568 Helicobacter pylori 210 -11538948 7502852804 hp0464 type i restriction enzyme r protein hsdr (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:contingency gene.; similar to egad:43825 percent) (le:8616) (re:11783) (di:complement) HPAE000561 AE000561 g2313568 Helicobacter pylori 26695 85962 -11538948

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903618	17307	39463	2205	734

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903627	17308	39464	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903630	17309	39465	276	91

Description

6500735091 vspim:hp0478 adenine specific dna methyltransferase (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0478 HP0478 Helicobacter pylori 210 -11538949 7000689615 adenine specific dna methyltransferase (db:pir2.dat) F64579 F64579 Helicobacter pylori 210 -11538949 7500958435 hp0478 adenine specific dna methyltransferase vspim (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to egad:7735 percent identity: 42.07;) (le:7401) (re:9038) (di:direct) HPAE000562 AE000562 g2313588 Helicobacter pylori 210 -11538949 7502852805 hp0478 adenine specific dna methyltransferase vspim (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to egad:7735 percent identity: 42.07;) (le:7401) (re:9038) (di:direct) HPAE000562 AE000562 g2313588 Helicobacter pylori 26695 85962 -11538949

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903635	17310	39466	1233	410

Description

6500735092 mfoki:hp0481 adenine specific dna methyltransferase (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0481 HP0481 Helicobacter pylori 210 -11538950 7500975634 hp0481 adenine specific dna methyltransferase mfoki (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to egad:19816 percent identity: 29.29;) (le:11713) (re:12348) (di:direct) HPAE000562 AE000562 g2313590 Helicobacter pylori 210 -11538950 7502852806 hp0481 adenine specific dna methyltransferase mfoki (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to egad:19816 percent identity: 29.29;) (le:11713) (re:12348) (di:direct) HPAE000562 AE000562 g2313590 Helicobacter pylori 26695 85962 -11538950

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903638	17311	39467	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903643	17312	39468	951	316

Description

GTC ORF with score 136 to: (fn:binds to gtp-bound form of rho and binds to) (sr:house mouse) (db:genpept-rod) (de:mus musculus p140mdia mrna, complete cds.) (nt:a formin related polyproline protein; similar to) (le:94) (re:3861) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903646	17313	39469	1992	663

Description

6500735093 gyrb:hp0501 dna gyrase:sub b gyrb:dna gyrase:sub b (gtcfc:10.8) (ec:5.99.1.3) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0501 HP0501 Helicobacter pylori 210 -11538951 5500685322 gyrb:hp0501 (sr:,campylobacter pylori) (ec:5.99.1.3) (de:dna gyrase subunit b,) (db:swissprot) GYRB_HELPY P55992 HELICOBACTER PYLORI 210 -11538951 7000685496 dna gyrase:sub b (cl:dna topoisomerase (atp-hydrolyzing) chain b) (db:pir2.dat) E64582 E64582 Helicobacter pylori 210 -11538951 7500882883 hp0501 dna gyrase:sub b gyrb (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:29202 percent identity: 45.96;) (le:10926) (re:13247) (di:direct) HPAE000564 AE000564 g2313611 Helicobacter pylori 210 -11538951 7502852807 hp0501 dna gyrase:sub b gyrb (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:29202 percent identity: 45.96;) (le:10926) (re:13247) (di:direct) HPAE000564 AE000564 g2313611 Helicobacter pylori 26695 85962 -11538951

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903649	17314	39470	480	159

Description

6500735094 endonuclease iii nth:endonuclease iii:nth (gtcfc:10.8) (ec:4.2.99.18) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0585 HP0585 Helicobacter pylori 210 -11538952 7000689910 endonuclease iii (cl:apurinic/apyrimidinic endonuclease class ii) (db:pir2.dat) A64593 A64593 Helicobacter pylori 210 -11538952 7500958706 hp0585 endonuclease iii nth (db:genpept-bct1) (de:helicobacter pylori section 50 of 134 of the complete genome.) (nt:similar to egad:28677 percent identity: 40.10;) (le:71) (re:727) (di:complement) HPAE000572 AE000572 g2313704 Helicobacter pylori 210 -11538952 7502852808 hp0585 endonuclease iii nth (db:genpept) (de:helicobacter pylori 26695 section 50 of 134 of the complete genome.) (nt:similar to egad:28677 percent identity: 40.10;) (le:71) (re:727) (di:complement) HPAE000572 AE000572 g2313704 Helicobacter pylori 26695 85962 -11538952

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903652	17315	39471	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903714	17316	39472	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903720	17317	39473	2214	737

Description

6500735095 res:hp0592 type iii triction enzyme r protein:type iii restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0592 HP0592 Helicobacter pylori 210 -11538953 7000690767 type iii restriction enzyme r protein (db:pir2.dat) H64593 H64593 Helicobacter pylori 210 -11538953 7500959531 hp0592 type iii restriction enzyme r protein res (db:genpept-bct1) (de:helicobacter pylori section 50 of 134 of the complete genome.) (nt:similar to egad:30631 percent identity: 30.63;) (le:7929) (re:10934) (di:direct) HPAE000572 AE000572 g2313710 Helicobacter pylori 210 -11538953 7502852809 hp0592 type iii restriction enzyme r protein res (db:genpept) (de:helicobacter pylori 26695 section 50 of 134 of the complete genome.) (nt:similar to egad:30631 percent identity: 30.63;) (le:7929) (re:10934) (di:direct) HPAE000572 AE000572 g2313710 Helicobacter pylori 26695 85962 -11538953

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903724	17318	39474	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903728	17319	39475	297	98

Description

6500735096 mod:hp0593 adenine specific dna methyltransferase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0593 HP0593 Helicobacter pylori 210 -11538954 7000689611 adenine specific dna methyltransferase (db:pir2.dat) A64594 A64594 Helicobacter pylori 210 -11538954 7500958430 hp0593 adenine specific dna methyltransferase mod (db:genpept-bct1) (de:helicobacter pylori section 51 of 134 of the complete genome.) (nt:similar to egad:7342 percent identity: 38.46;) (le:67) (re:1863) (di:direct) HPAE000573 AE000573 g2313713 Helicobacter pylori 210 -11538954 7502852810 hp0593 adenine specific dna methyltransferase mod (db:genpept) (de:helicobacter pylori 26695 section 51 of 134 of the complete genome.) (nt:similar to egad:7342 percent identity: 38.46;) (le:67) (re:1863) (di:direct) HPAE000573 AE000573 g2313713 Helicobacter pylori 26695 85962 -11538954

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903763	17320	39476	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903768	17321	39477	471	156

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903779	17322	39478	531	176

Description

6500735097 endonuclease iii (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0602 HP0602 Helicobacter pylori 210 -11538955 7000689911 endonuclease iii (db:pir2.dat) B64595 B64595 Helicobacter pylori 210 -11538955 7500958707 hp0602 endonuclease iii (db:genpept-bct1) (de:helicobacter pylori section 52 of 134 of the complete genome.) (nt:similar to egad:44038 percent identity: 36.60;) (le:1762) (re:2418) (di:direct) HPAE000574 AE000574 g2313723 Helicobacter pylori 210 -11538955 7502852811 hp0602 endonuclease iii (db:genpept) (de:helicobacter pylori 26695 section 52 of 134 of the complete genome.) (nt:similar to egad:44038 percent identity: 36.60;) (le:1762) (re:2418) (di:direct) HPAE000574 AE000574 g2313723 Helicobacter pylori 26695 85962 -11538955

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903781	17323	39479	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903783	17324	39480	735	244

Description

6500735098 dna ligase lig:dna ligase:lig (gtcfc:10.8) (ec:6.5.1.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0615 HP0615 Helicobacter pylori 210 -11538956 7500880524 liga:lig:hp0615 (sr:,campylobacter pylori) (ec:6.5.1.2) (de:dna ligase, (polydeoxyribonucleotide synthase (nad+))) (db:swissprot) DNLJ_HELPY O25336 HELICOBACTER PYLORI 210 -11538956 7000689899 dna ligase nad+ (cl:polydeoxyribonucleotide synthase (nad+)) (ec:6.5.1.2) (db:pir1.dat) G64596 G64596 Helicobacter pylori 210 -11538956 7500880526 hp0615 dna ligase lig (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:similar to egad:28109 percent identity: 40.12;) (le:617) (re:2587) (di:complement) HPAE000576 AE000576 g2313737 Helicobacter pylori 210 -11538956 7502852812 hp0615 dna ligase lig (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:similar to egad:28109 percent identity: 40.12;) (le:617) (re:2587) (di:complement) HPAE000576 AE000576 g2313737 Helicobacter pylori 26695 85962 -11538956

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903800	17325	39481	729	242

Description

6500735099 muts:hp0621 dna mismatch repair protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0621 HP0621 Helicobacter pylori 210 -11538957 7502852813 muts2:hp0621 (sr:,campylobacter pylori) (de:muts2 protein) (db:swissprot) MSU2_HELPY O25338 HELICOBACTER PYLORI 210 -11538957 7000689900 dna mismatch repair protein (db:pir2.dat) E64597 E64597 Helicobacter pylori 210 -11538957 7500958696 hp0621 dna mismatch repair protein muts (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:similar to egad:48571 percent identity: 32.58;) (le:7958) (re:10246) (di:complement) HPAE000576 AE000576 g2313742 Helicobacter pylori 210 -11538957 7502852814 hp0621 dna mismatch repair protein muts (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:similar to egad:48571 percent identity: 32.58;) (le:7958) (re:10246) (di:complement) HPAE000576 AE000576 g2313742 Helicobacter pylori 26695 85962 -11538957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903803	17326	39482	636	211

Description

6500735100 rnha:hp0661 ribonuclease h rnha:ribonuclease h (gtcfc:10.8) (ec:3.1.26.4) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0661 HP0661 Helicobacter pylori 210 -11538958 5500685889 rnha:hp0661 (sr:,campylobacter pylori) (ec:3.1.26.4) (de:ribonuclease h, (rnase h)) (db:swissprot) RNH_HELPY P56120 HELICOBACTER PYLORI 210 -11538958 7000686425 ribonuclease h (cl:ribonuclease h) (db:pir2.dat) E64602 E64602 Helicobacter pylori 210 -11538958 7500890451 hp0661 ribonuclease h rnha (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:27813 percent identity: 58.39;) (le:10142) (re:10573) (di:direct) HPAE000579 AE000579 g2313784 Helicobacter pylori 210 -11538958 7502852815 hp0661 ribonuclease h rnha (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:27813 percent identity: 58.39;) (le:10142) (re:10573) (di:direct) HPAE000579 AE000579 g2313784 Helicobacter pylori 26695 85962 -11538958

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903806	17327	39483	537	178

Description

6500735101 xerc:hp0675 integrase/recombinase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0675 HP0675 Helicobacter pylori 210 -11538959 7000690478 integrase/recombinase (db:pir2.dat) C64604 C64604 Helicobacter pylori 210 -11538959 7500959264 hp0675 integrase/recombinase xerc (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:similar to egad:24225 percent identity: 31.80;) (le:10477) (re:11565) (di:direct) HPAE000580 AE000580 g2313795 Helicobacter pylori 210 -11538959 7502852816 hp0675 integrase/recombinase xerc (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:similar to egad:24225 percent identity: 31.80;) (le:10477) (re:11565) (di:direct) HPAE000580 AE000580 g2313795 Helicobacter pylori 26695 85962 -11538959

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903807	17328	39484	564	187

Description

GTC ORF with score 320 to: (sr:thale cress) (db:genpept-pln1) (de:genomic sequence of arabidopsis bac f8a5, complete sequence.) (nt:highly similar to auxin-induced protein (aldo/keto) (le:73882:74320:74497) (re:74220:74422:74669) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903808	17329	39485	990	329

Description

6500735102 dat1:hp0676 methylated-dna--protein-cysteine methyltransferase:methylated-dna--protein-cysteinemethyltransferase (gtcfc:10.8) (ec:2.1.1.63) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0676 HP0676 Helicobacter pylori 210 -11538960 7000690518 methylated-dna--protein-cysteine methyltransferase (cl:methylated-dna--protein-cysteine s-methyltransferase homology) (db:pir2.dat) D64604 D64604 Helicobacter pylori 210 -11538960 7500959310 hp0676 methylated-dna--protein-cysteine (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:similar to egad:29038 percent identity: 40.97;) (le:61) (re:567) (di:complement) HPAE000581 AE000581 g2313803 Helicobacter pylori 210 -11538960 7502852817 hp0676 methylated-dna--protein-cysteine (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:similar to egad:29038 percent identity: 40.97;) (le:61) (re:567) (di:complement) HPAE000581 AE000581 g2313803 Helicobacter pylori 26695 85962 -11538960

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903814	17330	39486	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903830	17331	39487	510	169

Description

6500735103 gyra:hp0701 dna gyrase:sub a gyra:dna gyrase subunit a (gtcfc:10.8) (ec:5.99.1.3) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0701 HP0701 Helicobacter pylori 210 -11538961 75199 gyra:hp0701 (sr:,campylobacter pylori) (ec:5.99.1.3) (de:dna gyrase subunit a,) (db:swissprot) GYRA_HELPY P48370 HELICOBACTER PYLORI 210 -11538961 7000685494 dna gyrase:sub a (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (db:pir2.dat) E64607 E64607 Helicobacter pylori 210 -11538961 7500882875 hp0701 dna gyrase:sub a gyra (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:similar to egad:19444 percent identity: 97.45;) (le:1680) (re:4163) (di:direct) HPAE000583 AE000583 g2313826 Helicobacter pylori 210 -11538961 7502852818 hp0701 dna gyrase:sub a gyra (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:similar to egad:19444 percent identity: 97.45;) (le:1680) (re:4163) (di:direct) HPAE000583 AE000583 g2313826 Helicobacter pylori 26695 85962 -11538961

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903836	17332	39488	831	276

Description

6500735104 uvra:hp0705 excinuclease abc subunit a (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0705 HP0705 Helicobacter pylori 210 -11538962 7500893887 uvra:hp0705 (sr:,campylobacter pylori) (de:excinuclease abc subunit a) (db:swissprot) UVRA_HELPY P56474 HELICOBACTER PYLORI 210 -11538962 7000689378 excinuclease abc chain a:excision endonuclease abc::chain a:uvra protein (cl:excinuclease abc chain a:atp-binding cassette homology) (ec:3.1.-.-) (db:pir2.dat) A64608 A64608 Helicobacter pylori 210 -11538962 7500893889 hp0705 excinuclease abc subunit a uvra (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:similar to egad:28894 percent identity: 53.44;) (le:6450) (re:9257) (di:complement) HPAE000583 AE000583 g2313828 Helicobacter pylori 210 -11538962 7502852819 hp0705 excinuclease abc subunit a uvra (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:similar to egad:28894 percent identity: 53.44;) (le:6450) (re:9257) (di:complement) HPAE000583 AE000583 g2313828 Helicobacter pylori 26695 85962 -11538962

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903838	17333	39489	3045	1015

Description

6500735105 prrb:hp0790 anti-codon nuclease masking agent (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0790 HP0790 Helicobacter pylori 210 -11538963 7000689640 anti-codon nuclease masking agent (db:pir2.dat) F64618 F64618 Helicobacter pylori 210 -11538963 7500958457 hp0790 anti-codon nuclease masking agent prrb (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:similar to egad:9642 percent identity: 42.90;) (le:2031) (re:3326) (di:complement) HPAE000591 AE000591 g2313919 Helicobacter pylori 210 -11538963 7502852820 hp0790 anti-codon nuclease masking agent prrb (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:similar to egad:9642 percent identity: 42.90;) (le:2031) (re:3326) (di:complement) HPAE000591 AE000591 g2313919 Helicobacter pylori 26695 85962 -11538963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903867	17334	39490	792	263

Description

6500735106 uvrc:hp0821 excinuclease abc subunit c (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0821 HP0821 Helicobacter pylori 210 -11538964 7500893913 uvrc:hp0821 (sr:,campylobacter pylori) (de:excinuclease abc subunit c) (db:swissprot) UVRC_HELPY P56428 HELICOBACTER PYLORI 210 -11538964 7000689435 excinuclease abc chain c:excision endonuclease abc::chain c:uvrc protein (cl:excinuclease abc chain c) (ec:3.1.-.-) (db:pir2.dat) E64622 E64622 Helicobacter pylori 210 -11538964 7500893915 hp0821 excinuclease abc subunit c uvrc (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:27892 percent identity: 31.46;) (le:7813) (re:9597) (di:direct) HPAE000593 AE000593 g2313951 Helicobacter pylori 210 -11538964 7502852821 hp0821 excinuclease abc subunit c uvrc (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:27892 percent identity: 31.46;) (le:7813) (re:9597) (di:direct) HPAE000593 AE000593 g2313951 Helicobacter pylori 26695 85962 -11538964

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903874	17335	39491	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903880	17336	39492	339	112

Description

GTC ORF with score 169 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 37 kb genomic dna, clone c213.) (nt:similar to s.cerevisiae hlj1 protein: swiss_prot) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903881	17337	39493	882	293

Description

GTC ORF with score 307 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 37 kb genomic dna, clone c213.) (nt:similar to s.cerevisiae hlj1 protein: swiss_prot) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903885	17338	39494	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903898	17339	39495	495	164

Description

6500735107 hsdr:hp0846 type i restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0846 HP0846 Helicobacter pylori 210 -11538965 7000690757 type i restriction enzyme r protein (db:pir2.dat) F64625 F64625 Helicobacter pylori 210 -11538965 7500959523 hp0846 type i restriction enzyme r protein hsdr (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:similar to egad:10320 percent identity: 47.99;) (le:9359) (re:11959) (di:complement) HPAE000595 AE000595 g2313977 Helicobacter pylori 210 -11538965 7502852822 hp0846 type i restriction enzyme r protein hsdr (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:similar to egad:10320 percent identity: 47.99;) (le:9359) (re:11959) (di:complement) HPAE000595 AE000595 g2313977 Helicobacter pylori 26695 85962 -11538965

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903902	17340	39496	987	328

Description

6500735108 hsds:hp0848 type i restriction enzyme s protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0848 HP0848 Helicobacter pylori 210 -11538966 7000690761 type i restriction enzyme s protein (db:pir2.dat) H64625 H64625 Helicobacter pylori 210 -11538966 7500959527 hp0848 type i restriction enzyme s protein hsds (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:28863 percent identity: 36.99;) (le:279) (re:1175) (di:complement) HPAE000596 AE000596 g2313983 Helicobacter pylori 210 -11538966 7502852823 hp0848 type i restriction enzyme s protein hsds (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:28863 percent identity: 36.99;) (le:279) (re:1175) (di:complement) HPAE000596 AE000596 g2313983 Helicobacter pylori 26695 85962 -11538966

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903909	17341	39497	426	141

Description

6500735109 hsdm:hp0850 type i restriction enzyme m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0850 HP0850 Helicobacter pylori 210 -11538967 7000690753 type i restriction enzyme m protein (cl:type i site-specific deoxyribonuclease chain hsdm) (db:pir2.dat) B64626 B64626 Helicobacter pylori 210 -11538967 7500959519 hp0850 type i restriction enzyme m protein hsdm (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:7636 percent identity: 54.42;) (le:1560) (re:3143) (di:complement) HPAE000596 AE000596 g2313984 Helicobacter pylori 210 -11538967 7502852824 hp0850 type i restriction enzyme m protein hsdm (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:7636 percent identity: 54.42;) (le:1560) (re:3143) (di:complement) HPAE000596 AE000596 g2313984 Helicobacter pylori 26695 85962 -11538967

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903915	17342	39498	2019	672

Description

6500735110 ruvc:hp0877 holliday junction endodeoxyribonuclease (gtcfc:10.8) (ec:3.1.22.4) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0877 HP0877 Helicobacter pylori 210 -11538968 7502852825 ruvc:hp0877 (sr:,campylobacter pylori) (ec:3.1.22.4) (de:junction nuclease ruvc) (holliday juction resolvase ruvc)) (db:swissprot) RUVC_HELPY O25544 HELICOBACTER PYLORI 210 -11538968 7000689992 holliday junction endodeoxyribonuclease (cl:dna repair protein ruvc) (db:pir2.dat) E64629 E64629 Helicobacter pylori 210 -11538968 7500958772 hp0877 holliday junction endodeoxyribonuclease ruvc (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:similar to egad:13020 percent identity: 34.67;) (le:7140) (re:7613) (di:complement) HPAE000597 AE000597 g2314012 Helicobacter pylori 210 -11538968 7502852826 hp0877 holliday junction endodeoxyribonuclease ruvc (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:similar to egad:13020 percent identity: 34.67;) (le:7140) (re:7613) (di:complement) HPAE000597 AE000597 g2314012 Helicobacter pylori 26695 85962 -11538968

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ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903925	17343	39499	795	264

Description

6500735111 ruva:hp0883 holliday junction dna helicase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0883 HP0883 Helicobacter pylori 210 -11538969 7500891222 ruva:hp0883 (sr:,campylobacter pylori) (de:probable holliday junction dna helicase ruva) (db:swissprot) RUVA_HELPY O25549 HELICOBACTER PYLORI 210 -11538969 7000689991 holliday junction dna helicase (db:pir2.dat) C64630 C64630 Helicobacter pylori 210 -11538969 7500891224 hp0883 holliday junction dna helicase ruva (db:genpept-bct1) (de:helicobacter pylori section 76 of 134 of the complete genome.) (nt:similar to egad:28944 percent identity: 39.01;) (le:375) (re:926) (di:complement) HPAE000598 AE000598 g2314020 Helicobacter pylori 210 -11538969 7502852827 hp0883 holliday junction dna helicase ruva (db:genpept) (de:helicobacter pylori 26695 section 76 of 134 of the complete genome.) (nt:similar to egad:28944 percent identity: 39.01;) (le:375) (re:926) (di:complement) HPAE000598 AE000598 g2314020 Helicobacter pylori 26695 85962 -11538969

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903938	17344	39500	621	206

Description

6500735112 hindiim:hp0910 adenine specific dna methyltransferase (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0910 HP0910 Helicobacter pylori 210 -11538970 7000689616 site-specific dna-methyltransferase adenine-specific (cl:site-specific dna-methyltransferase (adenine-specific) hincii) (ec:2.1.1.72) (db:pir2.dat) F64633 F64633 Helicobacter pylori 210 -11538970 7500958436 hp0910 adenine specific dna methyltransferase (db:genpept-bct1) (de:helicobacter pylori section 78 of 134 of the complete genome.) (nt:similar to egad:29139 percent identity: 33.44;) (le:5163) (re:6302) (di:direct) HPAE000600 AE000600 g2314045 Helicobacter pylori 210 -11538970 7502852828 hp0910 adenine specific dna methyltransferase (db:genpept) (de:helicobacter pylori 26695 section 78 of 134 of the complete genome.) (nt:similar to egad:29139 percent identity: 33.44;) (le:5163) (re:6302) (di:direct) HPAE000600 AE000600 g2314045 Helicobacter pylori 26695 85962 -11538970

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903959	17345	39501	1026	341

Description

6500735113 recr:hp0925 recombinational dna repair protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0925 HP0925 Helicobacter pylori 210 -11538971 7500889592 recr:hp0925 (sr:,campylobacter pylori) (de:recombination protein recr) (db:swissprot) RECR_HELPY P56214 HELICOBACTER PYLORI 210 -11538971 7000690677 recombinational dna repair protein (db:pir2.dat) E64635 E64635 Helicobacter pylori 210 -11538971 7500889594 hp0925 recombinational dna repair protein recr (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:29069 percent identity: 36.46;) (le:9243) (re:9824) (di:direct) HPAE000602 AE000602 g2314062 Helicobacter pylori 210 -11538971 7502852829 hp0925 recombinational dna repair protein recr (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:29069 percent identity: 36.46;) (le:9243) (re:9824) (di:direct) HPAE000602 AE000602 g2314062 Helicobacter pylori 26695 85962 -11538971

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903962	17346	39502	255	84

Description

6500735114 xerd:hp0995 integrase/recombinase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP0995 HP0995 Helicobacter pylori 210 -11538972 7000690479 integrase/recombinase (db:pir2.dat) C64644 C64644 Helicobacter pylori 210 -11538972 7500959265 hp0995 integrase/recombinase xerd (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:similar to egad:24225 percent identity: 27.75;) (le:189) (re:1256) (di:complement) HPAE000608 AE000608 g2314140 Helicobacter pylori 210 -11538972 7502852830 hp0995 integrase/recombinase xerd (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:similar to egad:24225 percent identity: 27.75;) (le:189) (re:1256) (di:complement) HPAE000608 AE000608 g2314140 Helicobacter pylori 26695 85962 -11538972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903968	17347	39503	642	213

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903971	17348	39504	417	138

Description

6500735115 site-specific recombinase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1009 HP1009 Helicobacter pylori 210 -11538973 7000690709 site-specific recombinase (db:pir2.dat) A64646 A64646 Helicobacter pylori 210 -11538973 7500959476 hp1009 site-specific recombinase (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:similar to egad:15354 percent identity: 21.31;) (le:3523) (re:4083) (di:complement) HPAE000609 AE000609 g2314158 Helicobacter pylori 210 -11538973 7502852831 hp1009 site-specific recombinase (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:similar to egad:15354 percent identity: 21.31;) (le:3523) (re:4083) (di:complement) HPAE000609 AE000609 g2314158 Helicobacter pylori 26695 85962 -11538973

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903975	17349	39505	234	77

Description

6500735116 ruvb:hp1059 holliday junction dna helicase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1059 HP1059 Helicobacter pylori 210 -11538974 7500891236 ruvb:hp1059 (sr:,campylobacter pylori) (de:holliday junction dna helicase ruvb) (db:swissprot) RUVB_HELPY O25699 HELICOBACTER PYLORI 210 -11538974 7000689416 holliday junction dna helicase (cl:ruvb protein) (db:pir2.dat) C64652 C64652 Helicobacter pylori 210 -11538974 7500891238 hp1059 holliday junction dna helicase ruvb (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:similar to egad:28943 percent identity: 54.63;) (le:6341) (re:7351) (di:direct) HPAE000613 AE000613 g2314203 Helicobacter pylori 210 -11538974 7502852832 hp1059 holliday junction dna helicase ruvb (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:similar to egad:28943 percent identity: 54.63;) (le:6341) (re:7351) (di:direct) HPAE000613 AE000613 g2314203 Helicobacter pylori 26695 85962 -11538974

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903980	17350	39506	369	122

Description

6500735117 gidb:hp1063 glucose-inhibited division protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1063 HP1063 Helicobacter pylori 210 -11538975 7500882350 gidb:hp1063 (sr:,campylobacter pylori) (de:glucose inhibited division protein b) (db:swissprot) GIDB_HELPY O25703 HELICOBACTER PYLORI 210 -11538975 7000689963 glucose-inhibited division protein (db:pir2.dat) G64652 G64652 Helicobacter pylori 210 -11538975 7500882352 hp1063 glucose-inhibited division protein gidb (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:similar to egad:24336 percent identity: 32.89;) (le:9690) (re:10226) (di:direct) HPAE000613 AE000613 g2314206 Helicobacter pylori 210 -11538975 7502852833 hp1063 glucose-inhibited division protein gidb (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:similar to egad:24336 percent identity: 32.89;) (le:9690) (re:10226) (di:direct) HPAE000613 AE000613 g2314206 Helicobacter pylori 26695 85962 -11538975

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903989	17351	39507	3324	1107

Description

6500735118 uvrb:hp1114 excinuclease abc subunit b (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1114 HP1114 Helicobacter pylori 210 -11538976 5500686140 uvrb:hp1114 (sr:,campylobacter pylori) (de:excinuclease abc subunit b) (db:swissprot) UVRB_HELPY P94846 HELICOBACTER PYLORI 210 -11538976 7000686914 excinuclease abc chain b:excision endonuclease abc::chain b:uvrb protein (cl:excinuclease abc chain b:dead/h box helicase homology) (ec:3.1.-.-) (db:pir2.dat) B64659 B64659 Helicobacter pylori 210 -11538976 7500893898 hp1114 excinuclease abc subunit b uvrb (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to egad:28247 percent identity: 53.06;) (le:10421) (re:12397) (di:complement) HPAE000617 AE000617 g2314265 Helicobacter pylori 210 -11538976 7502852834 hp1114 excinuclease abc subunit b uvrb (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to egad:28247 percent identity: 53.06;) (le:10421) (re:12397) (di:complement) HPAE000617 AE000617 g2314265 Helicobacter pylori 26695 85962 -11538976

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501903997	17352	39508	669	222

Description

6500735119 bsp6im:hp1121 cytosine specific dna methyltransferase (gtcfc:10.8) (ec:2.1.1.73) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1121 HP1121 Helicobacter pylori 210 -11538977 7000689881 cytosine specific dna methyltransferase (db:pir2.dat) A64660 A64660 Helicobacter pylori 210 -11538977 7500958682 hp1121 cytosine specific dna methyltransferase (db:genpept-bct1) (de:helicobacter pylori section 96 of 134 of the complete genome.) (nt:similar to egad:17815 percent identity: 37.05;) (le:9386) (re:10324) (di:complement) HPAE000618 AE000618 g2314272 Helicobacter pylori 210 -11538977 7502852835 hp1121 cytosine specific dna methyltransferase (db:genpept) (de:helicobacter pylori 26695 section 96 of 134 of the complete genome.) (nt:similar to egad:17815 percent identity: 37.05;) (le:9386) (re:10324) (di:complement) HPAE000618 AE000618 g2314272 Helicobacter pylori 26695 85962 -11538977

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904008	17353	39509	204	67

Description

6500735120 ulcer associated adenine specific dna methyltransferase:ulcer associated adenine specific dnamethyltransferase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1208 HP1208 Helicobacter pylori 210 -11538978 7000689060 ulcer associated adenine specific dna methyltransferase (cl:site-specific methyltransferase (adenine-specific) nlaiii) (db:pir2.dat) H64670 H64670 Helicobacter pylori 210 -11538978 7500953973 hp1208 ulcer associated adenine specific dna (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to gp:1518454 percent identity: 93.43;) (le:8062) (re:9051) (di:complement) HPAE000626 AE000626 g2314368 Helicobacter pylori 210 -11538978 7502852836 hp1208 ulcer associated adenine specific dna (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to gp:1518454 percent identity: 93.43;) (le:8062) (re:9051) (di:complement) HPAE000626 AE000626 g2314368 Helicobacter pylori 26695 85962 -11538978

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904016	17354	39510	657	218

Description

6500735121 icea:hp1209 ulcer-associated gene restriction endonuclease (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1209 HP1209 Helicobacter pylori 210 -11538979 7500975642 hp1209 ulcer-associated gene restriction endonuclease (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to gp:1518453 percent identity: 95.51;) (le:9060) (re:9578) (di:complement) HPAE000626 AE000626 g2314369 Helicobacter pylori 210 -11538979 7502852837 hp1209 ulcer-associated gene restriction endonuclease (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to gp:1518453 percent identity: 95.51;) (le:9060) (re:9578) (di:complement) HPAE000626 AE000626 g2314369 Helicobacter pylori 26695 85962 -11538979

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904020	17355	39511	399	132

Description

GTC ORF with score 228 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k07h8.) (nt:contains similarity to n-terminal) (le:30904:31103:31786) (re:31050:31362:31927) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904024	17356	39512	438	145

Description

6500735122 holb:hp1231 dna polymerase iii delta prime subunit (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1231 HP1231 Helicobacter pylori 210 -11538980 7000689902 dna polymerase iii delta prime subunit (db:pir2.dat) G64673 G64673 Helicobacter pylori 210 -11538980 7500958698 hp1231 dna polymerase iii delta prime subunit holb (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to egad:20293 percent identity: 48.57;) (le:5364) (re:6020) (di:direct) HPAE000628 AE000628 g2314393 Helicobacter pylori 210 -11538980 7502852838 hp1231 dna polymerase iii delta prime subunit holb (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to egad:20293 percent identity: 48.57;) (le:5364) (re:6020) (di:direct) HPAE000628 AE000628 g2314393 Helicobacter pylori 26695 85962 -11538980

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904025	17357	39513	486	161

Description

6500735123 ssb:hp1245 single-strand dna-binding protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1245 HP1245 Helicobacter pylori 210 -11538981 7000690707 single-strand dna-binding protein (cl:bacterial single-stranded dna-binding protein:single-stranded dna-binding protein homology) (db:pir2.dat) E64675 E64675 Helicobacter pylori 210 -11538981 7500959474 hp1245 single-strand dna-binding protein ssb (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to egad:5232 percent identity: 32.56;) (le:460) (re:999) (di:complement) HPAE000630 AE000630 g2314411 Helicobacter pylori 210 -11538981 7502852839 hp1245 single-strand dna-binding protein ssb (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to egad:5232 percent identity: 32.56;) (le:460) (re:999) (di:complement) HPAE000630 AE000630 g2314411 Helicobacter pylori 26695 85962 -11538981

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904029	17358	39514	975	324

Description

GTC ORF with score 101 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, essa i ap2 contig fragmentno. 1.) (nt:similarity to ste11 proteine kinase homolog npk1,) (le:143936:144267:144762) (re:144206:144704:144843) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904032	17359	39515	774	257

Description

6500735124 rnhb:hp1323 ribonuclease hii rnhb:ribonuclease hii (gtcfc:10.8) (ec:3.1.26.4) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1323 HP1323 Helicobacter pylori 210 -11538982 5500685888 rnhb:hp1323 (sr:,campylobacter pylori) (ec:3.1.26.4) (de:ribonuclease hii, (rnase hii)) (db:swissprot) RNH2_HELPY P56121 HELICOBACTER PYLORI 210 -11538982 7000686424 ribonuclease hii (db:pir2.dat) C64685 C64685 Helicobacter pylori 210 -11538982 7500890449 hp1323 ribonuclease hii rnhb (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:similar to egad:28070 percent identity: 36.32;) (le:2031) (re:2660) (di:complement) HPAE000634 AE000634 g2314491 Helicobacter pylori 210 -11538982 7502852840 hp1323 ribonuclease hii rnhb (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:similar to egad:28070 percent identity: 36.32;) (le:2031) (re:2660) (di:complement) HPAE000634 AE000634 g2314491 Helicobacter pylori 26695 85962 -11538982

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904064	17360	39516	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904068	17361	39517	1602	533

Description

GTC ORF with score 508 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid f30a10, complete sequence.) (nt:predicted using genefinder; similarity to yeast) (le:16639:16822:17596:20108) (re:16774:17356:18266:20431) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904072	17362	39518	408	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904073	17363	39519	1287	428

Description

GTC ORF with score 1932 to: (db:genpept-pln1) (de:aspergillus fumigatus cytoplasmic metalloproteinase (mepb) gene,complete cds.) (nt:zinc metalloproteinase; pz-peptidase; member of the) (le:265:1629:2325) (re:1581:2269:2517) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904075	17364	39520	876	291

Description

6500735125 ung:hp1347 uracil-dna glycosylase (gtcfc:10.8) (ec:3.2.2.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1347 HP1347 Helicobacter pylori 210 -11538983 7500893812 ung:hp1347 (sr:,campylobacter pylori) (ec:3.2.2.-) (de:uracil-dna glycosylase, (udg)) (db:swissprot) UNG_HELPY P56397 HELICOBACTER PYLORI 210 -11538983 7000690789 uracil-dna glycosylase (cl:uracil-dna glycosylase) (db:pir2.dat) C64688 C64688 Helicobacter pylori 210 -11538983 7500893814 hp1347 uracil-dna glycosylase ung (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:5319 percent identity: 43.14;) (le:75) (re:776) (di:complement) HPAE000636 AE000636 g2314518 Helicobacter pylori 210 -11538983 7502852841 hp1347 uracil-dna glycosylase ung (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:5319 percent identity: 43.14;) (le:75) (re:776) (di:complement) HPAE000636 AE000636 g2314518 Helicobacter pylori 26695 85962 -11538983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904083	17365	39521	252	83

Description

GTC ORF with score 340 to: (db:genpept-pln1) (de:aspergillus fumigatus cytoplasmic metalloproteinase (mepb) gene,complete cds.) (nt:zinc metalloproteinase; pz-peptidase; member of the) (le:265:1629:2325) (re:1581:2269:2517) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904085	17366	39522	273	90

Description

GTC ORF with score 337 to: (db:genpept-pln1) (de:aspergillus fumigatus cytoplasmic metalloproteinase (mepb) gene,complete cds.) (nt:zinc metalloproteinase; pz-peptidase; member of the) (le:265:1629:2325) (re:1581:2269:2517) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904091	17367	39523	837	278

Description

6500735126 hinfim:hp1352 adenine specific dna methyltransferase (gtcfc:10.8) (ec:2.1.1.72) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1352 HP1352 Helicobacter pylori 210 -11538984 7000689061 adenine specific dna methyltransferase (cl:site-specific dna-methyltransferase (adenine-specific) hpai) (db:pir2.dat) H64688 H64688 Helicobacter pylori 210 -11538984 7500953975 hp1352 adenine specific dna methyltransferase hinfim (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:18054 percent identity: 62.50;) (le:5113) (re:6192) (di:complement) HPAE000636 AE000636 g2314521 Helicobacter pylori 210 -11538984 7502852842 hp1352 adenine specific dna methyltransferase hinfim (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:18054 percent identity: 62.50;) (le:5113) (re:6192) (di:complement) HPAE000636 AE000636 g2314521 Helicobacter pylori 26695 85962 -11538984

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904095	17368	39524	675	224

Description

GTC ORF with score 1151 to: (db:genpept-pln1) (de:aspergillus fumigatus cytoplasmic metalloproteinase (mepb) gene,complete cds.) (nt:zinc metalloproteinase; pz-peptidase; member of the) (le:265:1629:2325) (re:1581:2269:2517) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904112	17369	39525	219	72

Description

6500735127 putative adenine specific dna methyltransferase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1354 HP1354 Helicobacter pylori 210 -11538985 7000689613 adenine specific dna methyltransferase (db:pir2.dat) B64689 B64689 Helicobacter pylori 210 -11538985 7500958432 hp1354 putative adenine specific dna methyltransferase (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:20905 percent identity: 27.38;) (le:7431) (re:9938) (di:complement) HPAE000636 AE000636 g2314522 Helicobacter pylori 210 -11538985 7502852843 hp1354 putative adenine specific dna methyltransferase (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:20905 percent identity: 27.38;) (le:7431) (re:9938) (di:complement) HPAE000636 AE000636 g2314522 Helicobacter pylori 26695 85962 -11538985

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904125	17370	39526	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904127	17371	39527	333	110

Description

6500735128 mboiir:hp1366 type iis restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1366 HP1366 Helicobacter pylori 210 -11538986 7000690772 type iis restriction enzyme r protein (db:pir2.dat) F64690 F64690 Helicobacter pylori 210 -11538986 7500959536 hp1366 type iis restriction enzyme r protein mboiir (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:7691 percent identity: 37.14;) (le:72) (re:1343) (di:complement) HPAE000637 AE000637 g2314537 Helicobacter pylori 210 -11538986 7502852844 hp1366 type iis restriction enzyme r protein mboiir (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:7691 percent identity: 37.14;) (le:72) (re:1343) (di:complement) HPAE000637 AE000637 g2314537 Helicobacter pylori 26695 85962 -11538986

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904128	17372	39528	273	90

Description

6500735129 mod:hp1367 type iis restriction enzyme m1 protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1367 HP1367 Helicobacter pylori 210 -11538987 7000690769 type iis restriction enzyme m1 protein (cl:site-specific dna-methyltransferase (adenine-specific) hpai) (db:pir2.dat) G64690 G64690 Helicobacter pylori 210 -11538987 7500959533 hp1367 type iis restriction enzyme m1 protein mod (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:8041 percent identity: 59.27;) (le:1359) (re:2141) (di:complement) HPAE000637 AE000637 g2314538 Helicobacter pylori 210 -11538987 7502852845 hp1367 type iis restriction enzyme m1 protein mod (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:8041 percent identity: 59.27;) (le:1359) (re:2141) (di:complement) HPAE000637 AE000637 g2314538 Helicobacter pylori 26695 85962 -11538987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904134	17373	39529	516	171

Description

6500735130 mod:hp1368 type iis restriction enzyme m2 protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1368 HP1368 Helicobacter pylori 210 -11538988 7000690770 type iis restriction enzyme m2 protein (cl:site-specific dna-methyltransferase (adenine-specific) hpai) (db:pir2.dat) H64690 H64690 Helicobacter pylori 210 -11538988 7500959534 hp1368 type iis restriction enzyme m2 protein mod (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:7911 percent identity: 32.96;) (le:2128) (re:2991) (di:complement) HPAE000637 AE000637 g2314539 Helicobacter pylori 210 -11538988 7502852846 hp1368 type iis restriction enzyme m2 protein mod (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:7911 percent identity: 32.96;) (le:2128) (re:2991) (di:complement) HPAE000637 AE000637 g2314539 Helicobacter pylori 26695 85962 -11538988

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904138	17374	39530	270	89

Description

GTC ORF with score 203 to: (sr:aspergillus terreus (strain:imi16043) dna, clone_lib:lamda zapii) (db:genpept-pln1) (de:aspergillus terreus dhgo gene for dihydrogeodin oxidase, completecds (exon1-7).) (nt:copper binding site: 1224..1238, 1414..1431,) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904140	17375	39531	615	204

Description

6500735131 mod:hp1370 type iii restriction enzyme m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1370 HP1370 Helicobacter pylori 210 -11538989 7500975643 hp1370 type iii restriction enzyme m protein mod (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:28068 percent identity: 37.00;) (le:4802) (re:5668) (di:direct) HPAE000637 AE000637 g2314540 Helicobacter pylori 210 -11538989 7502852847 hp1370 type iii restriction enzyme m protein mod (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:28068 percent identity: 37.00;) (le:4802) (re:5668) (di:direct) HPAE000637 AE000637 g2314540 Helicobacter pylori 26695 85962 -11538989

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904142	17376	39532	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904143	17377	39533	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904145	17378	39534	825	275

Description

GTC ORF with score 823 to: (sr:aspergillus terreus (strain:imi16043) dna, clone_lib:lamda zapii) (db:genpept-pln1) (de:aspergillus terreus dhgo gene for dihydrogeodin oxidase, completecds (exon1-7).) (nt:copper binding site: 1224..1238, 1414..1431,) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904146	17379	39535	417	138

Description

6500735132 type iii restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1371 HP1371 Helicobacter pylori 210 -11538990 7000690766 type iii restriction enzyme r protein (db:pir2.dat) C64691 C64691 Helicobacter pylori 210 -11538990 7500959530 hp1371 type iii restriction enzyme r protein (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:21460 percent identity: 26.20;) (le:5679) (re:8585) (di:direct) HPAE000637 AE000637 g2314541 Helicobacter pylori 210 -11538990 7502852848 hp1371 type iii restriction enzyme r protein (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:21460 percent identity: 26.20;) (le:5679) (re:8585) (di:direct) HPAE000637 AE000637 g2314541 Helicobacter pylori 26695 85962 -11538990

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904157	17380	39536	1017	338

Description

6500735133 restriction modification system s subunit (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1383 HP1383 Helicobacter pylori 210 -11538991 7000690686 restriction modification system s subunit (db:pir2.dat) G64692 G64692 Helicobacter pylori 210 -11538991 7500959455 hp1383 restriction modification system s subunit (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:similar to egad:44312 percent identity: 38.05;) (le:5666) (re:6148) (di:direct) HPAE000638 AE000638 g2314551 Helicobacter pylori 210 -11538991 7502852849 hp1383 restriction modification system s subunit (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:similar to egad:44312 percent identity: 38.05;) (le:5666) (re:6148) (di:direct) HPAE000638 AE000638 g2314551 Helicobacter pylori 26695 85962 -11538991

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904164	17381	39537	609	202

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904175	17382	39538	684	228

Description

6500735134 recn:hp1393 dna repair protein recn:dna repair protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1393 HP1393 Helicobacter pylori 210 -11538992 7000689907 dna repair protein (db:pir2.dat) A64694 A64694 Helicobacter pylori 210 -11538992 7500958703 hp1393 dna repair protein recn (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:similar to egad:27905 percent identity: 28.27;) (le:2698) (re:4272) (di:complement) HPAE000639 AE000639 g2314562 Helicobacter pylori 210 -11538992 7502852850 hp1393 dna repair protein recn (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:similar to egad:27905 percent identity: 28.27;) (le:2698) (re:4272) (di:complement) HPAE000639 AE000639 g2314562 Helicobacter pylori 26695 85962 -11538992

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904203	17383	39539	792	263

Description

GTC ORF with score 517 to: (or:Caenorhabditis elegans) (db:genpept-inv) (de:caenorhabditis elegans cosmid vf39h21, complete sequence.) (nt:similarity to brugia peptidylprolyl isomerase) (le:3226:z81080:1778:z81080:2552) (re:3428:2038:2645) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904205	17384	39540	564	187

Description

6500735135 hsdr:hp1402 type i restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1402 HP1402 Helicobacter pylori 210 -11538993 7000690756 type i restriction enzyme r protein (db:pir2.dat) B64695 B64695 Helicobacter pylori 210 -11538993 7500959522 hp1402 type i restriction enzyme r protein hsdr (db:genpept-bct1) (de:helicobacter pylori section 118 of 134 of the complete genome.) (nt:similar to egad:10320 percent identity: 26.61;) (le:3623) (re:6604) (di:complement) HPAE000640 AE000640 g2314575 Helicobacter pylori 210 -11538993 7502852851 hp1402 type i restriction enzyme r protein hsdr (db:genpept) (de:helicobacter pylori 26695 section 118 of 134 of the completegenome.) (nt:similar to egad:10320 percent identity: 26.61;) (le:3623) (re:6604) (di:complement) HPAE000640 AE000640 g2314575 Helicobacter pylori 26695 85962 -11538993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904207	17385	39541	657	218

Description

6500735136 hsdm:hp1403 type i restriction enzyme m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1403 HP1403 Helicobacter pylori 210 -11538994 7000690754 type i restriction enzyme m protein (db:pir2.dat) C64695 C64695 Helicobacter pylori 210 -11538994 7500959520 hp1403 type i restriction enzyme m protein hsdm (db:genpept-bct1) (de:helicobacter pylori section 118 of 134 of the complete genome.) (nt:similar to egad:7636 percent identity: 37.08;) (le:6671) (re:9124) (di:direct) HPAE000640 AE000640 g2314576 Helicobacter pylori 210 -11538994 7502852852 hp1403 type i restriction enzyme m protein hsdm (db:genpept) (de:helicobacter pylori 26695 section 118 of 134 of the completegenome.) (nt:similar to egad:7636 percent identity: 37.08;) (le:6671) (re:9124) (di:direct) HPAE000640 AE000640 g2314576 Helicobacter pylori 26695 85962 -11538994

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904215	17386	39542	309	102

Description

6500735137 hsds:hp1404 type i restriction enzyme s protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1404 HP1404 Helicobacter pylori 210 -11538995 7000690759 type i restriction enzyme s protein (db:pir2.dat) D64695 D64695 Helicobacter pylori 210 -11538995 7500959525 hp1404 type i restriction enzyme s protein hsds (db:genpept-bct1) (de:helicobacter pylori section 118 of 134 of the complete genome.) (nt:similar to egad:44312 percent identity: 35.96;) (le:9121) (re:9411) (di:direct) HPAE000640 AE000640 g2314577 Helicobacter pylori 210 -11538995 7502852853 hp1404 type i restriction enzyme s protein hsds (db:genpept) (de:helicobacter pylori 26695 section 118 of 134 of the completegenome.) (nt:similar to egad:44312 percent identity: 35.96;) (le:9121) (re:9411) (di:direct) HPAE000640 AE000640 g2314577 Helicobacter pylori 26695 85962 -11538995

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904225	17387	39543	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904226	17388	39544	1308	435

Description

6500735138 bcgib:hp1471 type iis restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1471 HP1471 Helicobacter pylori 210 -11538996 7000690773 type iis restriction enzyme r protein (db:pir2.dat) G64703 G64703 Helicobacter pylori 210 -11538996 7500959537 hp1471 type iis restriction enzyme r protein bcgib (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:contingency gene.; similar to egad:18690 percent) (le:5479) (re:6672) (di:complement) HPAE000647 AE000647 g2314648 Helicobacter pylori 210 -11538996 7502852854 hp1471 type iis restriction enzyme r protein bcgib (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:contingency gene.; similar to egad:18690 percent) (le:5479) (re:6672) (di:complement) HPAE000647 AE000647 g2314648 Helicobacter pylori 26695 85962 -11538996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904229	17389	39545	1713	570

Description

GTC ORF with score 107 to: (sr:house mouse) (db:genpept-rod) (de:mus musculus transcriptional activator alpha-nac (naca) gene,complete cds.) (nt:putative muscle-specific transcriptional activator) (le:854:3527:10523:11084) (re:923:9442:10608:11161) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904274	17390	39546	1518	505

Description

6500735139 mod:hp1472 type iis restriction enzyme m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1472 HP1472 Helicobacter pylori 210 -11538997 7000690768 type iis restriction enzyme m protein (db:pir2.dat) H64703 H64703 Helicobacter pylori 210 -11538997 7500959532 hp1472 type iis restriction enzyme m protein mod (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:22981 percent identity: 32.45;) (le:6738) (re:8777) (di:complement) HPAE000647 AE000647 g2314649 Helicobacter pylori 210 -11538997 7502852855 hp1472 type iis restriction enzyme m protein mod (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:22981 percent identity: 32.45;) (le:6738) (re:8777) (di:complement) HPAE000647 AE000647 g2314649 Helicobacter pylori 26695 85962 -11538997

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904278	17391	39547	3696	1232

Description

6500735140 eco57ir:hp1517 type iis restriction enzyme r and m protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1517 HP1517 Helicobacter pylori 210 -11538998 7000690771 type iis restriction enzyme r and m protein (db:pir2.dat) E64709 E64709 Helicobacter pylori 210 -11538998 7500959535 hp1517 type iis restriction enzyme r and m protein (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:similar to egad:18483 percent identity: 26.74;) (le:10421) (re:14260) (di:complement) HPAE000649 AE000649 g2314695 Helicobacter pylori 210 -11538998 7502852856 hp1517 type iis restriction enzyme r and m protein (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:similar to egad:18483 percent identity: 26.74;) (le:10421) (re:14260) (di:complement) HPAE000649 AE000649 g2314695 Helicobacter pylori 26695 85962 -11538998

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904287	17392	39548	1131	376

Description

6500735141 res:hp1521 type iii triction enzyme r protein:type iii restriction enzyme r protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1521 HP1521 Helicobacter pylori 210 -11538999 7000690765 type iii restriction enzyme r protein (db:pir2.dat) A64710 A64710 Helicobacter pylori 210 -11538999 7500959529 hp1521 type iii restriction enzyme r protein res (db:genpept-bct1) (de:helicobacter pylori section 128 of 134 of the complete genome.) (nt:similar to egad:30631 percent identity: 33.12;) (le:2384) (re:5287) (di:complement) HPAE000650 AE000650 g2314701 Helicobacter pylori 210 -11538999 7502852857 hp1521 type iii restriction enzyme r protein res (db:genpept) (de:helicobacter pylori 26695 section 128 of 134 of the completegenome.) (nt:similar to egad:30631 percent identity: 33.12;) (le:2384) (re:5287) (di:complement) HPAE000650 AE000650 g2314701 Helicobacter pylori 26695 85962 -11538999

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904308	17393	39549	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904310	17394	39550	1311	436

Description

6500735142 lexa:hp1526 exodeoxyribonuclease (gtcfc:10.8) (ec:3.1.11.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1526 HP1526 Helicobacter pylori 210 -11539000 7000689913 exodeoxyribonuclease (cl:dna-(apurinic or apyrimidinic site) lyase) (db:pir2.dat) F64710 F64710 Helicobacter pylori 210 -11539000 7500958708 hp1526 exodeoxyribonuclease lexa (db:genpept-bct1) (de:helicobacter pylori section 128 of 134 of the complete genome.) (nt:similar to egad:16751 percent identity: 58.87;) (le:10212) (re:10964) (di:complement) HPAE000650 AE000650 g2314703 Helicobacter pylori 210 -11539000 7502852858 hp1526 exodeoxyribonuclease lexa (db:genpept) (de:helicobacter pylori 26695 section 128 of 134 of the completegenome.) (nt:similar to egad:16751 percent identity: 58.87;) (le:10212) (re:10964) (di:complement) HPAE000650 AE000650 g2314703 Helicobacter pylori 26695 85962 -11539000

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904317	17395	39551	708	235

Description

GTC ORF with score 122 to: (db:genpept-pln1) (de:pneumocystis carinii f. sp. carinii protease 1 gene, complete cds.) (nt:subtilisin-like serine protease; prt1(paga)) (le:1:577:674:798:988) (re:531:631:753:948:1364) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904327	17396	39552	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904352	17397	39553	411	136

Description

6500735143 dnaa:hp1529 chromosomal replication initiator protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1529 HP1529 Helicobacter pylori 210 -11539001 7000689713 chromosomal replication initiator protein (db:pir2.dat) A64711 A64711 Helicobacter pylori 210 -11539001 7500958521 hp1529 chromosomal replication initiator protein (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:similar to egad:14548 percent identity: 34.89;) (le:1827) (re:3200) (di:complement) HPAE000651 AE000651 g2314709 Helicobacter pylori 210 -11539001 7502852859 hp1529 chromosomal replication initiator protein (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:similar to egad:14548 percent identity: 34.89;) (le:1827) (re:3200) (di:complement) HPAE000651 AE000651 g2314709 Helicobacter pylori 26695 85962 -11539001

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904353	17398	39554	1734	577

Description

6500735144 trcf:hp1541 transcription-repair coupling factor (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1541 HP1541 Helicobacter pylori 210 -11539002 7500959506 mfd:hp1541 (sr:,campylobacter pylori) (de:transcription-repair coupling factor (trcf)) (db:swissprot) MFD_HELPY O26066 HELICOBACTER PYLORI 210 -11539002 7000690741 transcription-repair coupling factor (cl:dead/h box helicase homology) (db:pir2.dat) E64712 E64712 Helicobacter pylori 210 -11539002 7502852860 hp1541 transcription-repair coupling factor trcf (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:28258 percent identity: 37.66;) (le:2842) (re:5841) (di:complement) HPAE000652 AE000652 g2314723 Helicobacter pylori 210 -11539002 7502852861 hp1541 transcription-repair coupling factor trcf (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:28258 percent identity: 37.66;) (le:2842) (re:5841) (di:complement) HPAE000652 AE000652 g2314723 Helicobacter pylori 26695 85962 -11539002

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904370	17399	39555	285	94

Description

6500735145 helicase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-helicobacter pylori) HP1553 HP1553 Helicobacter pylori 210 -11539003 7000689984 helicase (db:pir2.dat) A64714 A64714 Helicobacter pylori 210 -11539003 7500958764 hp1553 helicase (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:18207 percent identity: 32.99;) (le:1833) (re:4670) (di:complement) HPAE000653 AE000653 g2314736 Helicobacter pylori 210 -11539003 7502852862 hp1553 helicase (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:18207 percent identity: 32.99;) (le:1833) (re:4670) (di:complement) HPAE000653 AE000653 g2314736 Helicobacter pylori 26695 85962 -11539003

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904371	17400	39556	408	135

Description

6500735146 paps:hp0640 polya polymerase paps:poly:a polymerase (gtcfc:10.9) (ec:2.7.7.19) (keggfc:14.1) (tigrfc:11.4) (db:gtc-helicobacter pylori) HP0640 HP0640 Helicobacter pylori 210 -11539004 7000690631 poly a polymerase (db:pir2.dat) H64599 H64599 Helicobacter pylori 210 -11539004 7500959411 hp0640 poly a polymerase paps (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:30998 percent identity: 37.44;) (le:2829) (re:4037) (di:direct) HPAE000578 AE000578 g2313761 Helicobacter pylori 210 -11539004 7502852863 hp0640 poly a polymerase paps (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:30998 percent identity: 37.44;) (le:2829) (re:4037) (di:direct) HPAE000578 AE000578 g2313761 Helicobacter pylori 26695 85962 -11539004

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904376	17401	39557	231	76

Description

6500735147 ribonuclease iii rnc:ribonuclease iii:rnc (gtcfc:10.9) (ec:3.1.26.3) (keggfc:14.1) (tigrfc:11.4) (db:gtc-helicobacter pylori) HP0662 HP0662 Helicobacter pylori 210 -11539005 5500685883 rnc:hp0662 (sr:,campylobacter pylori) (ec:3.1.26.3) (de:ribonuclease iii, (rnase iii)) (db:swissprot) RNC_HELPY P56118 HELICOBACTER PYLORI 210 -11539005 7000686422 ribonuclease iii (cl:ribonuclease iii:double-stranded rna-binding repeat homology) (db:pir2.dat) F64602 F64602 Helicobacter pylori 210 -11539005 7500890440 hp0662 ribonuclease iii rnc (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:8678 percent identity: 37.33;) (le:10582) (re:11304) (di:direct) HPAE000579 AE000579 g2313785 Helicobacter pylori 210 -11539005 7502852864 hp0662 ribonuclease iii rnc (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:8678 percent identity: 37.33;) (le:10582) (re:11304) (di:direct) HPAE000579 AE000579 g2313785 Helicobacter pylori 26695 85962 -11539005

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904386	17402	39558	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904388	17403	39559	345	114

Description

6500735148 omp2:hp0025 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0025 HP0025 Helicobacter pylori 210 -11539006 7000690571 outer membrane protein (db:pir2.dat) A64523 A64523 Helicobacter pylori 210 -11539006 7500959354 hp0025 h. pylori predicted coding region hp0025 (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:outer membrane protein (omp2); identified by) (le:195) (re:2330) (di:complement) HPAE000525 AE000525 g2313112 Helicobacter pylori 210 -11539006 7502852865 hp0025 h. pylori predicted coding region hp0025 (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:outer membrane protein (omp2); identified by) (le:195) (re:2330) (di:complement) HPAE000525 AE000525 g2313112 Helicobacter pylori 26695 85962 -11539006

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904394	17404	39560	393	130

Description

6500735149 hypothetical protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0078 HP0078 Helicobacter pylori 210 -11539007 7000690030 hypothetical protein hp0078 (db:pir2.dat) F64529 F64529 Helicobacter pylori 210 -11539007 7500958810 hp0078 h. pylori predicted coding region hp0078 (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6658) (re:6915) (di:direct) HPAE000529 AE000529 g2313159 Helicobacter pylori 210 -11539007 7502852866 hp0078 h. pylori predicted coding region hp0078 (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6658) (re:6915) (di:direct) HPAE000529 AE000529 g2313159 Helicobacter pylori 26695 85962 -11539007

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904397	17405	39561	201	66

Description

6500735150 omp3:hp0079 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0079 HP0079 Helicobacter pylori 210 -11539008 7000690594 outer membrane protein (db:pir2.dat) G64529 G64529 Helicobacter pylori 210 -11539008 7500959375 hp0079 h. pylori predicted coding region hp0079 (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:outer membrane protein (omp3); identified by) (le:6926) (re:8713) (di:direct) HPAE000529 AE000529 g2313160 Helicobacter pylori 210 -11539008 7502852867 hp0079 h. pylori predicted coding region hp0079 (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:outer membrane protein (omp3); identified by) (le:6926) (re:8713) (di:direct) HPAE000529 AE000529 g2313160 Helicobacter pylori 26695 85962 -11539008

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904403	17406	39562	303	100

Description

6500735151 omp4:hp0127 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0127 HP0127 Helicobacter pylori 210 -11539009 7000690595 outer membrane protein (db:pir2.dat) G64535 G64535 Helicobacter pylori 210 -11539009 7500959376 hp0127 h. pylori predicted coding region hp0127 (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:outer membrane protein (omp4); identified by) (le:7527) (re:8387) (di:direct) HPAE000534 AE000534 g2313212 Helicobacter pylori 210 -11539009 7502852868 hp0127 h. pylori predicted coding region hp0127 (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:outer membrane protein (omp4); identified by) (le:7527) (re:8387) (di:direct) HPAE000534 AE000534 g2313212 Helicobacter pylori 26695 85962 -11539009

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904405	17407	39563	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904406	17408	39564	240	80

Description

6500735152 cell binding factor 2 (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0175 HP0175 Helicobacter pylori 210 -11539010 5500686286 hp0175 (sr:,campylobacter pylori) (de:hypothetical protein hp0175 precursor) (db:swissprot) Y175_HELPY P56112 HELICOBACTER PYLORI 210 -11539010 7000687073 cell binding factor 2 (db:pir2.dat) G64541 G64541 Helicobacter pylori 210 -11539010 7500894819 hp0175 cell binding factor 2 (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:similar to egad:33124 percent identity: 34.90;) (le:246) (re:1145) (di:direct) HPAE000538 AE000538 g2313264 Helicobacter pylori 210 -11539010 7502852869 hp0175 cell binding factor 2 (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:similar to egad:33124 percent identity: 34.90;) (le:246) (re:1145) (di:direct) HPAE000538 AE000538 g2313264 Helicobacter pylori 26695 85962 -11539010

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904441	17409	39565	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904447	17410	39566	525	174

Description

6500735153 omp5:omp29:hp0227 outer membrane protein:omp5:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0227 HP0227 Helicobacter pylori 210 -11539011 7000690599 outer membrane protein omp5/omp29 (db:pir2.dat) C64548 C64548 Helicobacter pylori 210 -11539011 7500959380 hp0227 outer membrane protein omp5 (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.79;) (le:7381) (re:9456) (di:complement) HPAE000542 AE000542 g2313316 Helicobacter pylori 210 -11539011 7500959381 hp1342 h. pylori predicted coding region hp1342 (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:outer membrane protein (omp29); identified by) (le:7230) (re:9305) (di:direct) HPAE000635 AE000635 g2314516 Helicobacter pylori 210 -11539011 7502852870 hp0227 outer membrane protein omp5 (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.79;) (le:7381) (re:9456) (di:complement) HPAE000542 AE000542 g2313316 Helicobacter pylori 26695 85962 -11539011 7502852871 hp1342 h. pylori predicted coding region hp1342 (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:outer membrane protein (omp29); identified by) (le:7230) (re:9305) (di:direct) HPAE000635 AE000635 g2314516 Helicobacter pylori 26695 85962 -11539011

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904449	17411	39567	873	290

Description

6500735154 omp6:hp0229 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0229 HP0229 Helicobacter pylori 210 -11539012 7000690585 outer membrane protein (db:pir2.dat) E64548 E64548 Helicobacter pylori 210 -11539012 7500959367 hp0229 outer membrane protein omp6 (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 38.38;) (le:95) (re:1546) (di:complement) HPAE000543 AE000543 g2313322 Helicobacter pylori 210 -11539012 7502852872 hp0229 outer membrane protein omp6 (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 38.38;) (le:95) (re:1546) (di:complement) HPAE000543 AE000543 g2313322 Helicobacter pylori 26695 85962 -11539012

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904456	17412	39568	963	320

Description

6500735155 omp7:hp0252 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0252 HP0252 Helicobacter pylori 210 -11539013 7000690580 outer membrane protein (db:pir2.dat) D64551 D64551 Helicobacter pylori 210 -11539013 7500959362 hp0252 outer membrane protein omp7 (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:similar to egad:16664 percent identity: 30.56;) (le:8940) (re:10403) (di:direct) HPAE000544 AE000544 g2313344 Helicobacter pylori 210 -11539013 7502852873 hp0252 outer membrane protein omp7 (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:similar to egad:16664 percent identity: 30.56;) (le:8940) (re:10403) (di:direct) HPAE000544 AE000544 g2313344 Helicobacter pylori 26695 85962 -11539013

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904469	17413	39569	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904475	17414	39570	1689	562

Description

6500735156 omp8:hp0254 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0254 HP0254 Helicobacter pylori 210 -11539014 7000690592 outer membrane protein (db:pir2.dat) F64551 F64551 Helicobacter pylori 210 -11539014 7500959373 hp0254 outer membrane protein omp8 (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 37.64;) (le:10535) (re:11830) (di:direct) HPAE000544 AE000544 g2313345 Helicobacter pylori 210 -11539014 7502852874 hp0254 outer membrane protein omp8 (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 37.64;) (le:10535) (re:11830) (di:direct) HPAE000544 AE000544 g2313345 Helicobacter pylori 26695 85962 -11539014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904480	17415	39571	1704	567

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904492	17416	39572	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904504	17417	39573	567	188

Description

6500735157 toxin-like outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0289 HP0289 Helicobacter pylori 210 -11539015 7000690734 toxin-like outer membrane protein (db:pir2.dat) A64556 A64556 Helicobacter pylori 210 -11539015 7500959499 hp0289 toxin-like outer membrane protein (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:similar to egad:14373 percent identity: 30.59;) (le:9252) (re:17933) (di:direct) HPAE000547 AE000547 g2313383 Helicobacter pylori 210 -11539015 7502852875 hp0289 toxin-like outer membrane protein (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:similar to egad:14373 percent identity: 30.59;) (le:9252) (re:17933) (di:direct) HPAE000547 AE000547 g2313383 Helicobacter pylori 26695 85962 -11539015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904507	17418	39574	2583	860

Description

6500735158 omp9:hp0317 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0317 HP0317 Helicobacter pylori 210 -11539016 7000690586 outer membrane protein (db:pir2.dat) E64559 E64559 Helicobacter pylori 210 -11539016 7500959368 hp0317 outer membrane protein omp9 (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.31;) (le:8845) (re:11082) (di:complement) HPAE000549 AE000549 g2313410 Helicobacter pylori 210 -11539016 7502852876 hp0317 outer membrane protein omp9 (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.31;) (le:8845) (re:11082) (di:complement) HPAE000549 AE000549 g2313410 Helicobacter pylori 26695 85962 -11539016

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904512	17419	39575	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904527	17420	39576	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904528	17421	39577	711	236

Description

6500735159 omp10:hp0324 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0324 HP0324 Helicobacter pylori 210 -11539017 7000690581 outer membrane protein (db:pir2.dat) D64560 D64560 Helicobacter pylori 210 -11539017 7500959363 hp0324 h. pylori predicted coding region hp0324 (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:outer membrane protein (omp10); identified by) (le:5756) (re:6520) (di:complement) HPAE000550 AE000550 g2313429 Helicobacter pylori 210 -11539017 7502852877 hp0324 h. pylori predicted coding region hp0324 (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:outer membrane protein (omp10); identified by) (le:5756) (re:6520) (di:complement) HPAE000550 AE000550 g2313429 Helicobacter pylori 26695 85962 -11539017

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904542	17422	39578	2058	685

Description

6500735160 omp11:hp0472 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0472 HP0472 Helicobacter pylori 210 -11539018 7000690597 outer membrane protein (db:pir2.dat) H64578 H64578 Helicobacter pylori 210 -11539018 7500959378 hp0472 outer membrane protein omp11 (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 99.46;) (le:1649) (re:2209) (di:complement) HPAE000562 AE000562 g2313583 Helicobacter pylori 210 -11539018 7502852878 hp0472 outer membrane protein omp11 (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 99.46;) (le:1649) (re:2209) (di:complement) HPAE000562 AE000562 g2313583 Helicobacter pylori 26695 85962 -11539018

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904562	17423	39579	654	217

Description

6500735161 omp22:hp0477:hp0923 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0923 HP0923 Helicobacter pylori 210 -11539019 7000690587 outer membrane protein (db:pir2.dat) E64579 E64579 Helicobacter pylori 210 -11539019 7500959369 hp0477 h. pylori predicted coding region hp0477 (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:outer membrane protein (omp12); identified by) (le:6289) (re:7392) (di:direct) HPAE000562 AE000562 g2313591 Helicobacter pylori 210 -11539019 7502852879 hp0477 h. pylori predicted coding region hp0477 (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:outer membrane protein (omp12); identified by) (le:6289) (re:7392) (di:direct) HPAE000562 AE000562 g2313591 Helicobacter pylori 26695 85962 -11539019

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904600	17424	39580	270	89

Description

6500735162 membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0567 HP0567 Helicobacter pylori 210 -11539020 7000690514 membrane protein (db:pir2.dat) G64590 G64590 Helicobacter pylori 210 -11539020 7500959307 hp0567 membrane protein (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:similar to gp:1620467 percent identity: 26.36;) (le:8427) (re:9473) (di:direct) HPAE000570 AE000570 g2313674 Helicobacter pylori 210 -11539020 7502852880 hp0567 membrane protein (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:similar to gp:1620467 percent identity: 26.36;) (le:8427) (re:9473) (di:direct) HPAE000570 AE000570 g2313674 Helicobacter pylori 26695 85962 -11539020

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904602	17425	39581	930	309

Description

6500735163 toxin-like outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0610 HP0610 Helicobacter pylori 210 -11539021 7000690735 toxin-like outer membrane protein (db:pir2.dat) B64596 B64596 Helicobacter pylori 210 -11539021 7500959500 hp0610 toxin-like outer membrane protein (db:genpept-bct1) (de:helicobacter pylori section 53 of 134 of the complete genome.) (nt:similar to egad:14374 percent identity: 26.26;) (le:3833) (re:9664) (di:direct) HPAE000575 AE000575 g2313731 Helicobacter pylori 210 -11539021 7502852881 hp0610 toxin-like outer membrane protein (db:genpept) (de:helicobacter pylori 26695 section 53 of 134 of the complete genome.) (nt:similar to egad:14374 percent identity: 26.26;) (le:3833) (re:9664) (di:direct) HPAE000575 AE000575 g2313731 Helicobacter pylori 26695 85962 -11539021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904627	17426	39582	483	160

Description

6500735164 omp13:hp0638 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0638 HP0638 Helicobacter pylori 210 -11539022 7000690593 outer membrane protein (db:pir2.dat) F64599 F64599 Helicobacter pylori 210 -11539022 7500959374 hp0638 h. pylori predicted coding region hp0638 (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:contingency gene.; outer membrane protein (omp13);) (le:1126) (re:2043) (di:direct) HPAE000578 AE000578 g2313774 Helicobacter pylori 210 -11539022 7502852882 hp0638 h. pylori predicted coding region hp0638 (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:contingency gene.; outer membrane protein (omp13);) (le:1126) (re:2043) (di:direct) HPAE000578 AE000578 g2313774 Helicobacter pylori 26695 85962 -11539022

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904631	17427	39583	648	215

Description

6500735165 protective surface antigen d15 (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0655 HP0655 Helicobacter pylori 210 -11539023 7500975637 hp0655 protective surface antigen d15 (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:29390 percent identity: 27.51;) (le:1344) (re:4094) (di:direct) HPAE000579 AE000579 g2313780 Helicobacter pylori 210 -11539023 7502852883 hp0655 protective surface antigen d15 (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:29390 percent identity: 27.51;) (le:1344) (re:4094) (di:direct) HPAE000579 AE000579 g2313780 Helicobacter pylori 26695 85962 -11539023

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904636	17428	39584	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904646	17429	39585	321	106

Description

6500735166 omp14:hp0671 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0671 HP0671 Helicobacter pylori 210 -11539024 7000690596 outer membrane protein (db:pir2.dat) G64603 G64603 Helicobacter pylori 210 -11539024 7500959377 hp0671 outer membrane protein omp14 (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.00;) (le:6307) (re:7119) (di:direct) HPAE000580 AE000580 g2313793 Helicobacter pylori 210 -11539024 7502852884 hp0671 outer membrane protein omp14 (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.00;) (le:6307) (re:7119) (di:direct) HPAE000580 AE000580 g2313793 Helicobacter pylori 26695 85962 -11539024

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904662	17430	39586	906	301

Description

6500735167 omp15:hp0706 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0706 HP0706 Helicobacter pylori 210 -11539025 7000690574 outer membrane protein (db:pir2.dat) B64608 B64608 Helicobacter pylori 210 -11539025 7500959357 hp0706 outer membrane protein omp15 (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 33.51;) (le:9440) (re:10261) (di:direct) HPAE000583 AE000583 g2313829 Helicobacter pylori 210 -11539025 7502852885 hp0706 outer membrane protein omp15 (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 33.51;) (le:9440) (re:10261) (di:direct) HPAE000583 AE000583 g2313829 Helicobacter pylori 26695 85962 -11539025

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904669	17431	39587	702	233

Description

6500735168 omp18:hp0796 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0796 HP0796 Helicobacter pylori 210 -11539026 7000690582 outer membrane protein (db:pir2.dat) D64619 D64619 Helicobacter pylori 210 -11539026 7500959364 hp0796 h. pylori predicted coding region hp0796 (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:outer membrane protein (omp18); identified by) (le:9583) (re:10419) (di:complement) HPAE000591 AE000591 g2313927 Helicobacter pylori 210 -11539026 7502852886 hp0796 h. pylori predicted coding region hp0796 (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:outer membrane protein (omp18); identified by) (le:9583) (re:10419) (di:complement) HPAE000591 AE000591 g2313927 Helicobacter pylori 26695 85962 -11539026

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904670	17432	39588	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904695	17433	39589	2043	680

Description

GTC ORF with score 155 to: (fn:transcriptional regulation) (db:genpept-vrl) (de:human herpesvirus 6 replication origin-binding protein (hdrfo),partial cds, helicase-primase component (hdrf1), virion protein(hdlf1), putative helicase (hdrf2), putative ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904710	17434	39590	2553	851

Description

6500735169 ompp1:hp0839 outer membrane protein p1 (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0839 HP0839 Helicobacter pylori 210 -11539027 7000690600 outer membrane protein p1 (db:pir2.dat) G64624 G64624 Helicobacter pylori 210 -11539027 7500959382 hp0839 outer membrane protein p1 ompp1 (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:similar to egad:16316 percent identity: 23.27;) (le:2231) (re:3994) (di:direct) HPAE000595 AE000595 g2313971 Helicobacter pylori 210 -11539027 7502852887 hp0839 outer membrane protein p1 ompp1 (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:similar to egad:16316 percent identity: 23.27;) (le:2231) (re:3994) (di:direct) HPAE000595 AE000595 g2313971 Helicobacter pylori 26695 85962 -11539027

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904712	17435	39591	501	166

Description

6500735170 omp19:hp0896 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0896 HP0896 Helicobacter pylori 210 -11539028 7000690598 outer membrane protein (db:pir2.dat) H64631 H64631 Helicobacter pylori 210 -11539028 7500959379 hp0896 outer membrane protein omp19 (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:contingency gene.; similar to gp:1800185 percent) (le:2644) (re:4770) (di:complement) HPAE000599 AE000599 g2314032 Helicobacter pylori 210 -11539028 7502852888 hp0896 outer membrane protein omp19 (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:contingency gene.; similar to gp:1800185 percent) (le:2644) (re:4770) (di:complement) HPAE000599 AE000599 g2314032 Helicobacter pylori 26695 85962 -11539028

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904719	17436	39592	420	139

Description

6500735171 omp20:hp0912 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0912 HP0912 Helicobacter pylori 210 -11539029 7000689477 outer membrane protein omp20 (cl:helicobacter pylori outer membrane protein omp20) (db:pir2.dat) H64633 H64633 Helicobacter pylori 210 -11539029 7500955775 hp0912 h. pylori predicted coding region hp0912 (db:genpept-bct1) (de:helicobacter pylori section 78 of 134 of the complete genome.) (nt:outer membrane protein (omp20); identified by) (le:8852) (re:10399) (di:direct) HPAE000600 AE000600 g2314050 Helicobacter pylori 210 -11539029 7502852889 hp0912 h. pylori predicted coding region hp0912 (db:genpept) (de:helicobacter pylori 26695 section 78 of 134 of the complete genome.) (nt:outer membrane protein (omp20); identified by) (le:8852) (re:10399) (di:direct) HPAE000600 AE000600 g2314050 Helicobacter pylori 26695 85962 -11539029

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904721	17437	39593	1998	665

Description

6500735172 omp21:hp0913 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0913 HP0913 Helicobacter pylori 210 -11539030 7000689476 outer membrane protein omp21 (cl:helicobacter pylori outer membrane protein omp20) (db:pir2.dat) A64634 A64634 Helicobacter pylori 210 -11539030 7500955774 hp0913 outer membrane protein omp21 (db:genpept-bct1) (de:helicobacter pylori section 78 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 38.19;) (le:10421) (re:12010) (di:direct) HPAE000600 AE000600 g2314047 Helicobacter pylori 210 -11539030 7502852890 hp0913 outer membrane protein omp21 (db:genpept) (de:helicobacter pylori 26695 section 78 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 38.19;) (le:10421) (re:12010) (di:direct) HPAE000600 AE000600 g2314047 Helicobacter pylori 26695 85962 -11539030

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904723	17438	39594	2814	937

Description

6500735173 toxin-like outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP0922 HP0922 Helicobacter pylori 210 -11539031 7000690736 toxin-like outer membrane protein (db:pir2.dat) B64635 B64635 Helicobacter pylori 210 -11539031 7500959501 hp0922 toxin-like outer membrane protein (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:34276 percent identity: 29.55;) (le:71) (re:7660) (di:direct) HPAE000602 AE000602 g2314061 Helicobacter pylori 210 -11539031 7502852891 hp0922 toxin-like outer membrane protein (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:34276 percent identity: 29.55;) (le:71) (re:7660) (di:direct) HPAE000602 AE000602 g2314061 Helicobacter pylori 26695 85962 -11539031

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904724	17439	39595	1482	493

Description

6500735174 omp23:hp1107 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1107 HP1107 Helicobacter pylori 210 -11539032 7000690577 outer membrane protein (db:pir2.dat) C64658 C64658 Helicobacter pylori 210 -11539032 7500959359 hp1107 h. pylori predicted coding region hp1107 (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:outer membrane protein (omp23); identified by) (le:3969) (re:4661) (di:complement) HPAE000617 AE000617 g2314267 Helicobacter pylori 210 -11539032 7502852892 hp1107 h. pylori predicted coding region hp1107 (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:outer membrane protein (omp23); identified by) (le:3969) (re:4661) (di:complement) HPAE000617 AE000617 g2314267 Helicobacter pylori 26695 85962 -11539032

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904732	17440	39596	405	134

Description

6500735175 omp24:hp1113 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1113 HP1113 Helicobacter pylori 210 -11539033 7000690572 outer membrane protein (db:pir2.dat) A64659 A64659 Helicobacter pylori 210 -11539033 7500959355 hp1113 outer membrane protein omp24 (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.00;) (le:9577) (re:10410) (di:direct) HPAE000617 AE000617 g2314264 Helicobacter pylori 210 -11539033 7502852893 hp1113 outer membrane protein omp24 (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.00;) (le:9577) (re:10410) (di:direct) HPAE000617 AE000617 g2314264 Helicobacter pylori 26695 85962 -11539033

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904733	17441	39597	2331	776

Description

6500735176 omp25:hp1156 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1156 HP1156 Helicobacter pylori 210 -11539034 7000690583 outer membrane protein (db:pir2.dat) D64664 D64664 Helicobacter pylori 210 -11539034 7500959365 hp1156 h. pylori predicted coding region hp1156 (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:outer membrane protein (omp25); identified by) (le:9800) (re:11890) (di:direct) HPAE000621 AE000621 g2314315 Helicobacter pylori 210 -11539034 7502852894 hp1156 h. pylori predicted coding region hp1156 (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:outer membrane protein (omp25); identified by) (le:9800) (re:11890) (di:direct) HPAE000621 AE000621 g2314315 Helicobacter pylori 26695 85962 -11539034

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904740	17442	39598	474	157

Description

GTC ORF with score 146 to: (fn:helicase, helicase-primase complex) (db:genpept-vrl) (de:human herpesvirus 6 serotype b putative major immediate-earlygenes.) (nt:similar to hhv6a u86, region ie-b) (le:16386) (re:19235) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904741	17443	39599	432	143

Description

6500735177 omp26:hp1157 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1157 HP1157 Helicobacter pylori 210 -11539035 7000690589 outer membrane protein (db:pir2.dat) E64664 E64664 Helicobacter pylori 210 -11539035 7500959370 hp1157 h. pylori predicted coding region hp1157 (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:outer membrane protein (omp26); identified by) (le:11913) (re:15605) (di:direct) HPAE000621 AE000621 g2314316 Helicobacter pylori 210 -11539035 7502852895 hp1157 h. pylori predicted coding region hp1157 (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:outer membrane protein (omp26); identified by) (le:11913) (re:15605) (di:direct) HPAE000621 AE000621 g2314316 Helicobacter pylori 26695 85962 -11539035

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904746	17444	39600	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904750	17445	39601	285	94

Description

6500735178 omp27:hp1177 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1177 HP1177 Helicobacter pylori 210 -11539036 7000690573 outer membrane protein (db:pir2.dat) A64667 A64667 Helicobacter pylori 210 -11539036 7500959356 hp1177 outer membrane protein omp27 (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 36.98;) (le:7148) (re:9073) (di:complement) HPAE000623 AE000623 g2314334 Helicobacter pylori 210 -11539036 7502852896 hp1177 outer membrane protein omp27 (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to gp:1800185 percent identity: 36.98;) (le:7148) (re:9073) (di:complement) HPAE000623 AE000623 g2314334 Helicobacter pylori 26695 85962 -11539036

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904757	17446	39602	264	87

Description

6500735179 omp28:hp1243 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1243 HP1243 Helicobacter pylori 210 -11539037 7000690578 outer membrane protein (db:pir2.dat) C64675 C64675 Helicobacter pylori 210 -11539037 7500959360 hp1243 h. pylori predicted coding region hp1243 (db:genpept-bct1) (de:helicobacter pylori section 107 of 134 of the complete genome.) (nt:outer membrane protein (omp28); identified by) (le:7596) (re:9797) (di:complement) HPAE000629 AE000629 g2314407 Helicobacter pylori 210 -11539037 7502852897 hp1243 h. pylori predicted coding region hp1243 (db:genpept) (de:helicobacter pylori 26695 section 107 of 134 of the completegenome.) (nt:outer membrane protein (omp28); identified by) (le:7596) (re:9797) (di:complement) HPAE000629 AE000629 g2314407 Helicobacter pylori 26695 85962 -11539037

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904759	17447	39603	318	105

Description

GTC ORF with score 234 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome viii cosmid 9780.) (nt:weakly similar to 60 kd chaperonin (ricckettsia) (le:6925) (re:8238) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904762	17448	39604	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904764	17449	39605	294	97

Description

6500735180 omp30:hp1395 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1395 HP1395 Helicobacter pylori 210 -11539038 7000690579 outer membrane protein (db:pir2.dat) C64694 C64694 Helicobacter pylori 210 -11539038 7500959361 hp1395 h. pylori predicted coding region hp1395 (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:outer membrane protein (omp30); identified by) (le:5329) (re:6057) (di:direct) HPAE000639 AE000639 g2314569 Helicobacter pylori 210 -11539038 7502852898 hp1395 h. pylori predicted coding region hp1395 (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:outer membrane protein (omp30); identified by) (le:5329) (re:6057) (di:direct) HPAE000639 AE000639 g2314569 Helicobacter pylori 26695 85962 -11539038

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904766	17450	39606	549	182

Description

6500735181 60 kda inner-membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1450 HP1450 Helicobacter pylori 210 -11539039 7000689595 probable 60k inner membrane protein (cl:probable 60k inner membrane protein:stage iii sporulation protein homology) (db:pir2.dat) B64701 B64701 Helicobacter pylori 210 -11539039 7500955388 hp1450 60 kda inner-membrane protein (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:similar to egad:6113 percent identity: 40.00;) (le:991) (re:2634) (di:direct) HPAE000645 AE000645 g2314626 Helicobacter pylori 210 -11539039 7502852899 hp1450 60 kda inner-membrane protein (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:similar to egad:6113 percent identity: 40.00;) (le:991) (re:2634) (di:direct) HPAE000645 AE000645 g2314626 Helicobacter pylori 26695 85962 -11539039

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904770	17451	39607	414	137

Description

7500885108 lpp20:hp1456 membrane-associated lipoprotein:lipoprotein precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1456 HP1456 Helicobacter pylori 210 -11539040 82365 lpp20:hp1456 (sr:,campylobacter pylori) (de:lpp20 lipoprotein precursor) (db:swissprot) LP20_HELPY P53436 HELICOBACTER PYLORI 210 -11539040 7000685759 membrane-associated lipoprotein (db:pir2.dat) H64701 H64701 Helicobacter pylori 210 -11539040 7500885107 hp1456 membrane-associated lipoprotein lpp20 (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:similar to egad:34128 percent identity: 98.86;) (le:9304) (re:9831) (di:complement) HPAE000645 AE000645 g2314629 Helicobacter pylori 210 -11539040 7502852900 lpp20 conserved lipoprotein (db:genpept) (de:helicobacter pylori, strain j99 section 118 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1456) (le:9081) (re:9608) (di:complement) AE001557 AE001557 g4155961 Helicobacter pylori J99 85963 -11539040 6500735182 hp1456 membrane-associated lipoprotein lpp20 (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:similar to egad:34128 percent identity: 98.86;) (le:9304) (re:9831) (di:complement) HPAE000645 AE000645 g2314629 Helicobacter pylori 26695 85962 -11539040

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904776	17452	39608	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904787	17453	39609	1527	508

Description

6500735183 omp31:hp1469 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1469 HP1469 Helicobacter pylori 210 -11539041 7000690590 outer membrane protein (db:pir2.dat) E64703 E64703 Helicobacter pylori 210 -11539041 7500959371 hp1469 h. pylori predicted coding region hp1469 (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:outer membrane protein (omp31); identified by) (le:1872) (re:2618) (di:complement) HPAE000647 AE000647 g2314664 Helicobacter pylori 210 -11539041 7502852901 hp1469 h. pylori predicted coding region hp1469 (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:outer membrane protein (omp31); identified by) (le:1872) (re:2618) (di:complement) HPAE000647 AE000647 g2314664 Helicobacter pylori 26695 85962 -11539041

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904805	17454	39610	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904821	17455	39611	255	84

Description

6500735184 omp32:hp1501 outer membrane protein:h (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1501 HP1501 Helicobacter pylori 210 -11539042 7000690591 outer membrane protein (db:pir2.dat) E64707 E64707 Helicobacter pylori 210 -11539042 7500959372 hp1501 h. pylori predicted coding region hp1501 (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:outer membrane protein (omp32); identified by) (le:8629) (re:9795) (di:complement) HPAE000648 AE000648 g2314684 Helicobacter pylori 210 -11539042 7502852902 hp1501 h. pylori predicted coding region hp1501 (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:outer membrane protein (omp32); identified by) (le:8629) (re:9795) (di:complement) HPAE000648 AE000648 g2314684 Helicobacter pylori 26695 85962 -11539042

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904822	17456	39612	447	148

Description

6500735185 outer membrane protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1564 HP1564 Helicobacter pylori 210 -11539043 7000690584 outer membrane protein (cl:lipoprotein-28) (db:pir2.dat) D64715 D64715 Helicobacter pylori 210 -11539043 7500959366 hp1564 outer membrane protein (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:30554 percent identity: 39.85;) (le:4510) (re:5325) (di:direct) HPAE000654 AE000654 g2314748 Helicobacter pylori 210 -11539043 7502852903 hp1564 outer membrane protein (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:30554 percent identity: 39.85;) (le:4510) (re:5325) (di:direct) HPAE000654 AE000654 g2314748 Helicobacter pylori 26695 85962 -11539043

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904824	17457	39613	489	163

Description

6500735186 rlpa:hp1571 rare lipoprotein a (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-helicobacter pylori) HP1571 HP1571 Helicobacter pylori 210 -11539044 7000690675 rare lipoprotein a (db:pir2.dat) C64716 C64716 Helicobacter pylori 210 -11539044 7500959447 hp1571 rare lipoprotein a rlpa (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:27846 percent identity: 37.63;) (le:10254) (re:11201) (di:complement) HPAE000654 AE000654 g2314752 Helicobacter pylori 210 -11539044 7502852904 hp1571 rare lipoprotein a rlpa (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:27846 percent identity: 37.63;) (le:10254) (re:11201) (di:complement) HPAE000654 AE000654 g2314752 Helicobacter pylori 26695 85962 -11539044

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904825	17458	39614	963	320

Description

6500735187 rfaj:hp0159 lipopolysaccharide 1:2-glucosyltransferase (gtcfc:11.3) (ec:2.4.1.58) (keggfc:14.1) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0159 HP0159 Helicobacter pylori 210 -11539045 7000690501 lipopolysaccharide 1:2-glucosyltransferase (db:pir2.dat) G64539 G64539 Helicobacter pylori 210 -11539045 7500959292 hp0159 lipopolysaccharide 1:2-glucosyltransferase (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to egad:6220 percent identity: 28.90;) (le:11394) (re:12512) (di:complement) HPAE000536 AE000536 g2313238 Helicobacter pylori 210 -11539045 7502852905 hp0159 lipopolysaccharide 1:2-glucosyltransferase (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to egad:6220 percent identity: 28.90;) (le:11394) (re:12512) (di:complement) HPAE000536 AE000536 g2313238 Helicobacter pylori 26695 85962 -11539045

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904829	17459	39615	597	198

Description

6500735188 spore coat polysaccharide biosynthesis protein e (gtcfc:11.3:12.15) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0178 HP0178 Helicobacter pylori 210 -11539046 7000690717 spore coat polysaccharide biosynthesis protein e (db:pir2.dat) B64542 B64542 Helicobacter pylori 210 -11539046 7500959483 hp0178 spore coat polysaccharide biosynthesis protein (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:similar to egad:43682 percent identity: 36.25;) (le:3179) (re:4201) (di:complement) HPAE000538 AE000538 g2313267 Helicobacter pylori 210 -11539046 7502852906 hp0178 spore coat polysaccharide biosynthesis protein (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:similar to egad:43682 percent identity: 36.25;) (le:3179) (re:4201) (di:complement) HPAE000538 AE000538 g2313267 Helicobacter pylori 26695 85962 -11539046

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904830	17460	39616	543	181

Description

6500735189 rfac:hp0279 lipopolysaccharide heptosyltransferase-1 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0279 HP0279 Helicobacter pylori 210 -11539047 7000690505 lipopolysaccharide heptosyltransferase-1 (db:pir2.dat) G64554 G64554 Helicobacter pylori 210 -11539047 7500959297 hp0279 lipopolysaccharide heptosyltransferase-1 rfac (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:similar to egad:9485 percent identity: 31.65;) (le:8415) (re:9437) (di:direct) HPAE000546 AE000546 g2313369 Helicobacter pylori 210 -11539047 7502852907 hp0279 lipopolysaccharide heptosyltransferase-1 rfac (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:similar to egad:9485 percent identity: 31.65;) (le:8415) (re:9437) (di:direct) HPAE000546 AE000546 g2313369 Helicobacter pylori 26695 85962 -11539047

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904832	17461	39617	204	67

Description

6500735190 neua:hp0326 cmp-n-acetylneuraminic acid synthetase (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0326 HP0326 Helicobacter pylori 210 -11539048 7000689715 cmp-n-acetylneuraminic acid synthetase (db:pir2.dat) F64560 F64560 Helicobacter pylori 210 -11539048 7500958522 hp0326 cmp-n-acetylneuraminic acid synthetase neua (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:20217 percent identity: 31.92;) (le:7354) (re:8907) (di:direct) HPAE000550 AE000550 g2313424 Helicobacter pylori 210 -11539048 7502852908 hp0326 cmp-n-acetylneuraminic acid synthetase neua (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:20217 percent identity: 31.92;) (le:7354) (re:8907) (di:direct) HPAE000550 AE000550 g2313424 Helicobacter pylori 26695 85962 -11539048

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904838	17462	39618	267	88

Description

6500735191 spore coat polysaccharide biosynthesis protein c (gtcfc:11.3:12.15) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0366 HP0366 Helicobacter pylori 210 -11539049 7000690716 spore coat polysaccharide biosynthesis protein c (cl:erythromycin resistance protein) (db:pir2.dat) F64565 F64565 Helicobacter pylori 210 -11539049 7500959482 hp0366 spore coat polysaccharide biosynthesis protein (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:similar to egad:43683 percent identity: 35.34;) (le:5322) (re:6449) (di:complement) HPAE000553 AE000553 g2313467 Helicobacter pylori 210 -11539049 7502852909 hp0366 spore coat polysaccharide biosynthesis protein (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:similar to egad:43683 percent identity: 35.34;) (le:5322) (re:6449) (di:complement) HPAE000553 AE000553 g2313467 Helicobacter pylori 26695 85962 -11539049

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904841	17463	39619	1263	421

Description

6500735192 fucosyltransferase (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0379 HP0379 Helicobacter pylori 210 -11539050 7000689954 fucosyltransferase (db:pir2.dat) C64567 C64567 Helicobacter pylori 210 -11539050 7500958742 hp0379 fucosyltransferase (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:contingency gene.; similar to egad:4092 percent) (le:8693) (re:9970) (di:direct) HPAE000554 AE000554 g2313482 Helicobacter pylori 210 -11539050 7502852910 hp0379 fucosyltransferase (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:contingency gene.; similar to egad:4092 percent) (le:8693) (re:9970) (di:direct) HPAE000554 AE000554 g2313482 Helicobacter pylori 26695 85962 -11539050

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904853	17464	39620	408	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904890	17465	39621	513	170

Description

6500735193 capj:hp0421 type 1 capsular polysaccharide biosynthesis protein j:type 1 capsular polysaccharide biosynthesisprotein j (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0421 HP0421 Helicobacter pylori 210 -11539051 7000690752 type 1 capsular polysaccharide biosynthesis protein j (db:pir2.dat) E64572 E64572 Helicobacter pylori 210 -11539051 7500959518 hp0421 type 1 capsular polysaccharide biosynthesis (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to egad:19569 percent identity: 29.00;) (le:13578) (re:14747) (di:direct) HPAE000557 AE000557 g2313523 Helicobacter pylori 210 -11539051 7502852911 hp0421 type 1 capsular polysaccharide biosynthesis (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to egad:19569 percent identity: 29.00;) (le:13578) (re:14747) (di:direct) HPAE000557 AE000557 g2313523 Helicobacter pylori 26695 85962 -11539051

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904899	17466	39622	447	148

Description

6500735194 fucosyltransferase (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0651 HP0651 Helicobacter pylori 210 -11539052 7000689955 fucosyltransferase (db:pir2.dat) C64601 C64601 Helicobacter pylori 210 -11539052 7500958743 hp0651 fucosyltransferase (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:contingency gene.; similar to egad:4092 percent) (le:13014) (re:14444) (di:complement) HPAE000578 AE000578 g2313769 Helicobacter pylori 210 -11539052 7502852912 hp0651 fucosyltransferase (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:contingency gene.; similar to egad:4092 percent) (le:13014) (re:14444) (di:complement) HPAE000578 AE000578 g2313769 Helicobacter pylori 26695 85962 -11539052

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904904	17467	39623	1224	407

Description

6500735195 wbpb:hp0679 lipopolysaccharide biosynthesis protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0679 HP0679 Helicobacter pylori 210 -11539053 7000690503 lipopolysaccharide biosynthesis protein (db:pir2.dat) G64604 G64604 Helicobacter pylori 210 -11539053 7500959295 hp0679 lipopolysaccharide biosynthesis protein wbpb (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:similar to gp:1545848 percent identity: 42.79;) (le:1531) (re:2400) (di:complement) HPAE000581 AE000581 g2313805 Helicobacter pylori 210 -11539053 7502852913 hp0679 lipopolysaccharide biosynthesis protein wbpb (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:similar to gp:1545848 percent identity: 42.79;) (le:1531) (re:2400) (di:complement) HPAE000581 AE000581 g2313805 Helicobacter pylori 26695 85962 -11539053

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904905	17468	39624	1383	461

Description

6500735196 lex2b:hp0805 lipooligosaccharide 5g8 epitope biosynthesis-associated protein:lipooligosaccharide 5g8 epitopebiosynthesis-associated protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0805 HP0805 Helicobacter pylori 210 -11539054 7000689483 lipopolysaccharide 5g8 epitope biosynthesis-associated protein (cl:lipopolysaccharide biosynthesis-associated protein) (db:pir2.dat) E64620 E64620 Helicobacter pylori 210 -11539054 7500955782 hp0805 lipooligosaccharide 5g8 epitope (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:14804 percent identity: 36.89;) (le:4653) (re:5507) (di:complement) HPAE000592 AE000592 g2313935 Helicobacter pylori 210 -11539054 7502852914 hp0805 lipooligosaccharide 5g8 epitope (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:14804 percent identity: 36.89;) (le:4653) (re:5507) (di:complement) HPAE000592 AE000592 g2313935 Helicobacter pylori 26695 85962 -11539054

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904912	17469	39625	1032	343

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904917	17470	39626	294	97

Description

6500735197 lex2b:hp0826 lipooligosaccharide 5g8 epitope biosynthesis-associated protein:lipooligosaccharide 5g8 epitopebiosynthesis-associated protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0826 HP0826 Helicobacter pylori 210 -11539055 7000689482 lipopolysaccharide biosynthesis-associated protein lex2b (cl:lipopolysaccharide biosynthesis-associated protein) (db:pir2.dat) B64623 B64623 Helicobacter pylori 210 -11539055 7500955781 hp0826 lipooligosaccharide 5g8 epitope (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:14804 percent identity: 39.20;) (le:1551) (re:2372) (di:direct) HPAE000594 AE000594 g2313960 Helicobacter pylori 210 -11539055 7502852915 hp0826 lipooligosaccharide 5g8 epitope (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:14804 percent identity: 39.20;) (le:1551) (re:2372) (di:direct) HPAE000594 AE000594 g2313960 Helicobacter pylori 26695 85962 -11539055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904933	17471	39627	2688	895

Description

6500735198 algi:hp0855 alginate o-acetylation protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0855 HP0855 Helicobacter pylori 210 -11539056 7000689626 alginate o-acetylation protein (db:pir2.dat) G64626 G64626 Helicobacter pylori 210 -11539056 7500958444 hp0855 alginate o-acetylation protein algi (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:38563 percent identity: 41.83;) (le:8090) (re:9673) (di:direct) HPAE000596 AE000596 g2313988 Helicobacter pylori 210 -11539056 7502852916 hp0855 alginate o-acetylation protein algi (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:38563 percent identity: 41.83;) (le:8090) (re:9673) (di:direct) HPAE000596 AE000596 g2313988 Helicobacter pylori 26695 85962 -11539056

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904940	17472	39628	438	145

Description

6500735199 rfae:hp0858 adp-heptose synthase (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0858 HP0858 Helicobacter pylori 210 -11539057 7000689489 adp-heptose synthase (cl:hypothetical protein b3052) (db:pir2.dat) B64627 B64627 Helicobacter pylori 210 -11539057 7500955791 hp0858 adp-heptose synthase rfae (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:40002 percent identity: 40.59;) (le:11351) (re:12736) (di:complement) HPAE000596 AE000596 g2313990 Helicobacter pylori 210 -11539057 7502852917 hp0858 adp-heptose synthase rfae (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:40002 percent identity: 40.59;) (le:11351) (re:12736) (di:complement) HPAE000596 AE000596 g2313990 Helicobacter pylori 26695 85962 -11539057

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904949	17473	39629	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904954	17474	39630	609	202

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904956	17475	39631	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904967	17476	39632	393	130

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501904974	17477	39633	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905004	17478	39634	1059	352

Description

6500735200 kdta:hp0957 3-deoxy-d-manno-octulosonic-acid transferase (gtcfc:11.3) (ec:2.-.-.-) (keggfc:14.1) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP0957 HP0957 Helicobacter pylori 210 -11539058 7000689591 3-deoxy-d-manno-octulosonic-acid transferase (db:pir2.dat) E64639 E64639 Helicobacter pylori 210 -11539058 7500958412 hp0957 3-deoxy-d-manno-octulosonic-acid transferase (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:29274 percent identity: 35.90;) (le:9529) (re:10710) (di:complement) HPAE000604 AE000604 g2314094 Helicobacter pylori 210 -11539058 7502852918 hp0957 3-deoxy-d-manno-octulosonic-acid transferase (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:29274 percent identity: 35.90;) (le:9529) (re:10710) (di:complement) HPAE000604 AE000604 g2314094 Helicobacter pylori 26695 85962 -11539058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905009	17479	39635	402	133

Description

6500735201 lps biosynthesis protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1105 HP1105 Helicobacter pylori 210 -11539059 7000690506 lps biosynthesis protein (db:pir2.dat) A64658 A64658 Helicobacter pylori 210 -11539059 7500959299 hp1105 lps biosynthesis protein (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to egad:41941 percent identity: 28.68;) (le:1169) (re:2464) (di:complement) HPAE000617 AE000617 g2314258 Helicobacter pylori 210 -11539059 7502852919 hp1105 lps biosynthesis protein (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to egad:41941 percent identity: 28.68;) (le:1169) (re:2464) (di:complement) HPAE000617 AE000617 g2314258 Helicobacter pylori 26695 85962 -11539059

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905015	17480	39636	351	116

Description

GTC ORF with score 98 to: (sr:human) (db:genpept) (de:human dna sequence from clone 889n15 on chromosome xq22.1-22.3.contains part of the gene for a novel protein similar to x. laeviscortical thymocyte marker ctx, the possibly alternatively splicedgene...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905021	17481	39637	1134	377

Description

6500735202 rfaf:hp1191 adp-heptose-lps heptosyltransferase ii (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1191 HP1191 Helicobacter pylori 210 -11539060 7000689621 adp-heptose-lps heptosyltransferase ii (db:pir2.dat) G64668 G64668 Helicobacter pylori 210 -11539060 7500958440 hp1191 adp-heptose-lps heptosyltransferase ii rfaf (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to egad:28123 percent identity: 33.22;) (le:2727) (re:3776) (di:direct) HPAE000625 AE000625 g2314352 Helicobacter pylori 210 -11539060 7502852920 hp1191 adp-heptose-lps heptosyltransferase ii rfaf (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to egad:28123 percent identity: 33.22;) (le:2727) (re:3776) (di:direct) HPAE000625 AE000625 g2314352 Helicobacter pylori 26695 85962 -11539060

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905022	17482	39638	414	137

Description

6500735203 fibronectin/fibrinogen-binding protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1392 HP1392 Helicobacter pylori 210 -11539061 7000689921 fibronectin/fibrinogen-binding protein (db:pir2.dat) H64693 H64693 Helicobacter pylori 210 -11539061 7500958715 hp1392 fibronectin/fibrinogen-binding protein (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:similar to egad:15656 percent identity: 25.71;) (le:1394) (re:2701) (di:complement) HPAE000639 AE000639 g2314561 Helicobacter pylori 210 -11539061 7502852921 hp1392 fibronectin/fibrinogen-binding protein (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:similar to egad:15656 percent identity: 25.71;) (le:1394) (re:2701) (di:complement) HPAE000639 AE000639 g2314561 Helicobacter pylori 26695 85962 -11539061

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905025	17483	39639	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905030	17484	39640	684	227

Description

6500735204 rfaj:hp1416 lipopolysaccharide 1:2-glucosyltransferase (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1416 HP1416 Helicobacter pylori 210 -11539062 7000690502 lipopolysaccharide 1:2-glucosyltransferase (db:pir2.dat) H64696 H64696 Helicobacter pylori 210 -11539062 7500959294 hp1416 lipopolysaccharide 1:2-glucosyltransferase (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to egad:6220 percent identity: 29.21;) (le:1847) (re:2950) (di:direct) HPAE000642 AE000642 g2314591 Helicobacter pylori 210 -11539062 7502852922 hp1416 lipopolysaccharide 1:2-glucosyltransferase (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to egad:6220 percent identity: 29.21;) (le:1847) (re:2950) (di:direct) HPAE000642 AE000642 g2314591 Helicobacter pylori 26695 85962 -11539062

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905037	17485	39641	576	191

Description

6500735205 kpsf:hp1429 polysialic acid capsule expression protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1429 HP1429 Helicobacter pylori 210 -11539063 7000690635 polysialic acid capsule expression protein (cl:probable atp-binding protein gutq) (db:pir2.dat) E64698 E64698 Helicobacter pylori 210 -11539063 7500959414 hp1429 polysialic acid capsule expression protein (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:similar to egad:28666 percent identity: 45.95;) (le:3454) (re:4443) (di:complement) HPAE000643 AE000643 g2314601 Helicobacter pylori 210 -11539063 7502852923 hp1429 polysialic acid capsule expression protein (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:similar to egad:28666 percent identity: 45.95;) (le:3454) (re:4443) (di:complement) HPAE000643 AE000643 g2314601 Helicobacter pylori 26695 85962 -11539063

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905038	17486	39642	186	61

Description

6500735206 kdtb:hp1475 lipopolysaccharide core biosynthesis protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1475 HP1475 Helicobacter pylori 210 -11539064 7000690504 lipopolysaccharide core biosynthesis protein (cl:lipopolysaccharide core biosynthesis protein kdtb) (db:pir2.dat) C64704 C64704 Helicobacter pylori 210 -11539064 7500959296 hp1475 lipopolysaccharide core biosynthesis protein (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:9109 percent identity: 49.04;) (le:9948) (re:10421) (di:complement) HPAE000647 AE000647 g2314651 Helicobacter pylori 210 -11539064 7502852924 hp1475 lipopolysaccharide core biosynthesis protein (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:9109 percent identity: 49.04;) (le:9948) (re:10421) (di:complement) HPAE000647 AE000647 g2314651 Helicobacter pylori 26695 85962 -11539064

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905039	17487	39643	696	231

Description

GTC ORF with score 276 to: (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:2.1.1.63) (de:escherichia coli k-12 mg1655 section 200 of 400 of the completegenome.) (nt:f354; 100 pct identical to ada_ecoli sw: p06134) (le:5661) (re:6725) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905043	17488	39644	453	150

Description

6500735207 lps biosynthesis protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1578 HP1578 Helicobacter pylori 210 -11539065 7000690507 lps biosynthesis protein (db:pir2.dat) B64717 B64717 Helicobacter pylori 210 -11539065 7500959300 hp1578 lps biosynthesis protein (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:42710 percent identity: 28.09;) (le:3492) (re:4610) (di:complement) HPAE000655 AE000655 g2314763 Helicobacter pylori 210 -11539065 7502852925 hp1578 lps biosynthesis protein (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:42710 percent identity: 28.09;) (le:3492) (re:4610) (di:complement) HPAE000655 AE000655 g2314763 Helicobacter pylori 26695 85962 -11539065

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905044	17489	39645	297	98

Description

6500735208 llm:hp1581 methicillin resistance protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.3) (db:gtc-helicobacter pylori) HP1581 HP1581 Helicobacter pylori 210 -11539066 7000690515 methicillin resistance protein (db:pir2.dat) E64717 E64717 Helicobacter pylori 210 -11539066 7500959308 hp1581 methicillin resistance protein llm (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:23076 percent identity: 29.17;) (le:5690) (re:6700) (di:complement) HPAE000655 AE000655 g2314764 Helicobacter pylori 210 -11539066 7502852926 hp1581 methicillin resistance protein llm (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:23076 percent identity: 29.17;) (le:5690) (re:6700) (di:complement) HPAE000655 AE000655 g2314764 Helicobacter pylori 26695 85962 -11539066

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905052	17490	39646	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905117	17491	39647	366	121

Description

6500735209 flab:hp0115 flagellin b flab:flagellin b:flagellin n (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0115 HP0115 Helicobacter pylori 210 -11539067 7000689405 flagellin b:minor flagellin flab (cl:flagellin) (db:pir2.dat) C64534 C64534 Helicobacter pylori 210 -11539067 7500955406 hp0115 flagellin b flab (db:genpept-bct1) (de:helicobacter pylori section 11 of 134 of the complete genome.) (nt:similar to egad:20706 percent identity: 99.03;) (le:3162) (re:4706) (di:complement) HPAE000533 AE000533 g2313197 Helicobacter pylori 210 -11539067 7502852927 hp0115 flagellin b flab (db:genpept) (de:helicobacter pylori 26695 section 11 of 134 of the complete genome.) (nt:similar to egad:20706 percent identity: 99.03;) (le:3162) (re:4706) (di:complement) HPAE000533 AE000533 g2313197 Helicobacter pylori 26695 85962 -11539067

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905121	17492	39648	825	274

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905126	17493	39649	837	278

Description

GTC ORF with score 538 to: (sr:erwinia herbicola (strain eho10) dna) (db:genpept-bct1) (de:erwinia herbicola geranylgeranyl pyrophosphate synthase (crte),zeaxanthin glucosyl transferase (crtx), lycopene cyclase (crty),phyotene dehydogenase (crti), ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905138	17494	39650	1116	371

Description

6500735210 flir:hp0173 flagellar biosynthetic protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0173 HP0173 Helicobacter pylori 210 -11539068 7000689936 flagellar biosynthetic protein (db:pir2.dat) E64541 E64541 Helicobacter pylori 210 -11539068 7500958728 hp0173 flagellar biosynthetic protein flir (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to egad:8745 percent identity: 26.45;) (le:11121) (re:11888) (di:complement) HPAE000537 AE000537 g2313256 Helicobacter pylori 210 -11539068 7502852928 hp0173 flagellar biosynthetic protein flir (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to egad:8745 percent identity: 26.45;) (le:11121) (re:11888) (di:complement) HPAE000537 AE000537 g2313256 Helicobacter pylori 26695 85962 -11539068

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905143	17495	39651	879	293

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905145	17496	39652	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905146	17497	39653	576	191

Description

6500735211 hemagglutinin homolog:secreted protein-flagellar motility hpaa:secreted protein involved in flagellar motility (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0232 HP0232 Helicobacter pylori 210 -11539069 7000689941 flagellar motility secreted protein (db:pir2.dat) S70997 H64548 Helicobacter pylori 210 -11539069 7500958732 hp0232 secreted protein involved in flagellar motility (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to gp:1419555 percent identity: 99.18;) (le:3393) (re:4040) (di:direct) HPAE000543 AE000543 g2313324 Helicobacter pylori 210 -11539069 7502852929 hp0232 secreted protein involved in flagellar motility (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to gp:1419555 percent identity: 99.18;) (le:3393) (re:4040) (di:direct) HPAE000543 AE000543 g2313324 Helicobacter pylori 26695 85962 -11539069

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905147	17498	39654	279	92

Description

6500735212 flgi:hp0246 flagellar basal-body p-ring protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0246 HP0246 Helicobacter pylori 210 -11539070 7000689925 flagellar basal-body p-ring protein (cl:flagellar basal body p-ring protein flgi) (db:pir2.dat) F64550 F64550 Helicobacter pylori 210 -11539070 7500958719 hp0246 flagellar basal-body p-ring protein flgi (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:similar to egad:23939 percent identity: 37.94;) (le:1589) (re:2617) (di:complement) HPAE000544 AE000544 g2313339 Helicobacter pylori 210 -11539070 7502852930 hp0246 flagellar basal-body p-ring protein flgi (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:similar to egad:23939 percent identity: 37.94;) (le:1589) (re:2617) (di:complement) HPAE000544 AE000544 g2313339 Helicobacter pylori 26695 85962 -11539070

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905158	17499	39655	576	191

Description

GTC ORF with score 102 to: (sr:mice macrophage) (db:genpept-rod) (de:putative transcription regulator {clone t2, repetitive sequence}(mice, macrophage, mrna, 1263 nt).) (nt:method: conceptual translation supplied by author.) (le:55) (re:732) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905163	17500	39656	378	125

Description

6500735213 fla:hp0295 gellin b homolog:flagellin b homolog (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0295 HP0295 Helicobacter pylori 210 -11539071 7000689947 flagellin b homolog (db:pir2.dat) G64556 G64556 Helicobacter pylori 210 -11539071 7500958735 hp0295 flagellin b homolog fla (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:20706 percent identity: 32.90;) (le:1249) (re:3735) (di:complement) HPAE000548 AE000548 g2313393 Helicobacter pylori 210 -11539071 7502852931 hp0295 flagellin b homolog fla (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:20706 percent identity: 32.90;) (le:1249) (re:3735) (di:complement) HPAE000548 AE000548 g2313393 Helicobacter pylori 26695 85962 -11539071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905165	17501	39657	642	213

Description

6500735214 flgh:hp0325 flagellar basal-body l-ring protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0325 HP0325 Helicobacter pylori 210 -11539072 7000689923 flagellar basal-body l-ring protein (db:pir2.dat) E64560 E64560 Helicobacter pylori 210 -11539072 7500958717 hp0325 flagellar basal-body l-ring protein flgh (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:19556 percent identity: 32.69;) (le:6623) (re:7336) (di:direct) HPAE000550 AE000550 g2313423 Helicobacter pylori 210 -11539072 7502852932 hp0325 flagellar basal-body l-ring protein flgh (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:19556 percent identity: 32.69;) (le:6623) (re:7336) (di:direct) HPAE000550 AE000550 g2313423 Helicobacter pylori 26695 85962 -11539072

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905170	17502	39658	573	190

Description

6500735215 flag:hp0327 flagellar protein g (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0327 HP0327 Helicobacter pylori 210 -11539073 7000689945 flagellar protein g (db:pir2.dat) G64560 G64560 Helicobacter pylori 210 -11539073 7500958733 hp0327 flagellar protein g flag (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:43044 percent identity: 23.27;) (le:8904) (re:9446) (di:direct) HPAE000550 AE000550 g2313425 Helicobacter pylori 210 -11539073 7502852933 hp0327 flagellar protein g flag (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:43044 percent identity: 23.27;) (le:8904) (re:9446) (di:direct) HPAE000550 AE000550 g2313425 Helicobacter pylori 26695 85962 -11539073

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905178	17503	39659	819	272

Description

6500735216 flif:hp0351 flagellar basal-body m-ring protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0351 HP0351 Helicobacter pylori 210 -11539074 7000689924 flagellar basal-body m-ring protein (db:pir2.dat) G64563 G64563 Helicobacter pylori 210 -11539074 7500958718 hp0351 flagellar basal-body m-ring protein flif (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:similar to egad:20405 percent identity: 34.44;) (le:872) (re:2575) (di:direct) HPAE000552 AE000552 g2313452 Helicobacter pylori 210 -11539074 7502852934 hp0351 flagellar basal-body m-ring protein flif (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:similar to egad:20405 percent identity: 34.44;) (le:872) (re:2575) (di:direct) HPAE000552 AE000552 g2313452 Helicobacter pylori 26695 85962 -11539074

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905179	17504	39660	303	100

Description

6500735217 flig:hp0352 flagellar motor switch protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0352 HP0352 Helicobacter pylori 210 -11539075 7000689438 flagellar motor switch protein (cl:flagellar switch protein flig) (db:pir2.dat) H64563 H64563 Helicobacter pylori 210 -11539075 7500955492 hp0352 flagellar motor switch protein flig (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:similar to egad:38135 percent identity: 36.98;) (le:2593) (re:3624) (di:direct) HPAE000552 AE000552 g2313453 Helicobacter pylori 210 -11539075 7502852935 hp0352 flagellar motor switch protein flig (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:similar to egad:38135 percent identity: 36.98;) (le:2593) (re:3624) (di:direct) HPAE000552 AE000552 g2313453 Helicobacter pylori 26695 85962 -11539075

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905184	17505	39661	1062	353

Description

6500735218 flih:hp0353 flagellar export protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0353 HP0353 Helicobacter pylori 210 -11539076 7000689938 flagellar export protein (db:pir2.dat) A64564 A64564 Helicobacter pylori 210 -11539076 7500958729 hp0353 flagellar export protein flih (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:similar to egad:38108 percent identity: 29.05;) (le:3611) (re:4387) (di:direct) HPAE000552 AE000552 g2313454 Helicobacter pylori 210 -11539076 7502852936 hp0353 flagellar export protein flih (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:similar to egad:38108 percent identity: 29.05;) (le:3611) (re:4387) (di:direct) HPAE000552 AE000552 g2313454 Helicobacter pylori 26695 85962 -11539076

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905188	17506	39662	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905190	17507	39663	675	224

Description

6500735219 hpaa:hp0410 putative neuraminyllactose-binding:putative neuraminyllactose-binding hemagglutininhomolog (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0410 HP0410 Helicobacter pylori 210 -11539077 7000690643 probable neuraminyllactose-binding hemagglutinin homolog (db:pir2.dat) B64571 B64571 Helicobacter pylori 210 -11539077 7500959422 hp0410 putative neuraminyllactose-binding hemagglutinin (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to egad:34209 percent identity: 24.19;) (le:2223) (re:2972) (di:direct) HPAE000557 AE000557 g2313516 Helicobacter pylori 210 -11539077 7502852937 hp0410 putative neuraminyllactose-binding hemagglutinin (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to egad:34209 percent identity: 24.19;) (le:2223) (re:2972) (di:direct) HPAE000557 AE000557 g2313516 Helicobacter pylori 26695 85962 -11539077

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905215	17508	39664	447	148

Description

6500735220 flin:hp0584 flagellar switch protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0584 HP0584 Helicobacter pylori 210 -11539078 7000689946 flagellar switch protein (cl:flagellar motor switch protein) (db:pir2.dat) H64592 H64592 Helicobacter pylori 210 -11539078 7500958734 hp0584 flagellar switch protein flin (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:38123 percent identity: 39.73;) (le:13875) (re:14246) (di:complement) HPAE000571 AE000571 g2313688 Helicobacter pylori 210 -11539078 7502852938 hp0584 flagellar switch protein flin (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:38123 percent identity: 39.73;) (le:13875) (re:14246) (di:complement) HPAE000571 AE000571 g2313688 Helicobacter pylori 26695 85962 -11539078

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905216	17509	39665	222	73

Description

7500955405 flaa:hp0601 flagellin a flaa:flagellin a (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0601 HP0601 Helicobacter pylori 210 -11539079 7000689404 flaa flagellin a (cl:flagellin) (db:pir2.dat) A64595 A64595 Helicobacter pylori 210 -11539079 7500955404 hp0601 flagellin a flaa (db:genpept-bct1) (de:helicobacter pylori section 52 of 134 of the complete genome.) (nt:similar to egad:12921 percent identity: 99.80;) (le:112) (re:1644) (di:direct) HPAE000574 AE000574 g2313722 Helicobacter pylori 210 -11539079 7502852939 flaa flagellin a (db:genpept) (de:helicobacter pylori, strain j99 section 48 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0601) (le:7281) (re:8813) (di:direct) AE001487 AE001487 g4155099 Helicobacter pylori J99 85963 -11539079 6500735221 hp0601 flagellin a flaa (db:genpept) (de:helicobacter pylori 26695 section 52 of 134 of the complete genome.) (nt:similar to egad:12921 percent identity: 99.80;) (le:112) (re:1644) (di:direct) HPAE000574 AE000574 g2313722 Helicobacter pylori 26695 85962 -11539079

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905219	17510	39666	639	212

Description

6500735222 flip:hp0685 flagellar biosynthetic protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0685 HP0685 Helicobacter pylori 210 -11539080 5000696355 (de:(hp0685) (pn:flagellar biosynthetic protein:flip) (gn:flip) (gtcfc:11.3) (ec:) (keggfc:11.2) (tigrfc:3.4) (db:gtc-helicobacter pylori)) HP0685 HP0685 Helicobacter pylori 210 10316863

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905220	17511	39667	1479	492

Description

6500735223 flag:hp0751 polar flagellin flag:polar flagellin (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0751 HP0751 Helicobacter pylori 210 -11539081 7000690629 polar flagellin (db:pir2.dat) G64613 G64613 Helicobacter pylori 210 -11539081 7500959409 hp0751 polar flagellin flag (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:similar to egad:14382 percent identity: 21.90;) (le:9753) (re:10112) (di:direct) HPAE000587 AE000587 g2313876 Helicobacter pylori 210 -11539081 7502852940 hp0751 polar flagellin flag (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:similar to egad:14382 percent identity: 21.90;) (le:9753) (re:10112) (di:direct) HPAE000587 AE000587 g2313876 Helicobacter pylori 26695 85962 -11539081

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905257	17512	39668	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905261	17513	39669	1014	337

Description

6500735224 flid:hp0752 flagellar hook-associated protein 2 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0752 HP0752 Helicobacter pylori 210 -11539082 5500685225 flid:hp0752 (sr:,campylobacter pylori) (de:flagellar hook-associated protein 2 homolog) (db:swissprot) FLID_HELPY P96786 HELICOBACTER PYLORI 210 -11539082 7000685282 flagellar hook-associated protein 2 (db:pir2.dat) H64613 H64613 Helicobacter pylori 210 -11539082 7500881581 hp0752 flagellar hook-associated protein 2 flid (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:similar to egad:13626 percent identity: 28.88;) (le:10129) (re:12153) (di:direct) HPAE000587 AE000587 g2313877 Helicobacter pylori 210 -11539082 7502852941 hp0752 flagellar hook-associated protein 2 flid (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:similar to egad:13626 percent identity: 28.88;) (le:10129) (re:12153) (di:direct) HPAE000587 AE000587 g2313877 Helicobacter pylori 26695 85962 -11539082

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905264	17514	39670	489	162

Description

6500735225 flis:hp0753 flagellar protein flis:flagellar protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0753 HP0753 Helicobacter pylori 210 -11539083 7000689496 flagellar protein (cl:flagellar protein flis) (db:pir2.dat) A64614 A64614 Helicobacter pylori 210 -11539083 7500955796 hp0753 flagellar protein flis (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:similar to egad:13049 percent identity: 32.26;) (le:66) (re:446) (di:direct) HPAE000588 AE000588 g2313881 Helicobacter pylori 210 -11539083 7502852942 hp0753 flagellar protein flis (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:similar to egad:13049 percent identity: 32.26;) (le:66) (re:446) (di:direct) HPAE000588 AE000588 g2313881 Helicobacter pylori 26695 85962 -11539083

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905267	17515	39671	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905292	17516	39672	264	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905303	17517	39673	600	199

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905304	17518	39674	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905306	17519	39675	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905322	17520	39676	285	94

Description

6500735226 flhb:hp0770 flagellar biosynthetic protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0770 HP0770 Helicobacter pylori 210 -11539084 7500881571 flhb:hp0770 (sr:,campylobacter pylori) (de:flagellar biosynthetic protein flhb) (db:swissprot) FLHB_HELPY P56416 HELICOBACTER PYLORI 210 -11539084 7000689933 flagellar biosynthetic protein (cl:flagellar biosynthetic protein flhb) (db:pir2.dat) B64616 B64616 Helicobacter pylori 210 -11539084 7500881573 hp0770 flagellar biosynthetic protein flhb (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:similar to egad:7593 percent identity: 38.73;) (le:1902) (re:2978) (di:direct) HPAE000589 AE000589 g2313898 Helicobacter pylori 210 -11539084 7502852943 hp0770 flagellar biosynthetic protein flhb (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:similar to egad:7593 percent identity: 38.73;) (le:1902) (re:2978) (di:direct) HPAE000589 AE000589 g2313898 Helicobacter pylori 26695 85962 -11539084

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905341	17521	39677	399	132

Description

6500735227 hpaa:hp0797 flagellar sheath adhesin hpaa:neuraminyllactose-binding hemagglutinin precursor:n-acetylneuraminyllactose-binding fibrillar hemagglutinin receptor-binding subunit:nlbh:flagellar sheath adhesin (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0797 HP0797 Helicobacter pylori 210 -11539085 5500685362 hpaa:hp0797 (sr:,campylobacter pylori) (de:binding subunit) (nlbh) (flagellar sheath adhesin)) (db:swissprot) HPA0_HELPY P55969 HELICOBACTER PYLORI 210 -11539085 7000685553 hpaa adhesin a:flagellar sheath adhesin hpaa:n-acetylneuraminyllactose-binding fibrillar hemagglutinin receptor-binding subunit (db:pir2.dat) E64619 E64619 Helicobacter pylori 210 -11539085 7500883475 hp0797 flagellar sheath adhesin hpaa (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:similar to egad:34160 percent identity: 98.46;) (le:10448) (re:11230) (di:complement) HPAE000591 AE000591 g2313925 Helicobacter pylori 210 -11539085 7502852944 hp0797 flagellar sheath adhesin hpaa (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:similar to egad:34160 percent identity: 98.46;) (le:10448) (re:11230) (di:complement) HPAE000591 AE000591 g2313925 Helicobacter pylori 26695 85962 -11539085

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905349	17522	39678	411	136

Description

6500735228 mota:hp0815 flagellar motor rotation protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0815 HP0815 Helicobacter pylori 210 -11539086 7500885786 mota:hp0815 (sr:,campylobacter pylori) (de:chemotaxis mota protein (motility protein a)) (db:swissprot) MOTA_HELPY P56426 HELICOBACTER PYLORI 210 -11539086 7000689942 flagellar motor rotation protein (cl:flagellar motor rotation protein) (db:pir2.dat) G64621 G64621 Helicobacter pylori 210 -11539086 7500885788 hp0815 flagellar motor rotation protein mota (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:14089 percent identity: 32.93;) (le:2801) (re:3574) (di:direct) HPAE000593 AE000593 g2313947 Helicobacter pylori 210 -11539086 7502852945 mota putative chemotaxis protein motility protein (db:genpept) (de:helicobacter pylori, strain j99 section 67 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0815) (le:2802) (re:3575) (di:direct) AE001506 AE001506 g4155315 Helicobacter pylori J99 85963 -11539086 7502852946 hp0815 flagellar motor rotation protein mota (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:14089 percent identity: 32.93;) (le:2801) (re:3574) (di:direct) HPAE000593 AE000593 g2313947 Helicobacter pylori 26695 85962 -11539086

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905350	17523	39679	297	98

Description

6500735229 motb:hp0816 flagellar motor rotation protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0816 HP0816 Helicobacter pylori 210 -11539087 7500885798 motb:hp0816 (sr:,campylobacter pylori) (de:chemotaxis motb protein (motility protein b)) (db:swissprot) MOTB_HELPY P56427 HELICOBACTER PYLORI 210 -11539087 7000689943 flagellar motor rotation protein (db:pir2.dat) H64621 H64621 Helicobacter pylori 210 -11539087 7500885800 hp0816 flagellar motor rotation protein motb (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:13545 percent identity: 29.74;) (le:3577) (re:4350) (di:direct) HPAE000593 AE000593 g2313948 Helicobacter pylori 210 -11539087 7502852947 hp0816 flagellar motor rotation protein motb (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:13545 percent identity: 29.74;) (le:3577) (re:4350) (di:direct) HPAE000593 AE000593 g2313948 Helicobacter pylori 26695 85962 -11539087

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905365	17524	39680	1485	494

Description

6500735230 flaa1 protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0840 HP0840 Helicobacter pylori 210 -11539088 7000689922 flaa1 protein (cl:probable capsular polysaccharide biosynthesis protein d) (db:pir2.dat) H64624 H64624 Helicobacter pylori 210 -11539088 7500958716 hp0840 flaa1 protein (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:similar to egad:43081 percent identity: 60.21;) (le:3998) (re:4999) (di:direct) HPAE000595 AE000595 g2313972 Helicobacter pylori 210 -11539088 7502852948 hp0840 flaa1 protein (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:similar to egad:43081 percent identity: 60.21;) (le:3998) (re:4999) (di:direct) HPAE000595 AE000595 g2313972 Helicobacter pylori 26695 85962 -11539088

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905371	17525	39681	327	108

Description

6500735231 flge:hp0870 flagellar hook flge:flagellar hook protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0870 HP0870 Helicobacter pylori 210 -11539089 71916 flge:hp0870 (sr:,campylobacter pylori) (de:flagellar hook protein flge) (db:swissprot) FLGE_HELPY P50610 HELICOBACTER PYLORI 210 -11539089 7000685263 flge flagellar hook protein flge (db:pir2.dat) F64628 F64628 Helicobacter pylori 210 -11539089 7500881555 hp0870 flagellar hook flge (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:34181 percent identity: 98.89;) (le:20859) (re:23015) (di:complement) HPAE000596 AE000596 g2313997 Helicobacter pylori 210 -11539089 7502852949 hp0870 flagellar hook flge (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:34181 percent identity: 98.89;) (le:20859) (re:23015) (di:complement) HPAE000596 AE000596 g2313997 Helicobacter pylori 26695 85962 -11539089

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905381	17526	39682	312	103

Description

6500735232 flgd:hp0907 hook assembly protein:flagella (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0907 HP0907 Helicobacter pylori 210 -11539090 7000689996 hook assembly protein:flagella (db:pir2.dat) C64633 C64633 Helicobacter pylori 210 -11539090 7500958774 hp0907 hook assembly protein:flagella flgd (db:genpept-bct1) (de:helicobacter pylori section 78 of 134 of the complete genome.) (nt:similar to egad:20832 percent identity: 25.54;) (le:1794) (re:2699) (di:direct) HPAE000600 AE000600 g2314043 Helicobacter pylori 210 -11539090 7502852950 hp0907 hook assembly protein:flagella flgd (db:genpept) (de:helicobacter pylori 26695 section 78 of 134 of the complete genome.) (nt:similar to egad:20832 percent identity: 25.54;) (le:1794) (re:2699) (di:direct) HPAE000600 AE000600 g2314043 Helicobacter pylori 26695 85962 -11539090

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905406	17527	39683	690	229

Description

6500735233 flge:hp0908 flagellar hook flge:flagellar hook (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP0908 HP0908 Helicobacter pylori 210 -11539091 7000689939 flagellar hook (db:pir2.dat) D64633 D64633 Helicobacter pylori 210 -11539091 7500958730 hp0908 flagellar hook flge (db:genpept-bct1) (de:helicobacter pylori section 78 of 134 of the complete genome.) (nt:similar to egad:34181 percent identity: 30.49;) (le:2696) (re:4513) (di:direct) HPAE000600 AE000600 g2314044 Helicobacter pylori 210 -11539091 7502852951 hp0908 flagellar hook flge (db:genpept) (de:helicobacter pylori 26695 section 78 of 134 of the complete genome.) (nt:similar to egad:34181 percent identity: 30.49;) (le:2696) (re:4513) (di:direct) HPAE000600 AE000600 g2314044 Helicobacter pylori 26695 85962 -11539091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905416	17528	39684	432	143

Description

GTC ORF with score 202 to: (db:genpept-pln2) (de:emericella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj),(stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905424	17529	39685	210	69

Description

6500735234 fliy:hp1030 fliy protein fliy:protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1030 HP1030 Helicobacter pylori 210 -11539092 7000689950 fliy protein (db:pir2.dat) F64648 F64648 Helicobacter pylori 210 -11539092 7500958738 hp1030 fliy protein fliy (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to egad:14570 percent identity: 29.27;) (le:1641) (re:2504) (di:complement) HPAE000611 AE000611 g2314175 Helicobacter pylori 210 -11539092 7502852952 hp1030 fliy protein fliy (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to egad:14570 percent identity: 29.27;) (le:1641) (re:2504) (di:complement) HPAE000611 AE000611 g2314175 Helicobacter pylori 26695 85962 -11539092

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905425	17530	39686	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905429	17531	39687	1641	546

Description

6500735235 flim:hp1031 flagellar motor switch protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1031 HP1031 Helicobacter pylori 210 -11539093 7000689944 flagellar motor switch protein (cl:flagellar motor switch protein flim) (db:pir2.dat) G64648 G64648 Helicobacter pylori 210 -11539093 7500955361 hp1031 flagellar motor switch protein flim (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to egad:38124 percent identity: 34.41;) (le:2508) (re:3572) (di:complement) HPAE000611 AE000611 g2314176 Helicobacter pylori 210 -11539093 7502852953 hp1031 flagellar motor switch protein flim (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to egad:38124 percent identity: 34.41;) (le:2508) (re:3572) (di:complement) HPAE000611 AE000611 g2314176 Helicobacter pylori 26695 85962 -11539093

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905430	17532	39688	1296	431

Description

6500735236 flhf:hp1035 flagellar biosynthesis protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1035 HP1035 Helicobacter pylori 210 -11539094 7502852954 flhf:hp1035 (sr:,campylobacter pylori) (de:protein)) (db:swissprot) FLHF_HELPY O25679 HELICOBACTER PYLORI 210 -11539094 7000689931 flagellar biosynthesis protein (db:pir2.dat) C64649 C64649 Helicobacter pylori 210 -11539094 7500958725 hp1035 flagellar biosynthesis protein flhf (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to egad:7272 percent identity: 35.48;) (le:5512) (re:6891) (di:complement) HPAE000611 AE000611 g2314179 Helicobacter pylori 210 -11539094 7502852955 hp1035 flagellar biosynthesis protein flhf (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to egad:7272 percent identity: 35.48;) (le:5512) (re:6891) (di:complement) HPAE000611 AE000611 g2314179 Helicobacter pylori 26695 85962 -11539094

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905437	17533	39689	324	107

Description

GTC ORF with score 188 to: (fn:catalyzes hydroxylation at c-15 of) (db:genpept-pln1) (de:fusarium sporotrichioides isotrichodermin c-15 hydroxylase (tri11)gene, complete cds.) (nt:cytochrome p450 monooxygenase) (le:189:286:1132:1526:1757) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905441	17534	39690	972	323

Description

6500735237 flha:hp1041 flagellar biosynthesis protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1041 HP1041 Helicobacter pylori 210 -11539095 5500685224 flha:flba:hp1041 (sr:,campylobacter pylori) (de:flagellar biosynthesis protein flha) (db:swissprot) FLHA_HELPY O06758 HELICOBACTER PYLORI 210 -11539095 7000685277 flagellar biosynthesis protein (cl:regulatory protein lcrd) (db:pir2.dat) A64650 A64650 Helicobacter pylori 210 -11539095 7500881566 hp1041 flagellar biosynthesis protein flha (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to egad:30611 percent identity: 43.13;) (le:101) (re:2302) (di:direct) HPAE000612 AE000612 g2314189 Helicobacter pylori 210 -11539095 7502852956 hp1041 flagellar biosynthesis protein flha (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to egad:30611 percent identity: 43.13;) (le:101) (re:2302) (di:direct) HPAE000612 AE000612 g2314189 Helicobacter pylori 26695 85962 -11539095

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905442	17535	39691	408	135

Description

6500735238 flgg:hp1092 flagellar basal-body rod protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1092 HP1092 Helicobacter pylori 210 -11539096 7000689928 flagellar basal-body rod protein (db:pir2.dat) D64656 D64656 Helicobacter pylori 210 -11539096 7500958722 hp1092 flagellar basal-body rod protein flgg (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to egad:7063 percent identity: 35.48;) (le:1493) (re:2302) (di:direct) HPAE000616 AE000616 g2314244 Helicobacter pylori 210 -11539096 7502852957 hp1092 flagellar basal-body rod protein flgg (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to egad:7063 percent identity: 35.48;) (le:1493) (re:2302) (di:direct) HPAE000616 AE000616 g2314244 Helicobacter pylori 26695 85962 -11539096

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905444	17536	39692	600	200

Description

6500735239 flgk:hp1119 flagellar hook-associated protein 1 flgk:flagellar hook-associated protein 1:hap1 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1119 HP1119 Helicobacter pylori 210 -11539097 7000689940 flagellar hook-associated protein 1 (db:pir2.dat) G64659 G64659 Helicobacter pylori 210 -11539097 7500958731 hp1119 flagellar hook-associated protein 1 hap1 (db:genpept-bct1) (de:helicobacter pylori section 96 of 134 of the complete genome.) (nt:similar to egad:21528 percent identity: 27.56;) (le:7001) (re:8821) (di:complement) HPAE000618 AE000618 g2314271 Helicobacter pylori 210 -11539097 7502852958 hp1119 flagellar hook-associated protein 1 hap1 (db:genpept) (de:helicobacter pylori 26695 section 96 of 134 of the complete genome.) (nt:similar to egad:21528 percent identity: 27.56;) (le:7001) (re:8821) (di:complement) HPAE000618 AE000618 g2314271 Helicobacter pylori 26695 85962 -11539097

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905478	17537	39693	324	107

Description

6500735240 secreted protein involved in flagellar motility (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1192 HP1192 Helicobacter pylori 210 -11539098 7000690696 flagellar motility secreted protein hp1192 (db:pir2.dat) H64668 H64668 Helicobacter pylori 210 -11539098 7500959464 hp1192 secreted protein involved in flagellar motility (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to gp:1419559 percent identity: 72.53;) (le:3967) (re:4248) (di:complement) HPAE000625 AE000625 g2314353 Helicobacter pylori 210 -11539098 7502852959 hp1192 secreted protein involved in flagellar motility (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to gp:1419559 percent identity: 72.53;) (le:3967) (re:4248) (di:complement) HPAE000625 AE000625 g2314353 Helicobacter pylori 26695 85962 -11539098

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905479	17538	39694	855	284

Description

6500735241 pfla:hp1274 paralysed flagella protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1274 HP1274 Helicobacter pylori 210 -11539099 7000690607 paralysed flagella protein (db:pir2.dat) B64679 B64679 Helicobacter pylori 210 -11539099 7500959387 hp1274 paralysed flagella protein pfla (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:19905 percent identity: 23.92;) (le:17089) (re:19494) (di:direct) HPAE000631 AE000631 g2314439 Helicobacter pylori 210 -11539099 7502852960 hp1274 paralysed flagella protein pfla (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:19905 percent identity: 23.92;) (le:17089) (re:19494) (di:direct) HPAE000631 AE000631 g2314439 Helicobacter pylori 26695 85962 -11539099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905486	17539	39695	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905489	17540	39696	408	135

Description

7500958727 fliq:hp1419 flagellar biosynthetic protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1419 HP1419 Helicobacter pylori 210 -11539100 7000689934 flagellar biosynthetic protein (cl:flagellar biosynthesis-specific protein) (db:pir2.dat) C64697 C64697 Helicobacter pylori 210 -11539100 7000689935 hp1419 flagellar biosynthetic protein fliq (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to egad:22407 percent identity: 52.33;) (le:5473) (re:5739) (di:complement) HPAE000642 AE000642 g2314593 Helicobacter pylori 210 -11539100 7500958726 fliq membrane protein (db:genpept-bct1) (de:helicobacter pylori export type iii nucleotide binding protein(virb11), atpase (flii) and membrane protein (fliq) genes, completecds.) (nt:flagellar component; fliq) (le:2250) (re:2516) (di:direct) HPU75584 U75584 g2731647 Helicobacter pylori 210 -11539100 7502852961 fliq flagellar biosynthesis protein (db:genpept) (de:helicobacter pylori, strain j99 section 115 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1419) (le:7405) (re:7671) (di:complement) AE001554 AE001554 g4155919 Helicobacter pylori J99 85963 -11539100 6500735242 hp1419 flagellar biosynthetic protein fliq (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to egad:22407 percent identity: 52.33;) (le:5473) (re:5739) (di:complement) HPAE000642 AE000642 g2314593 Helicobacter pylori 26695 85962 -11539100

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905492	17541	39697	642	213

Description

6500735243 flii:hp1420 flagellar export protein atp synthase (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1420 HP1420 Helicobacter pylori 210 -11539101 5500685226 flii:hp1420 (sr:,campylobacter pylori) (ec:3.6.1.34) (de:flagellum-specific atp synthase,) (db:swissprot) FLII_HELPY O07025 HELICOBACTER PYLORI 210 -11539101 7000685291 flagellar export protein atp synthase (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (db:pir2.dat) D64697 D64697 Helicobacter pylori 210 -11539101 7500881600 hp1420 flagellar export protein atp synthase flii (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to sp:p23445 percent identity: 47.55;) (le:5750) (re:7054) (di:complement) HPAE000642 AE000642 g2314594 Helicobacter pylori 210 -11539101 7502852962 hp1420 flagellar export protein atp synthase flii (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to sp:p23445 percent identity: 47.55;) (le:5750) (re:7054) (di:complement) HPAE000642 AE000642 g2314594 Helicobacter pylori 26695 85962 -11539101

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905502	17542	39698	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905514	17543	39699	936	311

Description

6500735244 secreted protein involved in flagellar motility (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1462 HP1462 Helicobacter pylori 210 -11539102 7000690695 flagellar motility secreted protein hp1462 (db:pir2.dat) F64702 F64702 Helicobacter pylori 210 -11539102 7500959463 hp1462 secreted protein involved in flagellar motility (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:similar to gp:1419557 percent identity: 96.15;) (le:6366) (re:6884) (di:complement) HPAE000646 AE000646 g2314640 Helicobacter pylori 210 -11539102 7502852963 hp1462 secreted protein involved in flagellar motility (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:similar to gp:1419557 percent identity: 96.15;) (le:6366) (re:6884) (di:complement) HPAE000646 AE000646 g2314640 Helicobacter pylori 26695 85962 -11539102

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905520	17544	39700	1782	593

Description

7500958721 flie:hp1557 flagellar basal-body protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1557 HP1557 Helicobacter pylori 210 -11539103 7000689926 flagellar basal-body protein (db:pir2.dat) E64714 E64714 Helicobacter pylori 210 -11539103 7500958720 hp1557 flagellar basal-body protein flie (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:24081 percent identity: 37.00;) (le:9232) (re:9561) (di:complement) HPAE000653 AE000653 g2314740 Helicobacter pylori 210 -11539103 7502852964 flie flagellar hook-basal body complex protein (db:genpept) (de:helicobacter pylori, strain j99 section 129 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1557) (le:6987) (re:7316) (di:complement) AE001568 AE001568 g4156086 Helicobacter pylori J99 85963 -11539103 6500735245 hp1557 flagellar basal-body protein flie (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:24081 percent identity: 37.00;) (le:9232) (re:9561) (di:complement) HPAE000653 AE000653 g2314740 Helicobacter pylori 26695 85962 -11539103

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905529	17545	39701	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905542	17546	39702	1869	622

Description

6500735246 flgc:hp1558 flagellar basal-body rod protein:proximal rod protein:flagellar basal-body rod protein:proximal rod protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1558 HP1558 Helicobacter pylori 210 -11539104 7000689929 flagellar basal-body rod protein (cl:bacillus subtilis flagellar basal-body rod protein flgc) (db:pir2.dat) F64714 F64714 Helicobacter pylori 210 -11539104 7500958723 hp1558 flagellar basal-body rod protein flgc (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:38138 percent identity: 46.04;) (le:9689) (re:10174) (di:complement) HPAE000653 AE000653 g2314741 Helicobacter pylori 210 -11539104 7502852965 hp1558 flagellar basal-body rod protein flgc (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:38138 percent identity: 46.04;) (le:9689) (re:10174) (di:complement) HPAE000653 AE000653 g2314741 Helicobacter pylori 26695 85962 -11539104

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905553	17547	39703	501	166

Description

6500735247 flgb:hp1559 flagellar basal-body rod protein:proximal rod protein:flagellar basal-body rod protein:proximal rod protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1559 HP1559 Helicobacter pylori 210 -11539105 7000689930 flagellar basal-body rod protein (db:pir2.dat) G64714 G64714 Helicobacter pylori 210 -11539105 7500958724 hp1559 flagellar basal-body rod protein flgb (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:17514 percent identity: 31.01;) (le:10187) (re:10609) (di:complement) HPAE000653 AE000653 g2314742 Helicobacter pylori 210 -11539105 7502852966 hp1559 flagellar basal-body rod protein flgb (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:17514 percent identity: 31.01;) (le:10187) (re:10609) (di:complement) HPAE000653 AE000653 g2314742 Helicobacter pylori 26695 85962 -11539105

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905600	17548	39704	465	154

Description

6500735248 flhb:hp1575 flhb protein flhb:protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1575 HP1575 Helicobacter pylori 210 -11539106 7000689949 flhb protein (cl:helicobacter pylori flhb protein) (db:pir2.dat) G64716 G64716 Helicobacter pylori 210 -11539106 7500958737 hp1575 flhb protein flhb (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:33314 percent identity: 40.51;) (le:1534) (re:1806) (di:direct) HPAE000655 AE000655 g2314760 Helicobacter pylori 210 -11539106 7502852967 hp1575 flhb protein flhb (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:33314 percent identity: 40.51;) (le:1534) (re:1806) (di:direct) HPAE000655 AE000655 g2314760 Helicobacter pylori 26695 85962 -11539106

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905604	17549	39705	1302	433

Description

6500735249 flgg:hp1585 flagellar basal-body rod protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-helicobacter pylori) HP1585 HP1585 Helicobacter pylori 210 -11539107 7000689927 flgg flagellar basal body rod protein flgg (cl:rod protein flgf) (db:pir2.dat) A64718 A64718 Helicobacter pylori 210 -11539107 7500955365 hp1585 flagellar basal-body rod protein flgg (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:7063 percent identity: 47.69;) (le:9807) (re:10595) (di:direct) HPAE000655 AE000655 g2314768 Helicobacter pylori 210 -11539107 7502852968 hp1585 flagellar basal-body rod protein flgg (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:7063 percent identity: 47.69;) (le:9807) (re:10595) (di:direct) HPAE000655 AE000655 g2314768 Helicobacter pylori 26695 85962 -11539107

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905615	17550	39706	402	133

Description

6500735250 mray:hp0493 phospho-n-acetylmuramoyl-pentapeptide-transferase (gtcfc:11.4) (ec:2.7.8.13) (keggfc:7.3) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0493 HP0493 Helicobacter pylori 210 -11539108 7000689109 phospho-n-acetylmuramoyl-pentapeptide-transferase (cl:phospho-n-acetylmuramoyl-pentapeptide-transferase) (ec:2.7.8.13) (db:pir2.dat) E64581 E64581 Helicobacter pylori 210 -11539108 7500954173 hp0493 phospho-n-acetylmuramoyl-pentapeptide- (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:17985 percent identity: 45.24;) (le:2774) (re:3835) (di:direct) HPAE000564 AE000564 g2313604 Helicobacter pylori 210 -11539108 7502852969 hp0493 phospho-n-acetylmuramoyl-pentapeptide- (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:17985 percent identity: 45.24;) (le:2774) (re:3835) (di:direct) HPAE000564 AE000564 g2313604 Helicobacter pylori 26695 85962 -11539108

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905616	17551	39707	825	274

Description

6500735251 amia:hp0772 n-acetylmuramoyl-l-alanine amidase (gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0772 HP0772 Helicobacter pylori 210 -11539109 7000690537 n-acetylmuramoyl-l-alanine amidase (db:pir2.dat) D64616 D64616 Helicobacter pylori 210 -11539109 7500959324 hp0772 n-acetylmuramoyl-l-alanine amidase amia (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:similar to egad:10094 percent identity: 26.81;) (le:3807) (re:5129) (di:complement) HPAE000589 AE000589 g2313899 Helicobacter pylori 210 -11539109 7502852970 hp0772 n-acetylmuramoyl-l-alanine amidase amia (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:similar to egad:10094 percent identity: 26.81;) (le:3807) (re:5129) (di:complement) HPAE000589 AE000589 g2313899 Helicobacter pylori 26695 85962 -11539109

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905618	17552	39708	1185	394

Description

6500735252 pbp-1a:hp0597 penicillin-binding protein 1a (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0597 HP0597 Helicobacter pylori 210 -11539110 7000690609 penicillin-binding protein 1a (db:pir2.dat) E64594 E64594 Helicobacter pylori 210 -11539110 7500959388 hp0597 penicillin-binding protein 1a pbp-1a (db:genpept-bct1) (de:helicobacter pylori section 51 of 134 of the complete genome.) (nt:similar to egad:7204 percent identity: 33.69;) (le:4661) (re:6640) (di:complement) HPAE000573 AE000573 g2313714 Helicobacter pylori 210 -11539110 7502852971 hp0597 penicillin-binding protein 1a pbp-1a (db:genpept) (de:helicobacter pylori 26695 section 51 of 134 of the complete genome.) (nt:similar to egad:7204 percent identity: 33.69;) (le:4661) (re:6640) (di:complement) HPAE000573 AE000573 g2313714 Helicobacter pylori 26695 85962 -11539110

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905620	17553	39709	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905626	17554	39710	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905635	17555	39711	219	72

Description

6500735253 murz:hp0648 udp-n-acetylglucosamine enolpyruvyl transferase (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0648 HP0648 Helicobacter pylori 210 -11539111 5500685585 mura:murz:hp0648 (sr:,campylobacter pylori) (ec:2.5.1.7) (de:transferase) (ept)) (db:swissprot) MURA_HELPY P56189 HELICOBACTER PYLORI 210 -11539111 7000685884 udp-n-acetylglucosamine enolpyruvyl transferase (cl:udp-n-acetylglucosamine 1-carboxyvinyltransferase murz) (db:pir2.dat) H64600 H64600 Helicobacter pylori 210 -11539111 7500886093 hp0648 udp-n-acetylglucosamine enolpyruvyl transferase (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:28102 percent identity: 46.67;) (le:9638) (re:10906) (di:direct) HPAE000578 AE000578 g2313767 Helicobacter pylori 210 -11539111 7502852972 hp0648 udp-n-acetylglucosamine enolpyruvyl transferase (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:28102 percent identity: 46.67;) (le:9638) (re:10906) (di:direct) HPAE000578 AE000578 g2313767 Helicobacter pylori 26695 85962 -11539111

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905636	17556	39712	237	78

Description

6500735254 murf:hp0740 udp-murnac-pentapeptide presynthetase (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0740 HP0740 Helicobacter pylori 210 -11539112 7000690781 udp-murnac-pentapeptide presynthetase (db:pir2.dat) D64612 D64612 Helicobacter pylori 210 -11539112 7500959544 hp0740 udp-murnac-pentapeptide presynthetase murf (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:38148 percent identity: 25.70;) (le:11659) (re:13140) (di:direct) HPAE000586 AE000586 g2313862 Helicobacter pylori 210 -11539112 7502852973 hp0740 udp-murnac-pentapeptide presynthetase murf (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:38148 percent identity: 25.70;) (le:11659) (re:13140) (di:direct) HPAE000586 AE000586 g2313862 Helicobacter pylori 26695 85962 -11539112

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905639	17557	39713	420	139

Description

6500735255 mreb:hp0743 rod shape-determining protein (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP0743 HP0743 Helicobacter pylori 210 -11539113 5500685893 mrdb:roda:hp0743 (sr:,campylobacter pylori) (de:rod shape-determining protein roda) (db:swissprot) RODA_HELPY P56098 HELICOBACTER PYLORI 210 -11539113 7000686437 rod shape-determining protein (db:pir2.dat) G64612 G64612 Helicobacter pylori 210 -11539113 7500890491 hp0743 rod shape-determining protein mreb (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:similar to egad:21935 percent identity: 37.71;) (le:1080) (re:2225) (di:complement) HPAE000587 AE000587 g2313871 Helicobacter pylori 210 -11539113 7502852974 hp0743 rod shape-determining protein mreb (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:similar to egad:21935 percent identity: 37.71;) (le:1080) (re:2225) (di:complement) HPAE000587 AE000587 g2313871 Helicobacter pylori 26695 85962 -11539113

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905643	17558	39714	597	198

Description

6500735256 omp18:hp1125 peptidoglycan associated lipoprotein precursor (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1125 HP1125 Helicobacter pylori 210 -11539114 7000690614 peptidoglycan associated lipoprotein precursor (db:pir2.dat) E64660 E64660 Helicobacter pylori 210 -11539114 7500959393 hp1125 peptidoglycan associated lipoprotein precursor (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:40238 percent identity: 42.59;) (le:2163) (re:2702) (di:complement) HPAE000619 AE000619 g2314278 Helicobacter pylori 210 -11539114 7502852975 hp1125 peptidoglycan associated lipoprotein precursor (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:40238 percent identity: 42.59;) (le:2163) (re:2702) (di:complement) HPAE000619 AE000619 g2314278 Helicobacter pylori 26695 85962 -11539114

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905675	17559	39715	681	226

Description

6500735257 mrec:hp1372 rod shape-determining protein (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1372 HP1372 Helicobacter pylori 210 -11539115 7000690693 rod shape-determining protein (db:pir2.dat) D64691 D64691 Helicobacter pylori 210 -11539115 7500959461 hp1372 rod shape-determining protein mrec (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:27854 percent identity: 33.56;) (le:8635) (re:9381) (di:complement) HPAE000637 AE000637 g2314542 Helicobacter pylori 210 -11539115 7502852976 hp1372 rod shape-determining protein mrec (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:27854 percent identity: 33.56;) (le:8635) (re:9381) (di:complement) HPAE000637 AE000637 g2314542 Helicobacter pylori 26695 85962 -11539115

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905677	17560	39716	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905678	17561	39717	267	88

Description

6500735258 mreb:hp1373 rod shape-determining protein (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1373 HP1373 Helicobacter pylori 210 -11539116 7000689444 rod shape-determining protein (cl:rod shape-determining protein envb) (db:pir2.dat) E64691 E64691 Helicobacter pylori 210 -11539116 7500955517 hp1373 rod shape-determining protein mreb (db:genpept-bct1) (de:helicobacter pylori section 115 of 134 of the complete genome.) (nt:similar to egad:8106 percent identity: 51.87;) (le:9385) (re:10428) (di:complement) HPAE000637 AE000637 g2314543 Helicobacter pylori 210 -11539116 7502852977 hp1373 rod shape-determining protein mreb (db:genpept) (de:helicobacter pylori 26695 section 115 of 134 of the completegenome.) (nt:similar to egad:8106 percent identity: 51.87;) (le:9385) (re:10428) (di:complement) HPAE000637 AE000637 g2314543 Helicobacter pylori 26695 85962 -11539116

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905680	17562	39718	489	162

Description

6500735259 tage:hp1543 toxr-activated gene (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1543 HP1543 Helicobacter pylori 210 -11539117 7000690737 toxr-activated gene (db:pir2.dat) G64712 G64712 Helicobacter pylori 210 -11539117 7500959502 hp1543 toxr-activated gene tage (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:18571 percent identity: 37.15;) (le:6174) (re:7112) (di:complement) HPAE000652 AE000652 g2314724 Helicobacter pylori 210 -11539117 7502852978 hp1543 toxr-activated gene tage (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:18571 percent identity: 37.15;) (le:6174) (re:7112) (di:complement) HPAE000652 AE000652 g2314724 Helicobacter pylori 26695 85962 -11539117

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905681	17563	39719	315	104

Description

6500735260 tage:hp1544 toxr-activated gene (gtcfc:11.4) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1544 HP1544 Helicobacter pylori 210 -11539118 7000690738 toxr-activated gene (db:pir2.dat) H64712 H64712 Helicobacter pylori 210 -11539118 7500959503 hp1544 toxr-activated gene tage (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:18571 percent identity: 31.25;) (le:7121) (re:8047) (di:complement) HPAE000652 AE000652 g2314725 Helicobacter pylori 210 -11539118 7502852979 hp1544 toxr-activated gene tage (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:18571 percent identity: 31.25;) (le:7121) (re:8047) (di:complement) HPAE000652 AE000652 g2314725 Helicobacter pylori 26695 85962 -11539118

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905684	17564	39720	960	319

Description

6500735261 pbp2:hp1565 penicillin-binding protein 2 (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:3.2) (db:gtc-helicobacter pylori) HP1565 HP1565 Helicobacter pylori 210 -11539119 7000690610 penicillin-binding protein 2 (db:pir2.dat) E64715 E64715 Helicobacter pylori 210 -11539119 7500959389 hp1565 penicillin-binding protein 2 pbp2 (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:27848 percent identity: 35.04;) (le:5818) (re:7584) (di:complement) HPAE000654 AE000654 g2314749 Helicobacter pylori 210 -11539119 7502852980 hp1565 penicillin-binding protein 2 pbp2 (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:27848 percent identity: 35.04;) (le:5818) (re:7584) (di:complement) HPAE000654 AE000654 g2314749 Helicobacter pylori 26695 85962 -11539119

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905688	17565	39721	1818	605

Description

6500735262 lspa:ured:hp0074 lipoprotein signal peptidase:urease operon protein (gtcfc:10.7:11.1:12.10) (ec:3.4.23.36) (keggfc:14.1) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP0074 HP0074 Helicobacter pylori 210 -11539120 103870 lspa:ured:hp0074 (sr:,campylobacter pylori) (ec:3.4.23.36) (de:peptidase) (signal peptidase ii) (spase ii)) (db:swissprot) LSPA_HELPY P25178 HELICOBACTER PYLORI 210 -11539120 7000685768 lspa lipoprotein signal peptidase::ured protein (ec:3.4.23.36) (db:pir2.dat) B64529 B64529 Helicobacter pylori 210 -11539120 7500885172 hp0074 lipoprotein signal peptidase lspa (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:similar to egad:24320 percent identity: 96.99;) (le:2902) (re:3375) (di:complement) HPAE000529 AE000529 g2313155 Helicobacter pylori 210 -11539120 7502852981 hp0074 lipoprotein signal peptidase lspa (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:similar to egad:24320 percent identity: 96.99;) (le:2902) (re:3375) (di:complement) HPAE000529 AE000529 g2313155 Helicobacter pylori 26695 85962 -11539120

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905723	17566	39722	813	270

Description

6500735263 lepa:hp0355 gtp-binding membrane protein (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP0355 HP0355 Helicobacter pylori 210 -11539121 7500884921 lepa:hp0355 (sr:,campylobacter pylori) (de:gtp-binding protein lepa) (db:swissprot) LEPA_HELPY O25122 HELICOBACTER PYLORI 210 -11539121 7000689415 gtp-binding membrane protein lepa (cl:gtp-binding membrane protein lepa:translation elongation factor tu homology) (db:pir2.dat) C64564 C64564 Helicobacter pylori 210 -11539121 7500884923 hp0355 gtp-binding membrane protein lepa (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:similar to egad:27832 percent identity: 57.31;) (le:6237) (re:8045) (di:direct) HPAE000552 AE000552 g2313456 Helicobacter pylori 210 -11539121 7502852982 hp0355 gtp-binding membrane protein lepa (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:similar to egad:27832 percent identity: 57.31;) (le:6237) (re:8045) (di:direct) HPAE000552 AE000552 g2313456 Helicobacter pylori 26695 85962 -11539121

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905725	17567	39723	582	193

Description

6500735264 lepb:hp0576 signal peptidase i lepb:signal peptidase i (gtcfc:10.7:11.1:12.10) (ec:3.4.21.89) (keggfc:14.1) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP0576 HP0576 Helicobacter pylori 210 -11539122 7000690703 signal peptidase i (db:pir2.dat) H64591 H64591 Helicobacter pylori 210 -11539122 7500959470 hp0576 signal peptidase i lepb (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:27831 percent identity: 40.34;) (le:5495) (re:6367) (di:complement) HPAE000571 AE000571 g2313695 Helicobacter pylori 210 -11539122 7502852983 hp0576 signal peptidase i lepb (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:27831 percent identity: 40.34;) (le:5495) (re:6367) (di:complement) HPAE000571 AE000571 g2313695 Helicobacter pylori 26695 85962 -11539122

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905733	17568	39724	348	115

Description

6500735265 seca:hp0786 preprotein translocase subunit (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP0786 HP0786 Helicobacter pylori 210 -11539123 7500891451 seca:hp0786 (sr:,campylobacter pylori) (de:preprotein translocase seca subunit) (db:swissprot) SECA_HELPY O25475 HELICOBACTER PYLORI 210 -11539123 7000690637 preprotein translocase seca (cl:preprotein translocase seca:dead/h box helicase homology) (db:pir2.dat) B64618 B64618 Helicobacter pylori 210 -11539123 7500891453 hp0786 preprotein translocase subunit seca (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:similar to egad:29392 percent identity: 54.04;) (le:8552) (re:11149) (di:direct) HPAE000590 AE000590 g2313910 Helicobacter pylori 210 -11539123 7502852984 hp0786 preprotein translocase subunit seca (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:similar to egad:29392 percent identity: 54.04;) (le:8552) (re:11149) (di:direct) HPAE000590 AE000590 g2313910 Helicobacter pylori 26695 85962 -11539123

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905741	17569	39725	489	162

Description

6500735266 trigger factor tig:trigger factor:tig (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP0795 HP0795 Helicobacter pylori 210 -11539124 7500893182 tig:hp0795 (sr:,campylobacter pylori) (de:trigger factor (tf)) (db:swissprot) TIG_HELPY P56420 HELICOBACTER PYLORI 210 -11539124 7000689421 trigger factor (cl:trigger factor) (db:pir2.dat) C64619 C64619 Helicobacter pylori 210 -11539124 7500893184 hp0795 trigger factor tig (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:similar to egad:19730 percent identity: 27.65;) (le:8116) (re:9471) (di:complement) HPAE000591 AE000591 g2313924 Helicobacter pylori 210 -11539124 7502852985 hp0795 trigger factor tig (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:similar to egad:19730 percent identity: 27.65;) (le:8116) (re:9471) (di:complement) HPAE000591 AE000591 g2313924 Helicobacter pylori 26695 85962 -11539124

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905756	17570	39726	1914	637

Description

6500735267 ffh:hp1152 signal recognition particle protein (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP1152 HP1152 Helicobacter pylori 210 -11539125 5500685997 ffh:hp1152 (sr:,campylobacter pylori) (de:signal recognition particle protein (fifty-four homolog)) (db:swissprot) SR54_HELPY P56005 HELICOBACTER PYLORI 210 -11539125 7000686674 signal recognition particle protein (cl:signal recognition particle 54k protein) (db:pir2.dat) H64663 H64663 Helicobacter pylori 210 -11539125 7500892041 hp1152 signal recognition particle protein ffh (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:5600 percent identity: 41.44;) (le:4096) (re:5442) (di:complement) HPAE000621 AE000621 g2314305 Helicobacter pylori 210 -11539125 7502852986 hp1152 signal recognition particle protein ffh (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:5600 percent identity: 41.44;) (le:4096) (re:5442) (di:complement) HPAE000621 AE000621 g2314305 Helicobacter pylori 26695 85962 -11539125

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905767	17571	39727	657	218

Description

6500735268 secg:hp1255 protein translocation protein:low temperature (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP1255 HP1255 Helicobacter pylori 210 -11539126 7000690653 protein translocation protein:low temperature (db:pir2.dat) G64676 G64676 Helicobacter pylori 210 -11539126 7500959428 hp1255 protein translocation protein:low temperature (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to egad:23175 percent identity: 30.63;) (le:89) (re:694) (di:direct) HPAE000631 AE000631 g2314422 Helicobacter pylori 210 -11539126 7502852987 hp1255 protein translocation protein:low temperature (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to egad:23175 percent identity: 30.63;) (le:89) (re:694) (di:direct) HPAE000631 AE000631 g2314422 Helicobacter pylori 26695 85962 -11539126

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905772	17572	39728	900	299

Description

6500735269 secy:hp1300 preprotein translocase subunit (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP1300 HP1300 Helicobacter pylori 210 -11539127 7000690638 preprotein translocase secy (cl:preprotein translocase secy) (db:pir2.dat) D64682 D64682 Helicobacter pylori 210 -11539127 7500959416 hp1300 preprotein translocase subunit secy (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:5724 percent identity: 41.22;) (le:9767) (re:11029) (di:complement) HPAE000633 AE000633 g2314464 Helicobacter pylori 210 -11539127 7502852988 hp1300 preprotein translocase subunit secy (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:5724 percent identity: 41.22;) (le:9767) (re:11029) (di:complement) HPAE000633 AE000633 g2314464 Helicobacter pylori 26695 85962 -11539127

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905777	17573	39729	414	137

Description

6500735270 secf:hp1549 protein-export membrane protein (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP1549 HP1549 Helicobacter pylori 210 -11539128 7000690654 protein-export membrane protein (cl:escherichia coli preprotein translocase chain secf) (db:pir2.dat) E64713 E64713 Helicobacter pylori 210 -11539128 7500959429 hp1549 protein-export membrane protein secf (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:5842 percent identity: 35.12;) (le:12508) (re:13479) (di:complement) HPAE000652 AE000652 g2314729 Helicobacter pylori 210 -11539128 7502852989 hp1549 protein-export membrane protein secf (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:5842 percent identity: 35.12;) (le:12508) (re:13479) (di:complement) HPAE000652 AE000652 g2314729 Helicobacter pylori 26695 85962 -11539128

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905789	17574	39730	486	161

Description

6500735271 secd:hp1550 protein-export membrane protein (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.7) (db:gtc-helicobacter pylori) HP1550 HP1550 Helicobacter pylori 210 -11539129 7000690655 protein-export membrane protein (db:pir2.dat) F64713 F64713 Helicobacter pylori 210 -11539129 7500959430 hp1550 protein-export membrane protein secd (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:8173 percent identity: 38.94;) (le:13488) (re:14999) (di:complement) HPAE000652 AE000652 g2314730 Helicobacter pylori 210 -11539129 7502852990 hp1550 protein-export membrane protein secd (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:8173 percent identity: 38.94;) (le:13488) (re:14999) (di:complement) HPAE000652 AE000652 g2314730 Helicobacter pylori 26695 85962 -11539129

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905797	17575	39731	456	151

Description

6500735272 putp:hp0055 proline permease (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0055 HP0055 Helicobacter pylori 210 -11539130 7000689380 putp sodium/proline symporter:proline permease (cl:proline carrier protein) (db:pir2.dat) G64526 G64526 Helicobacter pylori 210 -11539130 7500955290 hp0055 proline permease putp (db:genpept-bct1) (de:helicobacter pylori section 5 of 134 of the complete genome.) (nt:similar to gp:1787251 percent identity: 51.35;) (le:5070) (re:6560) (di:complement) HPAE000527 AE000527 g2313133 Helicobacter pylori 210 -11539130 7502852991 hp0055 proline permease putp (db:genpept) (de:helicobacter pylori 26695 section 5 of 134 of the complete genome.) (nt:similar to gp:1787251 percent identity: 51.35;) (le:5070) (re:6560) (di:complement) HPAE000527 AE000527 g2313133 Helicobacter pylori 26695 85962 -11539130

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905800	17576	39732	1398	465

Description

GTC ORF with score 535 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c24c9.) (nt:spac24c9.11, unknown, len:775aa, similar eg. to) (le:27938:28057:29764:30132) (re:28007:29720:30084:30404) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905806	17577	39733	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905815	17578	39734	972	323

Description

GTC ORF with score 416 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c24c9.) (nt:spac24c9.11, unknown, len:775aa, similar eg. to) (le:27938:28057:29764:30132) (re:28007:29720:30084:30404) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905843	17579	39735	384	127

Description

6500735273 sdac:hp0133 serine transporter (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0133 HP0133 Helicobacter pylori 210 -11539131 7000689437 serine transporter (cl:threonine-serine permease) (db:pir2.dat) E64536 E64536 Helicobacter pylori 210 -11539131 7500955491 hp0133 serine transporter sdac (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:similar to egad:6484 percent identity: 44.64;) (le:1954) (re:3195) (di:complement) HPAE000535 AE000535 g2313219 Helicobacter pylori 210 -11539131 7502852992 hp0133 serine transporter sdac (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:similar to egad:6484 percent identity: 44.64;) (le:1954) (re:3195) (di:complement) HPAE000535 AE000535 g2313219 Helicobacter pylori 26695 85962 -11539131

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905844	17580	39736	2307	768

Description

6500735274 oppd:hp0250 oligopeptide abc transporter:atp-binding protein:oligopeptide abc transporter:atp-bindingprotein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0250 HP0250 Helicobacter pylori 210 -11539132 7000690564 oligopeptide abc transporter:atp-binding protein (cl:atp-binding cassette homology) (db:pir2.dat) B64551 B64551 Helicobacter pylori 210 -11539132 7500959348 hp0250 oligopeptide abc transporter:atp-binding (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:similar to gp:1736845 percent identity: 39.06;) (le:6022) (re:7572) (di:complement) HPAE000544 AE000544 g2313342 Helicobacter pylori 210 -11539132 7502852993 hp0250 oligopeptide abc transporter:atp-binding (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:similar to gp:1736845 percent identity: 39.06;) (le:6022) (re:7572) (di:complement) HPAE000544 AE000544 g2313342 Helicobacter pylori 26695 85962 -11539132

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905848	17581	39737	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905850	17582	39738	339	112

Description

GTC ORF with score 94 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1061.) (nt:unnamed protein product) (le:<1) (re:967) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905870	17583	39739	642	213

Description

6500735275 oppc:hp0251 oligopeptide abc transporter:permease protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0251 HP0251 Helicobacter pylori 210 -11539133 7000690566 oligopeptide abc transporter:permease protein (db:pir2.dat) C64551 C64551 Helicobacter pylori 210 -11539133 7500959350 hp0251 oligopeptide abc transporter:permease protein (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:similar to gp:1787498 percent identity: 31.41;) (le:7582) (re:8598) (di:complement) HPAE000544 AE000544 g2313343 Helicobacter pylori 210 -11539133 7502852994 hp0251 oligopeptide abc transporter:permease protein (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:similar to gp:1787498 percent identity: 31.41;) (le:7582) (re:8598) (di:complement) HPAE000544 AE000544 g2313343 Helicobacter pylori 26695 85962 -11539133

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905897	17584	39740	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905910	17585	39741	387	128

Description

GTC ORF with score 167 to: (or:Homo sapiens) (sr:human b-cell, cdna to mrna) (db:genpept-pri1) (de:human cyclic amp response element-binding protein (hb16) mrna, 3'end.) (nt:cyclic amp response element-binding protein (hb16)) (le:<1) (re:888) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905913	17586	39742	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905914	17587	39743	681	226

Description

6500735276 dppa:hp0298 dipeptide abc transporter:periplasmic dipeptide-binding protein:dipeptide abc transporter:periplasmicdipeptide-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0298 HP0298 Helicobacter pylori 210 -11539134 7000689357 dipeptide abc transporter:periplasmic dipeptide-binding protein (cl:dipeptide transport protein) (db:pir2.dat) B64557 B64557 Helicobacter pylori 210 -11539134 7500955176 hp0298 dipeptide abc transporter:periplasmic (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:9321 percent identity: 39.84;) (le:4689) (re:6338) (di:direct) HPAE000548 AE000548 g2313396 Helicobacter pylori 210 -11539134 7502852995 hp0298 dipeptide abc transporter:periplasmic (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:9321 percent identity: 39.84;) (le:4689) (re:6338) (di:direct) HPAE000548 AE000548 g2313396 Helicobacter pylori 26695 85962 -11539134

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905916	17588	39744	207	68

Description

6500735277 dppb:hp0299 dipeptide abc transporter:permease protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0299 HP0299 Helicobacter pylori 210 -11539135 7000689895 dipeptide abc transporter:permease protein (cl:transmembrane protein dppb) (db:pir2.dat) C64557 C64557 Helicobacter pylori 210 -11539135 7500958692 hp0299 dipeptide abc transporter:permease protein (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:8193 percent identity: 49.25;) (le:6349) (re:7353) (di:direct) HPAE000548 AE000548 g2313397 Helicobacter pylori 210 -11539135 7502852996 hp0299 dipeptide abc transporter:permease protein (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:8193 percent identity: 49.25;) (le:6349) (re:7353) (di:direct) HPAE000548 AE000548 g2313397 Helicobacter pylori 26695 85962 -11539135

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905918	17589	39745	306	101

Description

6500735278 dppc:hp0300 dipeptide abc transporter:permease protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0300 HP0300 Helicobacter pylori 210 -11539136 7000689896 dipeptide abc transporter:permease protein (cl:oligopeptide permease protein oppb) (db:pir2.dat) D64557 D64557 Helicobacter pylori 210 -11539136 7500958693 hp0300 dipeptide abc transporter:permease protein (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:9991 percent identity: 52.48;) (le:7353) (re:8210) (di:direct) HPAE000548 AE000548 g2313398 Helicobacter pylori 210 -11539136 7502852997 hp0300 dipeptide abc transporter:permease protein (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:9991 percent identity: 52.48;) (le:7353) (re:8210) (di:direct) HPAE000548 AE000548 g2313398 Helicobacter pylori 26695 85962 -11539136

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905926	17590	39746	399	132

Description

6500735279 dppd:hp0301 dipeptide abc transporter:atp-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0301 HP0301 Helicobacter pylori 210 -11539137 7000689362 dppd dipeptide transport atp-binding protein dppd (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) E64557 E64557 Helicobacter pylori 210 -11539137 7500955210 hp0301 dipeptide abc transporter:atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:30672 percent identity: 59.46;) (le:8222) (re:9085) (di:direct) HPAE000548 AE000548 g2313399 Helicobacter pylori 210 -11539137 7502852998 hp0301 dipeptide abc transporter:atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:30672 percent identity: 59.46;) (le:8222) (re:9085) (di:direct) HPAE000548 AE000548 g2313399 Helicobacter pylori 26695 85962 -11539137

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905932	17591	39747	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905934	17592	39748	321	106

Description

6500735280 dppf:hp0302 dipeptide abc transporter:atp-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0302 HP0302 Helicobacter pylori 210 -11539138 7000689361 dppf dipeptide transport atp-binding protein dppf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) F64557 F64557 Helicobacter pylori 210 -11539138 7500955194 hp0302 dipeptide abc transporter:atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:10112 percent identity: 54.75;) (le:9082) (re:9888) (di:direct) HPAE000548 AE000548 g2313400 Helicobacter pylori 210 -11539138 7502852999 hp0302 dipeptide abc transporter:atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:10112 percent identity: 54.75;) (le:9082) (re:9888) (di:direct) HPAE000548 AE000548 g2313400 Helicobacter pylori 26695 85962 -11539138

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905939	17593	39749	870	289

Description

6500735281 prowx:hp0818 osmoprotection protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0818 HP0818 Helicobacter pylori 210 -11539139 7000690568 osmoprotection protein (db:pir2.dat) B64622 B64622 Helicobacter pylori 210 -11539139 7500959352 hp0818 osmoprotection protein prowx (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:37692 percent identity: 30.37;) (le:4862) (re:6523) (di:direct) HPAE000593 AE000593 g2313949 Helicobacter pylori 210 -11539139 7502853000 hp0818 osmoprotection protein prowx (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:37692 percent identity: 30.37;) (le:4862) (re:6523) (di:direct) HPAE000593 AE000593 g2313949 Helicobacter pylori 26695 85962 -11539139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905945	17594	39750	579	192

Description

6500735282 prov:hp0819 osmoprotection protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0819 HP0819 Helicobacter pylori 210 -11539140 7000690569 osmoprotection protein (cl:atp-binding cassette homology) (db:pir2.dat) C64622 C64622 Helicobacter pylori 210 -11539140 7500959353 hp0819 osmoprotection protein prov (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:37691 percent identity: 38.27;) (le:6527) (re:7177) (di:direct) HPAE000593 AE000593 g2313950 Helicobacter pylori 210 -11539140 7502853001 hp0819 osmoprotection protein prov (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:37691 percent identity: 38.27;) (le:6527) (re:7177) (di:direct) HPAE000593 AE000593 g2313950 Helicobacter pylori 26695 85962 -11539140

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905953	17595	39751	966	321

Description

6500735283 prop:hp0936 proline/betaine transporter (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0936 HP0936 Helicobacter pylori 210 -11539141 7500975639 hp0936 proline/betaine transporter prop (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:similar to egad:8124 percent identity: 29.15;) (le:282) (re:1451) (di:complement) HPAE000603 AE000603 g2314076 Helicobacter pylori 210 -11539141 7502853002 hp0936 proline/betaine transporter prop (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:similar to egad:8124 percent identity: 29.15;) (le:282) (re:1451) (di:complement) HPAE000603 AE000603 g2314076 Helicobacter pylori 26695 85962 -11539141

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905967	17596	39752	1149	382

Description

6500735284 yckj:hp0939 amino acid abc transporter:permease protein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0939 HP0939 Helicobacter pylori 210 -11539142 7000689633 amino acid abc transporter:permease protein (cl:histidine permease protein m) (db:pir2.dat) C64637 C64637 Helicobacter pylori 210 -11539142 7500958451 hp0939 amino acid abc transporter:permease protein (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:similar to egad:30721 percent identity: 46.95;) (le:3357) (re:4070) (di:complement) HPAE000603 AE000603 g2314077 Helicobacter pylori 210 -11539142 7502853003 hp0939 amino acid abc transporter:permease protein (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:similar to egad:30721 percent identity: 46.95;) (le:3357) (re:4070) (di:complement) HPAE000603 AE000603 g2314077 Helicobacter pylori 26695 85962 -11539142

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905978	17597	39753	1026	341

Description

6500735285 yckk:hp0940 amino acid abc transporter:periplasmic binding protein:amino acid abc transporter:periplasmic bindingprotein (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0940 HP0940 Helicobacter pylori 210 -11539143 7000689632 amino acid abc transporter:periplasmic binding protein (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) D64637 D64637 Helicobacter pylori 210 -11539143 7500958450 hp0940 amino acid abc transporter:periplasmic binding (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:similar to egad:30720 percent identity: 41.53;) (le:4054) (re:4824) (di:complement) HPAE000603 AE000603 g2314078 Helicobacter pylori 210 -11539143 7502853004 hp0940 amino acid abc transporter:periplasmic binding (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:similar to egad:30720 percent identity: 41.53;) (le:4054) (re:4824) (di:complement) HPAE000603 AE000603 g2314078 Helicobacter pylori 26695 85962 -11539143

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501905993	17598	39754	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906000	17599	39755	261	86

Description

6500735286 daga:hp0942 d-alanine glycine permease (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP0942 HP0942 Helicobacter pylori 210 -11539144 7000689424 d-alanine/glycine transport protein:sodium-dependent (cl:sodium-dependent d-alanine/glycine transport protein) (db:pir2.dat) F64637 F64637 Helicobacter pylori 210 -11539144 7500955464 hp0942 d-alanine glycine permease daga (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:similar to egad:29366 percent identity: 44.47;) (le:6032) (re:7384) (di:complement) HPAE000603 AE000603 g2314080 Helicobacter pylori 210 -11539144 7502853005 hp0942 d-alanine glycine permease daga (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:similar to egad:29366 percent identity: 44.47;) (le:6032) (re:7384) (di:complement) HPAE000603 AE000603 g2314080 Helicobacter pylori 26695 85962 -11539144

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906015	17600	39756	1656	552

Description

6500735287 roce:hp1017 amino acid permease (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP1017 HP1017 Helicobacter pylori 210 -11539145 7000689358 amino acid permease roce (cl:arginine permease) (db:pir2.dat) A64647 A64647 Helicobacter pylori 210 -11539145 7500955178 hp1017 amino acid permease roce (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:similar to egad:24467 percent identity: 41.72;) (le:1226) (re:2785) (di:direct) HPAE000610 AE000610 g2314162 Helicobacter pylori 210 -11539145 7502853006 hp1017 amino acid permease roce (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:similar to egad:24467 percent identity: 41.72;) (le:1226) (re:2785) (di:direct) HPAE000610 AE000610 g2314162 Helicobacter pylori 26695 85962 -11539145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906033	17601	39757	2121	706

Description

6500735288 glnp:hp1169 glutamine abc transporter:permease protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP1169 HP1169 Helicobacter pylori 210 -11539146 7000689967 glutamine abc transporter:permease protein (cl:histidine permease protein m) (db:pir2.dat) A64666 A64666 Helicobacter pylori 210 -11539146 7500958751 hp1169 glutamine abc transporter:permease protein (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:9064 percent identity: 27.57;) (le:137) (re:790) (di:direct) HPAE000623 AE000623 g2314328 Helicobacter pylori 210 -11539146 7502853007 hp1169 glutamine abc transporter:permease protein (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:9064 percent identity: 27.57;) (le:137) (re:790) (di:direct) HPAE000623 AE000623 g2314328 Helicobacter pylori 26695 85962 -11539146

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906048	17602	39758	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906086	17603	39759	495	164

Description

6500735289 glnp:hp1170 glutamine abc transporter:permease protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP1170 HP1170 Helicobacter pylori 210 -11539147 7000689968 glutamine abc transporter:permease protein (db:pir2.dat) B64666 B64666 Helicobacter pylori 210 -11539147 7500958752 hp1170 glutamine abc transporter:permease protein (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:9064 percent identity: 30.88;) (le:792) (re:1463) (di:direct) HPAE000623 AE000623 g2314329 Helicobacter pylori 210 -11539147 7502853008 hp1170 glutamine abc transporter:permease protein (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:9064 percent identity: 30.88;) (le:792) (re:1463) (di:direct) HPAE000623 AE000623 g2314329 Helicobacter pylori 26695 85962 -11539147

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906095	17604	39760	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906096	17605	39761	3129	1042

Description

6500735290 glnq:hp1171 glutamine abc transporter:atp-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP1171 HP1171 Helicobacter pylori 210 -11539148 7000689363 glnq glutamine transport protein glnq (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) C64666 C64666 Helicobacter pylori 210 -11539148 7500955211 hp1171 glutamine abc transporter:atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:37772 percent identity: 51.90;) (le:1465) (re:2211) (di:direct) HPAE000623 AE000623 g2314330 Helicobacter pylori 210 -11539148 7502853009 hp1171 glutamine abc transporter:atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:37772 percent identity: 51.90;) (le:1465) (re:2211) (di:direct) HPAE000623 AE000623 g2314330 Helicobacter pylori 26695 85962 -11539148

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906097	17606	39762	1167	388

Description

6500735291 glnh:hp1172 glutamine abc transporter:periplasmic glutamine-binding protein:glutamine abc transporter:periplasmicglutamine-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP1172 HP1172 Helicobacter pylori 210 -11539149 7000689966 glutamine abc transporter:periplasmic glutamine-binding protein (db:pir2.dat) D64666 D64666 Helicobacter pylori 210 -11539149 7500958750 hp1172 glutamine abc transporter:periplasmic (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:37773 percent identity: 32.20;) (le:2260) (re:3093) (di:direct) HPAE000623 AE000623 g2314331 Helicobacter pylori 210 -11539149 7502853010 hp1172 glutamine abc transporter:periplasmic (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:37773 percent identity: 32.20;) (le:2260) (re:3093) (di:direct) HPAE000623 AE000623 g2314331 Helicobacter pylori 26695 85962 -11539149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906104	17607	39763	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906117	17608	39764	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906131	17609	39765	294	97

Description

6500735292 oppb:hp1251 oligopeptide abc transporter:permease protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP1251 HP1251 Helicobacter pylori 210 -11539150 7000690567 oligopeptide abc transporter:permease protein (db:pir2.dat) C64676 C64676 Helicobacter pylori 210 -11539150 7500959351 hp1251 oligopeptide abc transporter:permease protein (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to gp:1736843 percent identity: 59.60;) (le:5923) (re:6969) (di:complement) HPAE000630 AE000630 g2314415 Helicobacter pylori 210 -11539150 7502853011 hp1251 oligopeptide abc transporter:permease protein (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to gp:1736843 percent identity: 59.60;) (le:5923) (re:6969) (di:complement) HPAE000630 AE000630 g2314415 Helicobacter pylori 26695 85962 -11539150

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906132	17610	39766	690	229

Description

6500735293 oppa:hp1252 oligopeptide abc transporter:periplasmic oligopeptide-binding protein:oligopeptide abc transporter:periplasmicoligopeptide-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP1252 HP1252 Helicobacter pylori 210 -11539151 7000690565 oligopeptide abc transporter:periplasmic oligopeptide-binding protein (cl:periplasmic oligopeptide-binding protein) (db:pir2.dat) D64676 D64676 Helicobacter pylori 210 -11539151 7500959349 hp1252 oligopeptide abc transporter:periplasmic (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to egad:30669 percent identity: 28.71;) (le:6966) (re:8750) (di:complement) HPAE000630 AE000630 g2314416 Helicobacter pylori 210 -11539151 7502853012 hp1252 oligopeptide abc transporter:periplasmic (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to egad:30669 percent identity: 28.71;) (le:6966) (re:8750) (di:complement) HPAE000630 AE000630 g2314416 Helicobacter pylori 26695 85962 -11539151

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906133	17611	39767	828	275

Description

6500735294 glts:hp1506 glutamate permease (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-helicobacter pylori) HP1506 HP1506 Helicobacter pylori 210 -11539152 7000689360 glutamate permease (cl:sodium--glutamate symport carrier protein) (db:pir2.dat) B64708 B64708 Helicobacter pylori 210 -11539152 7500955182 hp1506 glutamate permease glts (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:14796 percent identity: 56.89;) (le:14529) (re:15755) (di:complement) HPAE000648 AE000648 g2314680 Helicobacter pylori 210 -11539152 7502853013 hp1506 glutamate permease glts (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:14796 percent identity: 56.89;) (le:14529) (re:15755) (di:complement) HPAE000648 AE000648 g2314680 Helicobacter pylori 26695 85962 -11539152

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906134	17612	39768	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906140	17613	39769	678	225

Description

6500735295 vaca:hp0887 vacuolating cytotoxin:vacuolating cytotoxin precursor (gtcfc:12.11) (keggfc:14.2) (tigrfc:4.3) (db:gtc-helicobacter pylori) HP0887 HP0887 Helicobacter pylori 210 -11539153 5500686145 vaca:hp0887 (sr:,campylobacter pylori) (de:vacuolating cytotoxin precursor) (db:swissprot) VAC0_HELPY P55981 HELICOBACTER PYLORI 210 -11539153 7000686932 vacuolating cytotoxin precursor (db:pir2.dat) G64630 G64630 Helicobacter pylori 210 -11539153 7500893946 hp0887 vacuolating cytotoxin (db:genpept-bct1) (de:helicobacter pylori section 76 of 134 of the complete genome.) (nt:similar to egad:14372 percent identity: 94.73;) (le:5972) (re:9844) (di:direct) HPAE000598 AE000598 g2314023 Helicobacter pylori 210 -11539153 7502853014 hp0887 vacuolating cytotoxin (db:genpept) (de:helicobacter pylori 26695 section 76 of 134 of the complete genome.) (nt:similar to egad:14372 percent identity: 94.73;) (le:5972) (re:9844) (di:direct) HPAE000598 AE000598 g2314023 Helicobacter pylori 26695 85962 -11539153

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906143	17614	39770	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906144	17615	39771	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906150	17616	39772	693	230

Description

6500735296 napa:hp0243 neutrophil activating protein:bacterioferritin:neutrophil-activating protein a:nap a:bacterioferritin (gtcfc:12.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-helicobacter pylori) HP0243 HP0243 Helicobacter pylori 210 -11539154 85219 napa:hp0243 (sr:,campylobacter pylori) (de:neutrophil-activating protein a (nap a) (bacterioferritin)) (db:swissprot) NAPA_HELPY P43313 HELICOBACTER PYLORI 210 -11539154 7000685914 neutrophil activating protein (cl:hypothetical protein hi1349) (db:pir2.dat) C64550 C64550 Helicobacter pylori 210 -11539154 7500886287 hp0243 neutrophil activating protein napa (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to egad:29611 percent identity: 95.83;) (le:13659) (re:14093) (di:complement) HPAE000543 AE000543 g2313332 Helicobacter pylori 210 -11539154 7502853015 hp0243 neutrophil activating protein napa (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to egad:29611 percent identity: 95.83;) (le:13659) (re:14093) (di:complement) HPAE000543 AE000543 g2313332 Helicobacter pylori 26695 85962 -11539154

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906157	17617	39773	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906180	17618	39774	564	187

Description

6500735297 chlorohydrolase (gtcfc:12.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-helicobacter pylori) HP0267 HP0267 Helicobacter pylori 210 -11539155 7000689712 chlorohydrolase (db:pir2.dat) C64553 C64553 Helicobacter pylori 210 -11539155 7500958520 hp0267 chlorohydrolase (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to gp:1655730 percent identity: 42.61;) (le:12474) (re:13703) (di:direct) HPAE000545 AE000545 g2313359 Helicobacter pylori 210 -11539155 7502853016 hp0267 chlorohydrolase (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to gp:1655730 percent identity: 42.61;) (le:12474) (re:13703) (di:direct) HPAE000545 AE000545 g2313359 Helicobacter pylori 26695 85962 -11539155

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906191	17619	39775	741	246

Description

6500735298 sodb:hp0389 superoxide dismutase:fe (gtcfc:12.12) (ec:1.15.1.1) (keggfc:14.1) (tigrfc:4.6) (db:gtc-helicobacter pylori) HP0389 HP0389 Helicobacter pylori 210 -11539156 7000689055 superoxide dismutase:fe/mn (cl:superoxide dismutase (mn)) (ec:1.15.1.1) (db:pir2.dat) E64568 E64568 Helicobacter pylori 210 -11539156 7500953944 hp0389 superoxide dismutase sodb (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:14911 percent identity: 98.59;) (le:6958) (re:7599) (di:complement) HPAE000555 AE000555 g2313490 Helicobacter pylori 210 -11539156 7502853017 hp0389 superoxide dismutase sodb (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:14911 percent identity: 98.59;) (le:6958) (re:7599) (di:complement) HPAE000555 AE000555 g2313490 Helicobacter pylori 26695 85962 -11539156

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906192	17620	39776	990	329

Description

6500735299 tdhf:hp1452 thiophene and furan oxidizer (gtcfc:12.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-helicobacter pylori) HP1452 HP1452 Helicobacter pylori 210 -11539157 7000690728 thiophene and furan oxidizer (cl:thiophen / furan oxidation protein:translation elongation factor tu homology) (db:pir2.dat) D64701 D64701 Helicobacter pylori 210 -11539157 7500959494 hp1452 thiophene and furan oxidizer tdhf (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:similar to egad:14211 percent identity: 37.56;) (le:3388) (re:4773) (di:direct) HPAE000645 AE000645 g2314627 Helicobacter pylori 210 -11539157 7502853018 hp1452 thiophene and furan oxidizer tdhf (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:similar to egad:14211 percent identity: 37.56;) (le:3388) (re:4773) (di:direct) HPAE000645 AE000645 g2314627 Helicobacter pylori 26695 85962 -11539157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906198	17621	39777	468	155

Description

6500735300 tsaa:hp1563 alkyl hydroperoxide reductase (gtcfc:12.12) (ec:1.6.4.-) (keggfc:14.1) (tigrfc:4.6) (db:gtc-helicobacter pylori) HP1563 HP1563 Helicobacter pylori 210 -11539158 57446 hp1563 (sr:,campylobacter pylori) (de:26 kd antigen) (db:swissprot) 26KD_HELPY P21762 HELICOBACTER PYLORI 210 -11539158 7000684463 alkyl hydroperoxide reductase::26k antigen (cl:alkyl hydroperoxide reductase c22 protein:alkyl hydroperoxidase c22 protein homology) (ec:1.6.4.-) (db:pir2.dat) C64715 C64715 Helicobacter pylori 210 -11539158 7500876085 hp1563 alkyl hydroperoxide reductase tsaa (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:17982 percent identity: 98.48;) (le:3774) (re:4370) (di:direct) HPAE000654 AE000654 g2314747 Helicobacter pylori 210 -11539158 7502853019 hp1563 alkyl hydroperoxide reductase tsaa (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:17982 percent identity: 98.48;) (le:3774) (re:4370) (di:direct) HPAE000654 AE000654 g2314747 Helicobacter pylori 26695 85962 -11539158

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906206	17622	39778	516	171

Description

6500735301 hypf:hp0048 transcriptional regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0048 HP0048 Helicobacter pylori 210 -11539159 7000690743 transcription regulator (cl:probabe transcription regulator hypf) (db:pir2.dat) H64525 H64525 Helicobacter pylori 210 -11539159 7500959508 hp0048 transcriptional regulator hypf (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:similar to egad:19428 percent identity: 34.47;) (le:8398) (re:10707) (di:complement) HPAE000526 AE000526 g2313122 Helicobacter pylori 210 -11539159 7502853020 hp0048 transcriptional regulator hypf (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:similar to egad:19428 percent identity: 34.47;) (le:8398) (re:10707) (di:complement) HPAE000526 AE000526 g2313122 Helicobacter pylori 26695 85962 -11539159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906211	17623	39779	1329	442

Description

6500735302 rpod:hp0088 rna polymerase sigma-70 factor (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0088 HP0088 Helicobacter pylori 210 -11539160 5500685913 rpod:hp0088 (sr:,campylobacter pylori) (de:rna polymerase sigma factor rpod (sigma-70)) (db:swissprot) RPSD_HELPY P55993 HELICOBACTER PYLORI 210 -11539160 7000686468 rna polymerase sigma-70 factor (cl:transcription initiation factor sigma katf homology:transcription initiation factor sigma region 1 homology) (db:pir2.dat) H64530 H64530 Helicobacter pylori 210 -11539160 7500890685 hp0088 rna polymerase sigma-70 factor rpod (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:similar to egad:29159 percent identity: 43.46;) (le:6707) (re:8722) (di:complement) HPAE000530 AE000530 g2313167 Helicobacter pylori 210 -11539160 7502853021 hp0088 rna polymerase sigma-70 factor rpod (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:similar to egad:29159 percent identity: 43.46;) (le:6707) (re:8722) (di:complement) HPAE000530 AE000530 g2313167 Helicobacter pylori 26695 85962 -11539160

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906213	17624	39780	2361	786

Description

6500735303 signal-transducing protein:histidine kinase (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0164 HP0164 Helicobacter pylori 210 -11539161 7000690704 signal-transducing protein:histidine kinase (db:pir2.dat) D64540 D64540 Helicobacter pylori 210 -11539161 7500959471 hp0164 signal-transducing protein:histidine kinase (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to egad:37673 percent identity: 27.06;) (le:3694) (re:4458) (di:complement) HPAE000537 AE000537 g2313251 Helicobacter pylori 210 -11539161 7502853022 hp0164 signal-transducing protein:histidine kinase (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to egad:37673 percent identity: 27.06;) (le:3694) (re:4458) (di:complement) HPAE000537 AE000537 g2313251 Helicobacter pylori 26695 85962 -11539161

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906241	17625	39781	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906243	17626	39782	375	124

Description

6500735304 ompr:hp0166 response regulator ompr:response regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0166 HP0166 Helicobacter pylori 210 -11539162 7000690684 response regulator (cl:ompr protein:response regulator homology) (db:pir2.dat) F64540 F64540 Helicobacter pylori 210 -11539162 7500959453 hp0166 response regulator ompr (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to egad:42966 percent identity: 51.02;) (le:5002) (re:5679) (di:complement) HPAE000537 AE000537 g2313252 Helicobacter pylori 210 -11539162 7502853023 hp0166 response regulator ompr (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to egad:42966 percent identity: 51.02;) (le:5002) (re:5679) (di:complement) HPAE000537 AE000537 g2313252 Helicobacter pylori 26695 85962 -11539162

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906245	17627	39783	489	162

Description

6500735305 msra:hp0224 peptide methionine sulfoxide reductase (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0224 HP0224 Helicobacter pylori 210 -11539163 7502853024 msra:hp0224 (sr:,campylobacter pylori) (de:peptide methionine sulfoxide reductase (peptide met(o) reductase)) (db:swissprot) PMSR_HELPY O25011 HELICOBACTER PYLORI 210 -11539163 7000690613 peptide methionine sulfoxide reductase (db:pir2.dat) H64547 H64547 Helicobacter pylori 210 -11539163 7500959392 hp0224 peptide methionine sulfoxide reductase msra (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:similar to egad:28444 percent identity: 66.77;) (le:4875) (re:5954) (di:direct) HPAE000542 AE000542 g2313314 Helicobacter pylori 210 -11539163 7502853025 hp0224 peptide methionine sulfoxide reductase msra (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:similar to egad:28444 percent identity: 66.77;) (le:4875) (re:5954) (di:direct) HPAE000542 AE000542 g2313314 Helicobacter pylori 26695 85962 -11539163

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906249	17628	39784	1245	414

Description

6500735306 atos:hp0244 signal-transducing protein:histidine kinase (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0244 HP0244 Helicobacter pylori 210 -11539164 7000690705 signal-transducing protein:histidine kinase (db:pir2.dat) D64550 D64550 Helicobacter pylori 210 -11539164 7500959472 hp0244 signal-transducing protein:histidine kinase (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:similar to egad:15380 percent identity: 30.00;) (le:133) (re:1278) (di:complement) HPAE000544 AE000544 g2313338 Helicobacter pylori 210 -11539164 7502853026 hp0244 signal-transducing protein:histidine kinase (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:similar to egad:15380 percent identity: 30.00;) (le:133) (re:1278) (di:complement) HPAE000544 AE000544 g2313338 Helicobacter pylori 26695 85962 -11539164

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906251	17629	39785	447	148

Description

7500955846 lytb:hp0400 penicillin tolerance protein (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0400 HP0400 Helicobacter pylori 210 -11539165 7000690608 penicillin tolerance protein (cl:penicillin tolerance protein) (db:pir2.dat) H64569 H64569 Helicobacter pylori 210 -11539165 7500955845 hp0400 penicillin tolerance protein lytb (db:genpept-bct1) (de:helicobacter pylori section 34 of 134 of the complete genome.) (nt:similar to egad:28020 percent identity: 30.58;) (le:91) (re:915) (di:complement) HPAE000556 AE000556 g2313506 Helicobacter pylori 210 -11539165 7502853027 lytb lysis tolerance protein (db:genpept) (de:helicobacter pylori, strain j99 section 88 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0400) (le:7015) (re:7839) (di:direct) AE001527 AE001527 g4155562 Helicobacter pylori J99 85963 -11539165 6500735307 hp0400 penicillin tolerance protein lytb (db:genpept) (de:helicobacter pylori 26695 section 34 of 134 of the complete genome.) (nt:similar to egad:28020 percent identity: 30.58;) (le:91) (re:915) (di:complement) HPAE000556 AE000556 g2313506 Helicobacter pylori 26695 85962 -11539165

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906254	17630	39786	801	266

Description

6500735308 response regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0703 HP0703 Helicobacter pylori 210 -11539166 7000690685 response regulator (cl:rna polymerase sigma factor interaction domain homology:response regulator homology) (db:pir2.dat) G64607 G64607 Helicobacter pylori 210 -11539166 7500959454 hp0703 response regulator (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:similar to egad:38658 percent identity: 44.20;) (le:4633) (re:5778) (di:direct) HPAE000583 AE000583 g2313827 Helicobacter pylori 210 -11539166 7502853028 hp0703 response regulator (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:similar to egad:38658 percent identity: 44.20;) (le:4633) (re:5778) (di:direct) HPAE000583 AE000583 g2313827 Helicobacter pylori 26695 85962 -11539166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906268	17631	39787	843	280

Description

6500735309 rpon:hp0714 rna polymerase sigma-54 factor (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0714 HP0714 Helicobacter pylori 210 -11539167 5500685895 rpon:hp0714 (sr:,campylobacter pylori) (de:rna polymerase sigma-54 factor) (db:swissprot) RP54_HELPY P56143 HELICOBACTER PYLORI 210 -11539167 7000686443 rna polymerase sigma-54 factor (db:pir2.dat) B64609 B64609 Helicobacter pylori 210 -11539167 7500890508 hp0714 rna polymerase sigma-54 factor rpon (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:similar to egad:14123 percent identity: 37.06;) (le:6937) (re:8181) (di:complement) HPAE000584 AE000584 g2313838 Helicobacter pylori 210 -11539167 7502853029 hp0714 rna polymerase sigma-54 factor rpon (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:similar to egad:14123 percent identity: 37.06;) (le:6937) (re:8181) (di:complement) HPAE000584 AE000584 g2313838 Helicobacter pylori 26695 85962 -11539167

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906272	17632	39788	546	182

Description

6500735310 transcriptional regulator:putative (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0727 HP0727 Helicobacter pylori 210 -11539168 7000690645 probable transcription regulator (db:pir2.dat) G64610 G64610 Helicobacter pylori 210 -11539168 7500959424 hp0727 transcriptional regulator:putative (db:genpept-bct1) (de:helicobacter pylori section 63 of 134 of the complete genome.) (nt:similar to egad:28002 percent identity: 33.33;) (le:9862) (re:10848) (di:complement) HPAE000585 AE000585 g2313849 Helicobacter pylori 210 -11539168 7502853030 hp0727 transcriptional regulator:putative (db:genpept) (de:helicobacter pylori 26695 section 63 of 134 of the complete genome.) (nt:similar to egad:28002 percent identity: 33.33;) (le:9862) (re:10848) (di:complement) HPAE000585 AE000585 g2313849 Helicobacter pylori 26695 85962 -11539168

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906274	17633	39789	1227	408

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906279	17634	39790	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906316	17635	39791	1110	370

Description

6500735311 sigma-54 interacting protein (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP0792 HP0792 Helicobacter pylori 210 -11539169 7000690702 sigma-54 interacting protein (cl:conserved hypothetical protein hi1117) (db:pir2.dat) H64618 H64618 Helicobacter pylori 210 -11539169 7500959469 hp0792 sigma-54 interacting protein (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:similar to egad:34138 percent identity: 97.72;) (le:5453) (re:6973) (di:complement) HPAE000591 AE000591 g2313921 Helicobacter pylori 210 -11539169 7502853031 hp0792 sigma-54 interacting protein (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:similar to egad:34138 percent identity: 97.72;) (le:5453) (re:6973) (di:complement) HPAE000591 AE000591 g2313921 Helicobacter pylori 26695 85962 -11539169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906319	17636	39792	390	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906328	17637	39793	687	228

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906330	17638	39794	372	123

Description

6500735312 response regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1021 HP1021 Helicobacter pylori 210 -11539170 7000690682 response regulator (db:pir2.dat) E64647 E64647 Helicobacter pylori 210 -11539170 7500959451 hp1021 response regulator (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:similar to egad:15562 percent identity: 28.70;) (le:5525) (re:6421) (di:direct) HPAE000610 AE000610 g2314165 Helicobacter pylori 210 -11539170 7502853032 hp1021 response regulator (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:similar to egad:15562 percent identity: 28.70;) (le:5525) (re:6421) (di:direct) HPAE000610 AE000610 g2314165 Helicobacter pylori 26695 85962 -11539170

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906331	17639	39795	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906333	17640	39796	297	98

Description

6500735313 hspr:hp1025 putative heat shock protein (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1025 HP1025 Helicobacter pylori 210 -11539171 7000690642 probable heat shock protein (cl:probable heat shock protein merr) (db:pir2.dat) A64648 A64648 Helicobacter pylori 210 -11539171 7500959421 hp1025 putative heat shock protein hspr (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:similar to egad:14005 percent identity: 46.15;) (le:9902) (re:10273) (di:direct) HPAE000610 AE000610 g2314167 Helicobacter pylori 210 -11539171 7502853033 hp1025 putative heat shock protein hspr (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:similar to egad:14005 percent identity: 46.15;) (le:9902) (re:10273) (di:direct) HPAE000610 AE000610 g2314167 Helicobacter pylori 26695 85962 -11539171

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906345	17641	39797	444	147

Description

6500735314 fur:hp1027 ferric uptake regulation protein (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1027 HP1027 Helicobacter pylori 210 -11539172 7502853034 fur:hp1027 (sr:,campylobacter pylori) (de:ferric uptake regulation protein (ferric uptake regulator)) (db:swissprot) FUR_HELPY O25671 HELICOBACTER PYLORI 210 -11539172 7000689918 ferric uptake regulation protein (cl:ferric uptake regulator) (db:pir2.dat) C64648 C64648 Helicobacter pylori 210 -11539172 7500958712 hp1027 ferric uptake regulation protein fur (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to egad:41845 percent identity: 39.86;) (le:110) (re:562) (di:direct) HPAE000611 AE000611 g2314174 Helicobacter pylori 210 -11539172 7502853035 hp1027 ferric uptake regulation protein fur (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to egad:41845 percent identity: 39.86;) (le:110) (re:562) (di:direct) HPAE000611 AE000611 g2314174 Helicobacter pylori 26695 85962 -11539172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906346	17642	39798	288	95

Description

6500735315 flia:hp1032 alternative transcription initiation factor:sigma-f:alternative transcription initiation factor:sigma-f (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1032 HP1032 Helicobacter pylori 210 -11539173 7000689631 alternative transcription initiation factor:sigma-f (db:pir2.dat) H64648 H64648 Helicobacter pylori 210 -11539173 7500958449 hp1032 alternative transcription initiation factor (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to egad:8747 percent identity: 34.60;) (le:3565) (re:4332) (di:complement) HPAE000611 AE000611 g2314177 Helicobacter pylori 210 -11539173 7502853036 hp1032 alternative transcription initiation factor (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to egad:8747 percent identity: 34.60;) (le:3565) (re:4332) (di:complement) HPAE000611 AE000611 g2314177 Helicobacter pylori 26695 85962 -11539173

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906355	17643	39799	231	76

Description

6500735316 response regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1043 HP1043 Helicobacter pylori 210 -11539174 7000690681 response regulator (db:pir2.dat) C64650 C64650 Helicobacter pylori 210 -11539174 7500959450 hp1043 response regulator (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to egad:35436 percent identity: 26.82;) (le:3919) (re:4590) (di:complement) HPAE000612 AE000612 g2314190 Helicobacter pylori 210 -11539174 7502853037 hp1043 response regulator (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to egad:35436 percent identity: 26.82;) (le:3919) (re:4590) (di:complement) HPAE000612 AE000612 g2314190 Helicobacter pylori 26695 85962 -11539174

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906362	17644	39800	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906366	17645	39801	1512	503

Description

6500735317 csta:hp1168 carbon starvation protein (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1168 HP1168 Helicobacter pylori 210 -11539175 5500685030 csta:hp1168 (sr:,campylobacter pylori) (de:carbon starvation protein a homolog) (db:swissprot) CSTA_HELPY P56190 HELICOBACTER PYLORI 210 -11539175 7000684932 carbon starvation protein (cl:carbon starvation protein) (db:pir2.dat) H64665 H64665 Helicobacter pylori 210 -11539175 7500879506 hp1168 carbon starvation protein csta (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:similar to egad:8578 percent identity: 59.81;) (le:7902) (re:9965) (di:complement) HPAE000622 AE000622 g2314324 Helicobacter pylori 210 -11539175 7502853038 hp1168 carbon starvation protein csta (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:similar to egad:8578 percent identity: 59.81;) (le:7902) (re:9965) (di:complement) HPAE000622 AE000622 g2314324 Helicobacter pylori 26695 85962 -11539175

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906372	17646	39802	561	186

Description

6500735318 tena:hp1287 transcriptional regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1287 HP1287 Helicobacter pylori 210 -11539176 7000690742 transcription regulator (db:pir2.dat) G64680 G64680 Helicobacter pylori 210 -11539176 7500959507 hp1287 transcriptional regulator tena (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:24145 percent identity: 34.65;) (le:1539) (re:2192) (di:complement) HPAE000633 AE000633 g2314455 Helicobacter pylori 210 -11539176 7502853039 hp1287 transcriptional regulator tena (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:24145 percent identity: 34.65;) (le:1539) (re:2192) (di:complement) HPAE000633 AE000633 g2314455 Helicobacter pylori 26695 85962 -11539176

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906375	17647	39803	1935	644

Description

6500735319 signal-transducing protein:histidine kinase (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1364 HP1364 Helicobacter pylori 210 -11539177 7000690706 signal-transducing protein:histidine kinase (db:pir2.dat) D64690 D64690 Helicobacter pylori 210 -11539177 7500959473 hp1364 signal-transducing protein:histidine kinase (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:16624 percent identity: 24.86;) (le:18690) (re:19883) (di:complement) HPAE000636 AE000636 g2314530 Helicobacter pylori 210 -11539177 7502853040 hp1364 signal-transducing protein:histidine kinase (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:16624 percent identity: 24.86;) (le:18690) (re:19883) (di:complement) HPAE000636 AE000636 g2314530 Helicobacter pylori 26695 85962 -11539177

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906379	17648	39804	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906386	17649	39805	336	111

Description

6500735320 response regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1365 HP1365 Helicobacter pylori 210 -11539178 7000690683 response regulator (cl:response regulator homology) (db:pir2.dat) E64690 E64690 Helicobacter pylori 210 -11539178 7500959452 hp1365 response regulator (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:41320 percent identity: 32.38;) (le:19858) (re:20499) (di:complement) HPAE000636 AE000636 g2314531 Helicobacter pylori 210 -11539178 7502853041 hp1365 response regulator (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:41320 percent identity: 32.38;) (le:19858) (re:20499) (di:complement) HPAE000636 AE000636 g2314531 Helicobacter pylori 26695 85962 -11539178

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906392	17650	39806	390	129

Description

6500735321 csra:hp1442 carbon storage regulator (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1442 HP1442 Helicobacter pylori 210 -11539179 7000689484 carbon storage regulator (cl:glycogen biosynthesis inhibitor) (db:pir2.dat) B64700 B64700 Helicobacter pylori 210 -11539179 7500955783 hp1442 carbon storage regulator csra (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to egad:8281 percent identity: 43.33;) (le:8522) (re:8752) (di:direct) HPAE000644 AE000644 g2314614 Helicobacter pylori 210 -11539179 7502853042 hp1442 carbon storage regulator csra (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to egad:8281 percent identity: 43.33;) (le:8522) (re:8752) (di:direct) HPAE000644 AE000644 g2314614 Helicobacter pylori 26695 85962 -11539179

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906393	17651	39807	237	78

Description

6500735322 regulatory protein dnir (gtcfc:12.13) (keggfc:14.2) (tigrfc:9.1) (db:gtc-helicobacter pylori) HP1572 HP1572 Helicobacter pylori 210 -11539180 7000690678 regulatory protein dnir (db:pir2.dat) D64716 D64716 Helicobacter pylori 210 -11539180 7500959448 hp1572 regulatory protein dnir (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to gp:1552781 percent identity: 31.87;) (le:11201) (re:12319) (di:complement) HPAE000654 AE000654 g2314753 Helicobacter pylori 210 -11539180 7502853043 hp1572 regulatory protein dnir (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to gp:1552781 percent identity: 31.87;) (le:11201) (re:12319) (di:complement) HPAE000654 AE000654 g2314753 Helicobacter pylori 26695 85962 -11539180

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906399	17652	39808	255	84

Description

6500735323 lctp:hp0140 l-lactate permease (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-helicobacter pylori) HP0140 HP0140 Helicobacter pylori 210 -11539181 7000690496 l-lactate permease (cl:l-lactate permease) (db:pir2.dat) D64537 D64537 Helicobacter pylori 210 -11539181 7500959288 hp0140 l-lactate permease lctp (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:similar to egad:8633 percent identity: 58.67;) (le:8702) (re:10351) (di:direct) HPAE000535 AE000535 g2313224 Helicobacter pylori 210 -11539181 7502853044 hp0140 l-lactate permease lctp (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:similar to egad:8633 percent identity: 58.67;) (le:8702) (re:10351) (di:direct) HPAE000535 AE000535 g2313224 Helicobacter pylori 26695 85962 -11539181

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906402	17653	39809	747	248

Description

6500735324 lctp:hp0141 l-lactate permease (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-helicobacter pylori) HP0141 HP0141 Helicobacter pylori 210 -11539182 7000690497 l-lactate permease (cl:l-lactate permease) (db:pir2.dat) E64537 E64537 Helicobacter pylori 210 -11539182 7500959289 hp0141 l-lactate permease lctp (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:similar to egad:8633 percent identity: 55.49;) (le:10408) (re:12063) (di:direct) HPAE000535 AE000535 g2313225 Helicobacter pylori 210 -11539182 7502853045 hp0141 l-lactate permease lctp (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:similar to egad:8633 percent identity: 55.49;) (le:10408) (re:12063) (di:direct) HPAE000535 AE000535 g2313225 Helicobacter pylori 26695 85962 -11539182

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906404	17654	39810	219	72

Description

6500735325 dcua:hp0724 anaerobic c4-dicarboxylate transport protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-helicobacter pylori) HP0724 HP0724 Helicobacter pylori 210 -11539183 7502853046 dcua:hp0724 (sr:,campylobacter pylori) (de:anaerobic c4-dicarboxylate transporter dcua) (db:swissprot) DCUA_HELPY O25425 HELICOBACTER PYLORI 210 -11539183 7000689456 dicarboxylate membrane-transporter protein a (cl:dicarboxylate membrane-transporter protein a) (db:pir2.dat) D64610 D64610 Helicobacter pylori 210 -11539183 7500955731 hp0724 anaerobic c4-dicarboxylate transport protein (db:genpept-bct1) (de:helicobacter pylori section 63 of 134 of the complete genome.) (nt:similar to egad:17984 percent identity: 53.81;) (le:5393) (re:6724) (di:direct) HPAE000585 AE000585 g2313848 Helicobacter pylori 210 -11539183 7502853047 hp0724 anaerobic c4-dicarboxylate transport protein (db:genpept) (de:helicobacter pylori 26695 section 63 of 134 of the complete genome.) (nt:similar to egad:17984 percent identity: 53.81;) (le:5393) (re:6724) (di:direct) HPAE000585 AE000585 g2313848 Helicobacter pylori 26695 85962 -11539183

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906408	17655	39811	696	231

Description

6500735326 kgtp:hp1091 alpha-ketoglutarate permease (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-helicobacter pylori) HP1091 HP1091 Helicobacter pylori 210 -11539184 7000689630 alpha-ketoglutarate permease (cl:citrate utilization determinant) (db:pir2.dat) C64656 C64656 Helicobacter pylori 210 -11539184 7500958448 hp1091 alpha-ketoglutarate permease kgtp (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to egad:5589 percent identity: 45.87;) (le:160) (re:1440) (di:direct) HPAE000616 AE000616 g2314243 Helicobacter pylori 210 -11539184 7502853048 hp1091 alpha-ketoglutarate permease kgtp (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to egad:5589 percent identity: 45.87;) (le:160) (re:1440) (di:direct) HPAE000616 AE000616 g2314243 Helicobacter pylori 26695 85962 -11539184

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906411	17656	39812	654	217

Description

6500735327 glup:hp1174 glucose/galactose transporter (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-helicobacter pylori) HP1174 HP1174 Helicobacter pylori 210 -11539185 7500882581 glup:hp1174 (sr:,campylobacter pylori) (de:putative glucose/galactose transporter) (db:swissprot) GLUP_HELPY O25788 HELICOBACTER PYLORI 210 -11539185 7000689964 glucose/galactose transporter (db:pir2.dat) F64666 F64666 Helicobacter pylori 210 -11539185 7500882583 hp1174 glucose/galactose transporter glup (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:41134 percent identity: 53.59;) (le:4038) (re:5261) (di:complement) HPAE000623 AE000623 g2314332 Helicobacter pylori 210 -11539185 7502853049 hp1174 glucose/galactose transporter glup (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:41134 percent identity: 53.59;) (le:4038) (re:5261) (di:complement) HPAE000623 AE000623 g2314332 Helicobacter pylori 26695 85962 -11539185

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906412	17657	39813	285	94

Description

6500735328 nupc:hp1180 pyrimidine nucleoside transport protein (gtcfc:12.3) (keggfc:14.2) (tigrfc:13.6) (db:gtc-helicobacter pylori) HP1180 HP1180 Helicobacter pylori 210 -11539186 7000690665 pyrimidine nucleoside transport protein (cl:pyrimidine nucleoside transport protein nupc) (db:pir2.dat) D64667 D64667 Helicobacter pylori 210 -11539186 7500959438 hp1180 pyrimidine nucleoside transport protein nupc (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:30360 percent identity: 32.91;) (le:11480) (re:12736) (di:complement) HPAE000623 AE000623 g2314337 Helicobacter pylori 210 -11539186 7502853050 hp1180 pyrimidine nucleoside transport protein nupc (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:30360 percent identity: 32.91;) (le:11480) (re:12736) (di:complement) HPAE000623 AE000623 g2314337 Helicobacter pylori 26695 85962 -11539186

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906413	17658	39814	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906414	17659	39815	309	102

Description

6500735329 pnuc:hp1290 nicotinamide mononucleotide transporter (gtcfc:12.3) (keggfc:14.2) (tigrfc:13.6) (db:gtc-helicobacter pylori) HP1290 HP1290 Helicobacter pylori 210 -11539187 7000690556 nicotinamide mononucleotide transporter (db:pir2.dat) B64681 B64681 Helicobacter pylori 210 -11539187 7500959343 hp1290 nicotinamide mononucleotide transporter pnuc (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:6089 percent identity: 28.00;) (le:3809) (re:4471) (di:direct) HPAE000633 AE000633 g2314456 Helicobacter pylori 210 -11539187 7502853051 hp1290 nicotinamide mononucleotide transporter pnuc (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:6089 percent identity: 28.00;) (le:3809) (re:4471) (di:direct) HPAE000633 AE000633 g2314456 Helicobacter pylori 26695 85962 -11539187

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906416	17660	39816	300	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906435	17661	39817	741	246

Description

6500735330 nark:hp0313 nitrite extrusion protein (gtcfc:12.4) (keggfc:14.2) (tigrfc:13.3) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_)) HP0313 HP0313 Helicobacter pylori 210 -11539188 7000690560 nitrite extrusion protein (cl:nitrite extrusion protein) (db:pir2.dat) A64559 A64559 Helicobacter pylori 210 -11539188 7500959345 hp0313 nitrite extrusion protein nark (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:similar to egad:30454 percent identity: 23.56;) (le:5938) (re:7083) (di:complement) HPAE000549 AE000549 g2313408 Helicobacter pylori 210 -11539188 7502853052 hp0313 nitrite extrusion protein nark (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:similar to egad:30454 percent identity: 23.56;) (le:5938) (re:7083) (di:complement) HPAE000549 AE000549 g2313408 Helicobacter pylori 26695 85962 -11539188

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906442	17662	39818	222	73

Description

6500735331 moda:hp0473 molybdenum abc transporter:periplasmic molybdate-binding protein:molybdenum abc transporter:periplasmicmolybdate-binding protein (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) HP0473 HP0473 Helicobacter pylori 210 -11539189 7000690523 molybdenum abc transporter:periplasmic molybdate-binding protein (cl:molybdate-binding periplasmic protein) (db:pir2.dat) A64579 A64579 Helicobacter pylori 210 -11539189 7500959314 hp0473 molybdenum abc transporter:periplasmic (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to gp:1800186 percent identity: 95.93;) (le:2435) (re:3175) (di:direct) HPAE000562 AE000562 g2313584 Helicobacter pylori 210 -11539189 7502853053 hp0473 molybdenum abc transporter:periplasmic (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to gp:1800186 percent identity: 95.93;) (le:2435) (re:3175) (di:direct) HPAE000562 AE000562 g2313584 Helicobacter pylori 26695 85962 -11539189

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906447	17663	39819	336	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906448	17664	39820	1194	397

Description

6500735332 modb:hp0474 molybdenum abc transporter:permease protein (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) HP0474 HP0474 Helicobacter pylori 210 -11539190 7000690524 molybdenum abc transporter:permease protein (cl:maltose transport protein malg) (db:pir2.dat) B64579 B64579 Helicobacter pylori 210 -11539190 7500959315 hp0474 molybdenum abc transporter:permease protein (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to egad:28680 percent identity: 28.71;) (le:3197) (re:3871) (di:direct) HPAE000562 AE000562 g2313585 Helicobacter pylori 210 -11539190 7502853054 hp0474 molybdenum abc transporter:permease protein (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to egad:28680 percent identity: 28.71;) (le:3197) (re:3871) (di:direct) HPAE000562 AE000562 g2313585 Helicobacter pylori 26695 85962 -11539190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906467	17665	39821	453	150

Description

GTC ORF with score 117 to: (sr:norway rat) (db:genpept-rod) (de:rattus norvegicus brain-enriched guanylate kinase-associatedprotein 1 mrna, complete cds.) (nt:protein enriched in the postsynaptic density) (le:99) (re:1934) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906484	17666	39822	546	181

Description

6500735333 modd:hp0475 molybdenum abc transporter:atp-binding protein (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) HP0475 HP0475 Helicobacter pylori 210 -11539191 7000690522 molybdenum abc transporter:atp-binding protein (cl:atp-binding cassette homology) (db:pir2.dat) C64579 C64579 Helicobacter pylori 210 -11539191 7500959313 hp0475 molybdenum abc transporter:atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to egad:8781 percent identity: 38.38;) (le:3868) (re:4665) (di:direct) HPAE000562 AE000562 g2313586 Helicobacter pylori 210 -11539191 7502853055 hp0475 molybdenum abc transporter:atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to egad:8781 percent identity: 38.38;) (le:3868) (re:4665) (di:direct) HPAE000562 AE000562 g2313586 Helicobacter pylori 26695 85962 -11539191

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906492	17667	39823	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906501	17668	39824	1581	526

Description

6500735334 phosphate permease (gtcfc:12.4) (keggfc:14.2) (tigrfc:13.3) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_)) HP1491 HP1491 Helicobacter pylori 210 -11539192 7000690619 phosphate permease (db:pir2.dat) C64706 C64706 Helicobacter pylori 210 -11539192 7500959398 hp1491 phosphate permease (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:28595 percent identity: 34.80;) (le:82) (re:1683) (di:complement) HPAE000648 AE000648 g2314671 Helicobacter pylori 210 -11539192 7502853056 hp1491 phosphate permease (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:28595 percent identity: 34.80;) (le:82) (re:1683) (di:complement) HPAE000648 AE000648 g2314671 Helicobacter pylori 26695 85962 -11539192

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906502	17669	39825	312	103

Description

6500735335 kefb:hp0471 glutathione-regulated potassium-efflux system protein:glutathione-regulated potassium-efflux systemprotein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP0471 HP0471 Helicobacter pylori 210 -11539193 7000689969 glutathione-regulated potassium-efflux system protein (db:pir2.dat) G64578 G64578 Helicobacter pylori 210 -11539193 7500958754 hp0471 glutathione-regulated potassium-efflux system (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to gp:1800183 percent identity: 99.28;) (le:79) (re:1329) (di:complement) HPAE000562 AE000562 g2313582 Helicobacter pylori 210 -11539193 7502853057 hp0471 glutathione-regulated potassium-efflux system (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to gp:1800183 percent identity: 99.28;) (le:79) (re:1329) (di:complement) HPAE000562 AE000562 g2313582 Helicobacter pylori 26695 85962 -11539193

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906514	17670	39826	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906524	17671	39827	876	291

Description

6500735336 putative potassium channel protein:putative (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP0490 HP0490 Helicobacter pylori 210 -11539194 7000690644 probable potassium channel protein (db:pir2.dat) B64581 B64581 Helicobacter pylori 210 -11539194 7500959423 hp0490 putative potassium channel protein:putative (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:45122 percent identity: 25.75;) (le:240) (re:1376) (di:complement) HPAE000564 AE000564 g2313603 Helicobacter pylori 210 -11539194 7502853058 hp0490 putative potassium channel protein:putative (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:45122 percent identity: 25.75;) (le:240) (re:1376) (di:complement) HPAE000564 AE000564 g2313603 Helicobacter pylori 26695 85962 -11539194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906530	17672	39828	1065	354

Description

6500735337 feca:hp0686 iron iii dicitrate transport protein (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.5) (db:gtc-helicobacter pylori) HP0686 HP0686 Helicobacter pylori 210 -11539195 7000690485 iron iii dicitrate transport protein (cl:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pir2.dat) F64605 F64605 Helicobacter pylori 210 -11539195 7500959271 hp0686 iron iii dicitrate transport protein feca (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:similar to egad:10491 percent identity: 29.69;) (le:8256) (re:10559) (di:complement) HPAE000581 AE000581 g2313808 Helicobacter pylori 210 -11539195 7502853059 hp0686 iron iii dicitrate transport protein feca (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:similar to egad:10491 percent identity: 29.69;) (le:8256) (re:10559) (di:complement) HPAE000581 AE000581 g2313808 Helicobacter pylori 26695 85962 -11539195

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906543	17673	39829	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906556	17674	39830	744	247

Description

6500735338 feob:hp0687 iron ii transport protein:iron:ii transport protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP0687 HP0687 Helicobacter pylori 210 -11539196 7000690482 iron ii transport protein (cl:ferrous iron transport protein b:translation elongation factor tu homology) (db:pir2.dat) G64605 G64605 Helicobacter pylori 210 -11539196 7500959268 hp0687 iron ii transport protein feob (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:similar to egad:7439 percent identity: 33.60;) (le:154) (re:2082) (di:complement) HPAE000582 AE000582 g2313813 Helicobacter pylori 210 -11539196 7502853060 hp0687 iron ii transport protein feob (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:similar to egad:7439 percent identity: 33.60;) (le:154) (re:2082) (di:complement) HPAE000582 AE000582 g2313813 Helicobacter pylori 26695 85962 -11539196

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906567	17675	39831	570	189

Description

6500735339 feca:hp0807 iron iii dicitrate transport protein (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.5) (db:gtc-helicobacter pylori) HP0807 HP0807 Helicobacter pylori 210 -11539197 7000690486 iron iii dicitrate transport protein (cl:tonb-dependent receptor amino-terminal homology:tonb-dependent receptor carboxyl-terminal homology) (db:pir2.dat) G64620 G64620 Helicobacter pylori 210 -11539197 7500959272 hp0807 iron iii dicitrate transport protein feca (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:10491 percent identity: 28.53;) (le:6226) (re:8589) (di:complement) HPAE000592 AE000592 g2313936 Helicobacter pylori 210 -11539197 7502853061 hp0807 iron iii dicitrate transport protein feca (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:10491 percent identity: 28.53;) (le:6226) (re:8589) (di:complement) HPAE000592 AE000592 g2313936 Helicobacter pylori 26695 85962 -11539197

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906577	17676	39832	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906608	17677	39833	882	293

Description

GTC ORF with score 110 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome 1 bac f5o8 sequence, completesequence.) (nt:strong similarity to pfam pf|00069 eukaryotic) (le:21143:21479:21726) (re:21388:21640:21873) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906628	17678	39834	300	99

Description

6500735340 fece:hp0888 iron iii dicitrate abc transporter:atp-binding protein (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.5) (db:gtc-helicobacter pylori) HP0888 HP0888 Helicobacter pylori 210 -11539198 5500686442 hp0888 (sr:,campylobacter pylori) (de:probable iron chelatin transport atp-binding protein hp0888) (db:swissprot) Y888_HELPY O05732 HELICOBACTER PYLORI 210 -11539198 7000687096 iron iii dicitrate abc transporter:atp-binding protein (cl:atp-binding cassette homology) (db:pir2.dat) H64630 H64630 Helicobacter pylori 210 -11539198 1500692145 hp0888 iron iii dicitrate abc transporter:atp-binding (db:genpept-bct1) (de:helicobacter pylori section 76 of 134 of the complete genome.) (nt:similar to egad:28280 percent identity: 34.43;) (le:9904) (re:10671) (di:complement) HPAE000598 AE000598 g2314024 Helicobacter pylori 210 -11539198 7500895615 fepc fepc (db:genpept-bct2) (de:helicobacter pylori vapd (vapd), vdld (vdld), vdlc (vdlc), hemu(hemu) and fepc (fepc) genes, complete cds.) (le:3372) (re:4139) (di:direct) HPU94318 U94318 g2072456 Helicobacter pylori 210 -11539198 5000696483 hp0888 iron iii dicitrate abc transporter:atp-binding (db:genpept) (de:helicobacter pylori 26695 section 76 of 134 of the complete genome.) (nt:similar to egad:28280 percent identity: 34.43;) (le:9904) (re:10671) (di:complement) HPAE000598 AE000598 g2314024 Helicobacter pylori 26695 85962 -11539198

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906632	17679	39835	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906636	17680	39836	1353	450

Description

6500735341 fecd:hp0889 iron iii dicitrate abc transporter:permease protein (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.5) (db:gtc-helicobacter pylori) HP0889 HP0889 Helicobacter pylori 210 -11539199 5500686443 hp0889 (sr:,campylobacter pylori) (de:probable iron chelatin transport system permease protein hp0889) (db:swissprot) Y889_HELPY O05731 HELICOBACTER PYLORI 210 -11539199 7000687097 iron iii dicitrate abc transporter:permease protein (db:pir2.dat) A64631 A64631 Helicobacter pylori 210 -11539199 1500692144 hp0889 iron iii dicitrate abc transporter:permease (db:genpept-bct1) (de:helicobacter pylori section 76 of 134 of the complete genome.) (nt:similar to egad:7245 percent identity: 38.32;) (le:10671) (re:11651) (di:complement) HPAE000598 AE000598 g2314025 Helicobacter pylori 210 -11539199 7500895616 hemu hemu (db:genpept-bct2) (de:helicobacter pylori vapd (vapd), vdld (vdld), vdlc (vdlc), hemu(hemu) and fepc (fepc) genes, complete cds.) (le:2392) (re:3372) (di:direct) HPU94318 U94318 g2072455 Helicobacter pylori 210 -11539199 5000696484 hp0889 iron iii dicitrate abc transporter:permease (db:genpept) (de:helicobacter pylori 26695 section 76 of 134 of the complete genome.) (nt:similar to egad:7245 percent identity: 38.32;) (le:10671) (re:11651) (di:complement) HPAE000598 AE000598 g2314025 Helicobacter pylori 26695 85962 -11539199

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906660	17681	39837	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906665	17682	39838	924	307

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906666	17683	39839	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906686	17684	39840	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906690	17685	39841	489	162

Description

6500735342 czca:hp0969 cation efflux system protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP0969 HP0969 Helicobacter pylori 210 -11539200 7000689696 cation efflux system protein (cl:cation efflux system membrane protein czca) (db:pir2.dat) A64641 A64641 Helicobacter pylori 210 -11539200 7500958507 hp0969 cation efflux system protein czca (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:similar to egad:14773 percent identity: 37.32;) (le:6743) (re:9805) (di:complement) HPAE000605 AE000605 g2314107 Helicobacter pylori 210 -11539200 7502853062 hp0969 cation efflux system protein czca (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:similar to egad:14773 percent identity: 37.32;) (le:6743) (re:9805) (di:complement) HPAE000605 AE000605 g2314107 Helicobacter pylori 26695 85962 -11539200

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906700	17686	39842	717	238

Description

6500735343 copa:hp1072 copper-transporting atpase:p-type:copper-transporting atpase (gtcfc:12.5) (ec:3.6.1.36) (keggfc:14.1) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1072 HP1072 Helicobacter pylori 210 -11539201 5500685003 copa:hp1072 (sr:,campylobacter pylori) (ec:3.6.1.36) (de:copper-transporting atpase,) (db:swissprot) COA0_HELPY P55989 HELICOBACTER PYLORI 210 -11539201 7000684857 copper-transporting atpase::p-type (cl:enterococcus copper-transporting atpase copa:atpase nucleotide-binding domain homology:atpase transduction domain homology:heavy-metal-associated homology) (ec:3.6.1.-) (db:pir1.dat) H64653 H64653 Helicobacter pylori 210 -11539201 7500878971 hp1072 copper-transporting atpase:p-type copa (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:similar to egad:15377 percent identity: 93.94;) (le:4416) (re:6653) (di:direct) HPAE000614 AE000614 g2314221 Helicobacter pylori 210 -11539201 7502853063 hp1072 copper-transporting atpase:p-type copa (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:similar to egad:15377 percent identity: 93.94;) (le:4416) (re:6653) (di:direct) HPAE000614 AE000614 g2314221 Helicobacter pylori 26695 85962 -11539201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906705	17687	39843	456	151

Description

6500735344 copp:hp1073 cop associated protein:copper ion binding protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1073 HP1073 Helicobacter pylori 210 -11539202 1500686913 copp:hp1073 (sr:,campylobacter pylori) (de:cop associated protein (copper ion binding protein)) (db:swissprot) COPP_HELPY Q48271 HELICOBACTER PYLORI 210 -11539202 7000684871 heavy-metal-binding protein hp1073:copper-ion-binding protein copp homolog (cl:mercuric resistance operon regulatory protein:heavy-metal-associated homology) (db:pir1.dat) A64654 A64654 Helicobacter pylori 210 -11539202 7500879097 hp1073 copper ion binding protein copp (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:similar to egad:17393 percent identity: 92.42;) (le:6654) (re:6854) (di:direct) HPAE000614 AE000614 g2314224 Helicobacter pylori 210 -11539202 7502853064 hp1073 copper ion binding protein copp (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:similar to egad:17393 percent identity: 92.42;) (le:6654) (re:6854) (di:direct) HPAE000614 AE000614 g2314224 Helicobacter pylori 26695 85962 -11539202

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906707	17688	39844	321	106

Description

6500735345 nixa:hp1077 nickel transport protein:high-affinity nickel-transport protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1077 HP1077 Helicobacter pylori 210 -11539203 1500686981 nixa:hp1077 (sr:,campylobacter pylori) (de:high-affinity nickel-transport protein nixa) (db:swissprot) NIXA_HELPY Q48262 HELICOBACTER PYLORI 210 -11539203 7000685971 nixa nickel transport protein (db:pir2.dat) S53113 E64654 Helicobacter pylori 210 -11539203 7500886485 hp1077 nickel transport protein nixa (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:similar to egad:33273 percent identity: 98.70;) (le:9813) (re:10808) (di:complement) HPAE000614 AE000614 g2314223 Helicobacter pylori 210 -11539203 7502853065 hp1077 nickel transport protein nixa (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:similar to egad:33273 percent identity: 98.70;) (le:9813) (re:10808) (di:complement) HPAE000614 AE000614 g2314223 Helicobacter pylori 26695 85962 -11539203

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906712	17689	39845	282	93

Description

6500735346 napa:hp1183 na+/h+ antiporter (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1183 HP1183 Helicobacter pylori 210 -11539204 7000690539 na+/h+ antiporter (db:pir2.dat) G64667 G64667 Helicobacter pylori 210 -11539204 7500959326 hp1183 na+/h+ antiporter napa (db:genpept-bct1) (de:helicobacter pylori section 102 of 134 of the complete genome.) (nt:similar to egad:6297 percent identity: 26.57;) (le:2413) (re:3564) (di:complement) HPAE000624 AE000624 g2314343 Helicobacter pylori 210 -11539204 7502853066 hp1183 na+/h+ antiporter napa (db:genpept) (de:helicobacter pylori 26695 section 102 of 134 of the completegenome.) (nt:similar to egad:6297 percent identity: 26.57;) (le:2413) (re:3564) (di:complement) HPAE000624 AE000624 g2314343 Helicobacter pylori 26695 85962 -11539204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906727	17690	39846	2745	914

Description

6500735347 czca:hp1328 cation efflux system protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1328 HP1328 Helicobacter pylori 210 -11539205 7000689698 cation efflux system protein (db:pir2.dat) H64685 H64685 Helicobacter pylori 210 -11539205 7500958509 hp1328 cation efflux system protein czca (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:similar to egad:13059 percent identity: 28.85;) (le:6132) (re:7148) (di:direct) HPAE000634 AE000634 g2314493 Helicobacter pylori 210 -11539205 7502853067 hp1328 cation efflux system protein czca (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:similar to egad:13059 percent identity: 28.85;) (le:6132) (re:7148) (di:direct) HPAE000634 AE000634 g2314493 Helicobacter pylori 26695 85962 -11539205

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906738	17691	39847	771	256

Description

6500735348 czca:hp1329 cation efflux system protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1329 HP1329 Helicobacter pylori 210 -11539206 7000689697 cation efflux system protein (cl:cation efflux system membrane protein czca) (db:pir2.dat) A64686 A64686 Helicobacter pylori 210 -11539206 7500958508 hp1329 cation efflux system protein czca (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:similar to egad:14773 percent identity: 31.32;) (le:7149) (re:10256) (di:direct) HPAE000634 AE000634 g2314494 Helicobacter pylori 210 -11539206 7502853068 hp1329 cation efflux system protein czca (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:similar to egad:14773 percent identity: 31.32;) (le:7149) (re:10256) (di:direct) HPAE000634 AE000634 g2314494 Helicobacter pylori 26695 85962 -11539206

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906743	17692	39848	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906750	17693	39849	654	217

Description

6500735349 cora:hp1344 magnesium and cobalt transport protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1344 HP1344 Helicobacter pylori 210 -11539207 7000690509 magnesium and cobalt transport protein (cl:magnesium and cobalt transport protein) (db:pir2.dat) H64687 H64687 Helicobacter pylori 210 -11539207 7500959303 hp1344 magnesium and cobalt transport protein cora (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:8227 percent identity: 26.32;) (le:10197) (re:11153) (di:complement) HPAE000635 AE000635 g2314510 Helicobacter pylori 210 -11539207 7502853069 hp1344 magnesium and cobalt transport protein cora (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:8227 percent identity: 26.32;) (le:10197) (re:11153) (di:complement) HPAE000635 AE000635 g2314510 Helicobacter pylori 26695 85962 -11539207

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906751	17694	39850	708	235

Description

6500735350 feca:hp1400 iron iii dicitrate transport protein (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.5) (db:gtc-helicobacter pylori) HP1400 HP1400 Helicobacter pylori 210 -11539208 7000690487 iron iii dicitrate transport protein (db:pir2.dat) H64694 H64694 Helicobacter pylori 210 -11539208 7500959273 hp1400 iron iii dicitrate transport protein feca (db:genpept-bct1) (de:helicobacter pylori section 118 of 134 of the complete genome.) (nt:similar to egad:10491 percent identity: 26.32;) (le:299) (re:2827) (di:direct) HPAE000640 AE000640 g2314573 Helicobacter pylori 210 -11539208 7502853070 hp1400 iron iii dicitrate transport protein feca (db:genpept) (de:helicobacter pylori 26695 section 118 of 134 of the completegenome.) (nt:similar to egad:10491 percent identity: 26.32;) (le:299) (re:2827) (di:direct) HPAE000640 AE000640 g2314573 Helicobacter pylori 26695 85962 -11539208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906775	17695	39851	615	204

Description

6500735351 nhaa:hp1552 na+/h+ antiporter (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1552 HP1552 Helicobacter pylori 210 -11539209 7000690540 na+/h+ antiporter (cl:na+/h+-exchanging protein nhaa) (db:pir2.dat) H64713 H64713 Helicobacter pylori 210 -11539209 7500959327 hp1552 na+/h+ antiporter nhaa (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:7232 percent identity: 49.20;) (le:493) (re:1809) (di:complement) HPAE000653 AE000653 g2314735 Helicobacter pylori 210 -11539209 7502853071 hp1552 na+/h+ antiporter nhaa (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:7232 percent identity: 49.20;) (le:493) (re:1809) (di:complement) HPAE000653 AE000653 g2314735 Helicobacter pylori 26695 85962 -11539209

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906792	17696	39852	366	121

Description

6500735352 ceue:hp1561 iron iii abc transporter:periplasmic iron-binding protein:iron:iii abc transporter:periplasmiciron-binding protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1561 HP1561 Helicobacter pylori 210 -11539210 7000690483 iron iii abc transporter:periplasmic iron-binding protein (db:pir2.dat) A64715 A64715 Helicobacter pylori 210 -11539210 7500959269 hp1561 iron iii abc transporter:periplasmic (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:40381 percent identity: 27.52;) (le:1324) (re:2331) (di:complement) HPAE000654 AE000654 g2314745 Helicobacter pylori 210 -11539210 7502853072 hp1561 iron iii abc transporter:periplasmic (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:40381 percent identity: 27.52;) (le:1324) (re:2331) (di:complement) HPAE000654 AE000654 g2314745 Helicobacter pylori 26695 85962 -11539210

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906793	17697	39853	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906801	17698	39854	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906807	17699	39855	252	83

Description

6500735353 ceue:hp1562 iron iii abc transporter:periplasmic iron-binding protein:iron:iii abc transporter:periplasmiciron-binding protein (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-helicobacter pylori) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) HP1562 HP1562 Helicobacter pylori 210 -11539211 7000690484 iron iii abc transporter:periplasmic iron-binding protein (db:pir2.dat) B64715 B64715 Helicobacter pylori 210 -11539211 7500959270 hp1562 iron iii abc transporter:periplasmic (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:40381 percent identity: 28.17;) (le:2532) (re:3533) (di:complement) HPAE000654 AE000654 g2314746 Helicobacter pylori 210 -11539211 7502853073 hp1562 iron iii abc transporter:periplasmic (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:40381 percent identity: 28.17;) (le:2532) (re:3533) (di:complement) HPAE000654 AE000654 g2314746 Helicobacter pylori 26695 85962 -11539211

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906809	17700	39856	372	123

Description

6500735354 abc transporter:atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0179 HP0179 Helicobacter pylori 210 -11539212 7000689601 abc transporter:atp-binding protein (cl:atp-binding cassette homology) (db:pir2.dat) C64542 C64542 Helicobacter pylori 210 -11539212 7500958420 hp0179 abc transporter:atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:similar to gp:1786703 percent identity: 66.67;) (le:4205) (re:4846) (di:complement) HPAE000538 AE000538 g2313268 Helicobacter pylori 210 -11539212 7502853074 hp0179 abc transporter:atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:similar to gp:1786703 percent identity: 66.67;) (le:4205) (re:4846) (di:complement) HPAE000538 AE000538 g2313268 Helicobacter pylori 26695 85962 -11539212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906813	17701	39857	525	174

Description

GTC ORF with score 355 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:f348; 37 pct identical (8 gaps) to 335 residues of) (le:4235) (re:5281) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906820	17702	39858	213	70

Description

6500735355 hunadc-1:hp0214 sodium-dependent transporter (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0214 HP0214 Helicobacter pylori 210 -11539213 7000690713 sodium-dependent transporter (db:pir2.dat) F64546 F64546 Helicobacter pylori 210 -11539213 7500959479 hp0214 sodium-dependent transporter hunadc-1 (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:similar to egad:26418 percent identity: 36.55;) (le:7582) (re:9240) (di:direct) HPAE000541 AE000541 g2313304 Helicobacter pylori 210 -11539213 7502853075 hp0214 sodium-dependent transporter hunadc-1 (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:similar to egad:26418 percent identity: 36.55;) (le:7582) (re:9240) (di:direct) HPAE000541 AE000541 g2313304 Helicobacter pylori 26695 85962 -11539213

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906822	17703	39859	495	164

Description

6500735356 sodium-and chloride-dependent transporter (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0497 HP0497 Helicobacter pylori 210 -11539214 7000690711 sodium-and chloride-dependent transporter (cl:gamma-aminobutyric acid transporter) (db:pir2.dat) A64582 A64582 Helicobacter pylori 210 -11539214 7500959477 hp0497 sodium-and chloride-dependent transporter (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:28678 percent identity: 31.69;) (le:5982) (re:7310) (di:direct) HPAE000564 AE000564 g2313607 Helicobacter pylori 210 -11539214 7502853076 hp0497 sodium-and chloride-dependent transporter (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:28678 percent identity: 31.69;) (le:5982) (re:7310) (di:direct) HPAE000564 AE000564 g2313607 Helicobacter pylori 26695 85962 -11539214

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906829	17704	39860	783	260

Description

6500735357 sodium-and chloride-dependent transporter (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0498 HP0498 Helicobacter pylori 210 -11539215 7000690712 sodium-and chloride-dependent transporter (cl:gamma-aminobutyric acid transporter) (db:pir2.dat) B64582 B64582 Helicobacter pylori 210 -11539215 7500959478 hp0498 sodium-and chloride-dependent transporter (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to egad:28678 percent identity: 30.75;) (le:7321) (re:8649) (di:direct) HPAE000564 AE000564 g2313608 Helicobacter pylori 210 -11539215 7502853077 hp0498 sodium-and chloride-dependent transporter (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to egad:28678 percent identity: 30.75;) (le:7321) (re:8649) (di:direct) HPAE000564 AE000564 g2313608 Helicobacter pylori 26695 85962 -11539215

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906863	17705	39861	402	133

Description

6500735358 spab:hp0600 multidrug resistance protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0600 HP0600 Helicobacter pylori 210 -11539216 7000690534 multidrug resistance protein (cl:atp-binding cassette homology) (db:pir2.dat) H64594 H64594 Helicobacter pylori 210 -11539216 7500959321 hp0600 multidrug resistance protein spab (db:genpept-bct1) (de:helicobacter pylori section 51 of 134 of the complete genome.) (nt:similar to egad:14698 percent identity: 29.65;) (le:9158) (re:10939) (di:complement) HPAE000573 AE000573 g2313717 Helicobacter pylori 210 -11539216 7502853078 hp0600 multidrug resistance protein spab (db:genpept) (de:helicobacter pylori 26695 section 51 of 134 of the complete genome.) (nt:similar to egad:14698 percent identity: 29.65;) (le:9158) (re:10939) (di:complement) HPAE000573 AE000573 g2313717 Helicobacter pylori 26695 85962 -11539216

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906877	17706	39862	1140	379

Description

6500735359 acrb:hp0607 acriflavine resistance protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0607 HP0607 Helicobacter pylori 210 -11539217 7000689609 acriflavine resistance protein (db:pir2.dat) G64595 G64595 Helicobacter pylori 210 -11539217 7500958427 hp0607 acriflavine resistance protein acrb (db:genpept-bct1) (de:helicobacter pylori section 52 of 134 of the complete genome.) (nt:similar to egad:29368 percent identity: 29.74;) (le:6290) (re:9376) (di:direct) HPAE000574 AE000574 g2313726 Helicobacter pylori 210 -11539217 5000696502 hp0607 acriflavine resistance protein acrb (db:genpept) (de:helicobacter pylori 26695 section 52 of 134 of the complete genome.) (nt:similar to egad:29368 percent identity: 29.74;) (le:6290) (re:9376) (di:direct) HPAE000574 AE000574 g2313726 Helicobacter pylori 26695 85962 -11539217

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906888	17707	39863	2937	978

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906890	17708	39864	753	250

Description

6500735360 abc transporter:atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0613 HP0613 Helicobacter pylori 210 -11539218 7000689603 abc transporter:atp-binding protein (cl:atp-binding cassette homology) (db:pir2.dat) E64596 E64596 Helicobacter pylori 210 -11539218 7500958422 hp0613 abc transporter:atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 53 of 134 of the complete genome.) (nt:similar to egad:32943 percent identity: 31.07;) (le:10480) (re:11181) (di:complement) HPAE000575 AE000575 g2313732 Helicobacter pylori 210 -11539218 7502853079 hp0613 abc transporter:atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 53 of 134 of the complete genome.) (nt:similar to egad:32943 percent identity: 31.07;) (le:10480) (re:11181) (di:complement) HPAE000575 AE000575 g2313732 Helicobacter pylori 26695 85962 -11539218

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906949	17709	39865	747	248

Description

6500735361 abc transporter:atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0715 HP0715 Helicobacter pylori 210 -11539219 7000689372 abc transporter:atp-binding protein (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) C64609 C64609 Helicobacter pylori 210 -11539219 7500955264 hp0715 abc transporter:atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:similar to egad:24569 percent identity: 52.32;) (le:8184) (re:8906) (di:complement) HPAE000584 AE000584 g2313839 Helicobacter pylori 210 -11539219 7502853080 hp0715 abc transporter:atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:similar to egad:24569 percent identity: 52.32;) (le:8184) (re:8906) (di:complement) HPAE000584 AE000584 g2313839 Helicobacter pylori 26695 85962 -11539219

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906952	17710	39866	498	165

Description

6500735362 yhes:hp0853 abc transporter:atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP0853 HP0853 Helicobacter pylori 210 -11539220 7000689604 abc transporter:atp-binding protein (cl:atp-binding cassette homology) (db:pir2.dat) E64626 E64626 Helicobacter pylori 210 -11539220 7500958423 hp0853 abc transporter:atp-binding protein yhes (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:29805 percent identity: 36.34;) (le:5168) (re:6769) (di:complement) HPAE000596 AE000596 g2313986 Helicobacter pylori 210 -11539220 7502853081 hp0853 abc transporter:atp-binding protein yhes (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:29805 percent identity: 36.34;) (le:5168) (re:6769) (di:complement) HPAE000596 AE000596 g2313986 Helicobacter pylori 26695 85962 -11539220

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906979	17711	39867	228	75

Description

6500735363 msba:hp1082 multidrug resistance protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1082 HP1082 Helicobacter pylori 210 -11539221 7000690532 multidrug resistance protein (cl:atp-binding cassette homology) (db:pir2.dat) B64655 B64655 Helicobacter pylori 210 -11539221 7500959319 hp1082 multidrug resistance protein msba (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:similar to egad:27895 percent identity: 32.36;) (le:1276) (re:2931) (di:complement) HPAE000615 AE000615 g2314232 Helicobacter pylori 210 -11539221 7502853082 hp1082 multidrug resistance protein msba (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:similar to egad:27895 percent identity: 32.36;) (le:1276) (re:2931) (di:complement) HPAE000615 AE000615 g2314232 Helicobacter pylori 26695 85962 -11539221

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906980	17712	39868	225	74

Description

6500735364 multidrug-efflux transporter (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1181 HP1181 Helicobacter pylori 210 -11539222 7000690535 multidrug-efflux transporter (db:pir2.dat) E64667 E64667 Helicobacter pylori 210 -11539222 7500959322 hp1181 multidrug-efflux transporter (db:genpept-bct1) (de:helicobacter pylori section 102 of 134 of the complete genome.) (nt:similar to egad:40944 percent identity: 29.06;) (le:293) (re:1624) (di:direct) HPAE000624 AE000624 g2314341 Helicobacter pylori 210 -11539222 7502853083 hp1181 multidrug-efflux transporter (db:genpept) (de:helicobacter pylori 26695 section 102 of 134 of the completegenome.) (nt:similar to egad:40944 percent identity: 29.06;) (le:293) (re:1624) (di:direct) HPAE000624 AE000624 g2314341 Helicobacter pylori 26695 85962 -11539222

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906983	17713	39869	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906984	17714	39870	1527	508

Description

GTC ORF with score 1056 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0433.) (nt:similar to saccharomyces cerevisiae putative) (le:<1) (re:1703) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501906993	17715	39871	588	195

Description

6500735365 heta:hp1206 multidrug resistance protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1206 HP1206 Helicobacter pylori 210 -11539223 7000690533 multidrug resistance protein (cl:atp-binding cassette homology) (db:pir2.dat) F64670 F64670 Helicobacter pylori 210 -11539223 7500959320 hp1206 multidrug resistance protein heta (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:similar to egad:8906 percent identity: 26.18;) (le:5448) (re:7184) (di:direct) HPAE000626 AE000626 g2314367 Helicobacter pylori 210 -11539223 7502853084 hp1206 multidrug resistance protein heta (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:similar to egad:8906 percent identity: 26.18;) (le:5448) (re:7184) (di:direct) HPAE000626 AE000626 g2314367 Helicobacter pylori 26695 85962 -11539223

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907003	17716	39872	450	149

Description

6500735366 yhcg:hp1220 abc transporter:atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1220 HP1220 Helicobacter pylori 210 -11539224 7000689602 abc transporter:atp-binding protein (db:pir2.dat) D64672 D64672 Helicobacter pylori 210 -11539224 7500958421 hp1220 abc transporter:atp-binding protein yhcg (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:similar to egad:37848 percent identity: 31.53;) (le:8099) (re:8785) (di:complement) HPAE000627 AE000627 g2314379 Helicobacter pylori 210 -11539224 7502853085 hp1220 abc transporter:atp-binding protein yhcg (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:similar to egad:37848 percent identity: 31.53;) (le:8099) (re:8785) (di:complement) HPAE000627 AE000627 g2314379 Helicobacter pylori 26695 85962 -11539224

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907023	17717	39873	471	156

Description

6500735367 hpn:hp1427 histidine-rich:metal binding polypeptide (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1427 HP1427 Helicobacter pylori 210 -11539225 7000685554 histidine-rich:metal binding polypeptide (db:pir2.dat) C64698 C64698 Helicobacter pylori 210 -11539225 7500958769 hp1427 histidine-rich:metal binding polypeptide hpn (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:similar to egad:34120 percent identity: 100.00;) (le:2006) (re:2188) (di:complement) HPAE000643 AE000643 g2314604 Helicobacter pylori 210 -11539225 243519 hpn hpn (db:genpept-bct1) (de:helicobacter pylori histidine-rich, metal binding polypeptide (hpn)gene, complete cds.) (nt:histidine-rich, metal binding polypeptide) (le:451) (re:633) (di:direct) HPU26361 U26361 g836667 Helicobacter pylori 210 -11539225 1500686955 jhp1320 putative histidine-rich metal-binding protein (db:genpept) (de:helicobacter pylori, strain j99 section 116 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1427) (le:937) (re:1119) (di:complement) AE001555 AE001555 g4155931 Helicobacter pylori J99 85963 -11539225 5000696510 hp1427 histidine-rich:metal binding polypeptide hpn (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:similar to egad:34120 percent identity: 100.00;) (le:2006) (re:2188) (di:complement) HPAE000643 AE000643 g2314604 Helicobacter pylori 26695 85962 -11539225

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907024	17718	39874	648	215

Description

6500735368 histidine and glutamine-rich protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1432 HP1432 Helicobacter pylori 210 -11539226 7500975644 hp1432 histidine and glutamine-rich protein (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:similar to egad:34120 percent identity: 50.00;) (le:7603) (re:7821) (di:direct) HPAE000643 AE000643 g2314605 Helicobacter pylori 210 -11539226 7502853086 hp1432 histidine and glutamine-rich protein (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:similar to egad:34120 percent identity: 50.00;) (le:7603) (re:7821) (di:direct) HPAE000643 AE000643 g2314605 Helicobacter pylori 26695 85962 -11539226

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907035	17719	39875	384	127

Description

6500735369 hi1087:hp1465 abc transporter:atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1465 HP1465 Helicobacter pylori 210 -11539227 7000689600 abc transporter:atp-binding protein (cl:atp-binding cassette homology) (db:pir2.dat) A64703 A64703 Helicobacter pylori 210 -11539227 7500958419 hp1465 abc transporter:atp-binding protein hi1087 (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:similar to egad:28098 percent identity: 37.79;) (le:8452) (re:9237) (di:complement) HPAE000646 AE000646 g2314642 Helicobacter pylori 210 -11539227 7502853087 hp1465 abc transporter:atp-binding protein hi1087 (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:similar to egad:28098 percent identity: 37.79;) (le:8452) (re:9237) (di:complement) HPAE000646 AE000646 g2314642 Helicobacter pylori 26695 85962 -11539227

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907036	17720	39876	459	152

Description

6500735370 abc:hp1576 abc transporter:atp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1576 HP1576 Helicobacter pylori 210 -11539228 7000689605 abc transporter:atp-binding protein (cl:atp-binding cassette homology) (db:pir2.dat) H64716 H64716 Helicobacter pylori 210 -11539228 7500958424 hp1576 abc transporter:atp-binding protein abc (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:29254 percent identity: 48.16;) (le:1828) (re:2811) (di:direct) HPAE000655 AE000655 g2314761 Helicobacter pylori 210 -11539228 7502853088 hp1576 abc transporter:atp-binding protein abc (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:29254 percent identity: 48.16;) (le:1828) (re:2811) (di:direct) HPAE000655 AE000655 g2314761 Helicobacter pylori 26695 85962 -11539228

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907037	17721	39877	654	218

Description

6500735371 yaee:hp1577 abc transporter:permease protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-helicobacter pylori) HP1577 HP1577 Helicobacter pylori 210 -11539229 7000689606 abc transporter:permease protein (cl:probable transport protein yaee) (db:pir2.dat) A64717 A64717 Helicobacter pylori 210 -11539229 7500958425 hp1577 abc transporter:permease protein yaee (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:9654 percent identity: 43.06;) (le:2813) (re:3460) (di:direct) HPAE000655 AE000655 g2314762 Helicobacter pylori 210 -11539229 7502853089 hp1577 abc transporter:permease protein yaee (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:9654 percent identity: 43.06;) (le:2813) (re:3460) (di:direct) HPAE000655 AE000655 g2314762 Helicobacter pylori 26695 85962 -11539229

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907041	17722	39878	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907051	17723	39879	774	257

Description

6500735372 pfr:hp0653 nonheme iron-containing ferritin (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP0653 HP0653 Helicobacter pylori 210 -11539230 72431 pfr:hp0653 (sr:,campylobacter pylori) (de:nonheme iron-containing ferritin) (db:swissprot) FTN_HELPY P52093 HELICOBACTER PYLORI 210 -11539230 7500881782 hp0653 nonheme iron-containing ferritin pfr (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:17893 percent identity: 99.40;) (le:15122) (re:15625) (di:complement) HPAE000578 AE000578 g2313771 Helicobacter pylori 210 -11539230 7502853090 hp0653 nonheme iron-containing ferritin pfr (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:17893 percent identity: 99.40;) (le:15122) (re:15625) (di:complement) HPAE000578 AE000578 g2313771 Helicobacter pylori 26695 85962 -11539230

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907053	17724	39880	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907059	17725	39881	963	320

Description

6500735373 frpb:hp0876 iron-regulated outer membrane protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP0876 HP0876 Helicobacter pylori 210 -11539231 7000690489 iron-regulated outer membrane protein (cl:iron-regulated outer membrane protein) (db:pir2.dat) D64629 D64629 Helicobacter pylori 210 -11539231 7500959275 hp0876 iron-regulated outer membrane protein frpb (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:similar to egad:40658 percent identity: 27.60;) (le:4764) (re:7139) (di:direct) HPAE000597 AE000597 g2314011 Helicobacter pylori 210 -11539231 7502853091 hp0876 iron-regulated outer membrane protein frpb (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:similar to egad:40658 percent identity: 27.60;) (le:4764) (re:7139) (di:direct) HPAE000597 AE000597 g2314011 Helicobacter pylori 26695 85962 -11539231

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907076	17726	39882	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907101	17727	39883	870	289

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907104	17728	39884	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907107	17729	39885	405	134

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907108	17730	39886	828	275

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907114	17731	39887	1545	515

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907115	17732	39888	804	267

Description

6500735374 frpb:hp0915 iron-regulated outer membrane protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP0915 HP0915 Helicobacter pylori 210 -11539232 7000690488 iron-regulated outer membrane protein (db:pir2.dat) C64634 C64634 Helicobacter pylori 210 -11539232 7500959274 hp0915 iron-regulated outer membrane protein frpb (db:genpept-bct1) (de:helicobacter pylori section 79 of 134 of the complete genome.) (nt:similar to egad:40658 percent identity: 28.12;) (le:2272) (re:3960) (di:complement) HPAE000601 AE000601 g2314052 Helicobacter pylori 210 -11539232 7502853092 hp0915 iron-regulated outer membrane protein frpb (db:genpept) (de:helicobacter pylori 26695 section 79 of 134 of the complete genome.) (nt:similar to egad:40658 percent identity: 28.12;) (le:2272) (re:3960) (di:complement) HPAE000601 AE000601 g2314052 Helicobacter pylori 26695 85962 -11539232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907120	17733	39889	984	327

Description

6500735375 frpb:hp0916 iron-regulated outer membrane protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP0916 HP0916 Helicobacter pylori 210 -11539233 7000690490 iron-regulated outer membrane protein (cl:tonb-dependent receptor amino-terminal homology) (db:pir2.dat) D64634 D64634 Helicobacter pylori 210 -11539233 7500959276 hp0916 iron-regulated outer membrane protein frpb (db:genpept-bct1) (de:helicobacter pylori section 79 of 134 of the complete genome.) (nt:similar to egad:40658 percent identity: 28.80;) (le:3960) (re:4709) (di:complement) HPAE000601 AE000601 g2314053 Helicobacter pylori 210 -11539233 7502853093 hp0916 iron-regulated outer membrane protein frpb (db:genpept) (de:helicobacter pylori 26695 section 79 of 134 of the complete genome.) (nt:similar to egad:40658 percent identity: 28.80;) (le:3960) (re:4709) (di:complement) HPAE000601 AE000601 g2314053 Helicobacter pylori 26695 85962 -11539233

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907121	17734	39890	1476	491

Description

6500735376 exbd:hp1129 biopolymer transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP1129 HP1129 Helicobacter pylori 210 -11539234 7502853094 hp1129 (sr:,campylobacter pylori) (de:putative biopolymer transport exbd-like protein 1) (db:swissprot) EXD1_HELPY O25754 HELICOBACTER PYLORI 210 -11539234 7000689659 biopolymer transport protein (db:pir2.dat) A64661 A64661 Helicobacter pylori 210 -11539234 7500958473 hp1129 biopolymer transport protein exbd (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:13326 percent identity: 29.66;) (le:4863) (re:5264) (di:complement) HPAE000619 AE000619 g2314280 Helicobacter pylori 210 -11539234 7502853095 hp1129 biopolymer transport protein exbd (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:13326 percent identity: 29.66;) (le:4863) (re:5264) (di:complement) HPAE000619 AE000619 g2314280 Helicobacter pylori 26695 85962 -11539234

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907144	17735	39891	912	303

Description

6500735377 exbb:hp1130 biopolymer transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP1130 HP1130 Helicobacter pylori 210 -11539235 7502853096 hp1130 (sr:,campylobacter pylori) (de:putative biopolymer transport exbb-like protein 1) (db:swissprot) EXB1_HELPY O25755 HELICOBACTER PYLORI 210 -11539235 7000689660 biopolymer transport protein (db:pir2.dat) B64661 B64661 Helicobacter pylori 210 -11539235 7500958474 hp1130 biopolymer transport protein exbb (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:23986 percent identity: 33.53;) (le:5317) (re:5886) (di:complement) HPAE000619 AE000619 g2314281 Helicobacter pylori 210 -11539235 7502853097 hp1130 biopolymer transport protein exbb (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:23986 percent identity: 33.53;) (le:5317) (re:5886) (di:complement) HPAE000619 AE000619 g2314281 Helicobacter pylori 26695 85962 -11539235

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907147	17736	39892	411	136

Description

GTC ORF with score 174 to: (or:Anolis pulchellus) (fn:precursor of yolk proteins, serum transport) (db:genpept-vrt) (de:anolis pulchellus vitellogenin mrna, partial cds.) (nt:apvtg5; similar to chicken and xenopus phosvitin) (le:<1) (re:546) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907149	17737	39893	606	201

Description

6500735378 exbb:hp1339 biopolymer transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP1339 HP1339 Helicobacter pylori 210 -11539236 7502853098 exbb:hp1339 (sr:,campylobacter pylori) (de:biopolymer transport exbb protein) (db:swissprot) EXBB_HELPY O25897 HELICOBACTER PYLORI 210 -11539236 7000689443 biopolymer transport protein (cl:biopolymer transport protein) (db:pir2.dat) C64687 C64687 Helicobacter pylori 210 -11539236 7500955513 hp1339 biopolymer transport protein exbb (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:28889 percent identity: 46.76;) (le:5330) (re:5830) (di:direct) HPAE000635 AE000635 g2314506 Helicobacter pylori 210 -11539236 7502853099 hp1339 biopolymer transport protein exbb (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:28889 percent identity: 46.76;) (le:5330) (re:5830) (di:direct) HPAE000635 AE000635 g2314506 Helicobacter pylori 26695 85962 -11539236

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907150	17738	39894	549	182

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907171	17739	39895	375	124

Description

6500735379 exbd:hp1340 biopolymer transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP1340 HP1340 Helicobacter pylori 210 -11539237 7502853100 exbd:hp1340 (sr:,campylobacter pylori) (de:biopolymer transport exbd protein) (db:swissprot) EXBD_HELPY O25898 HELICOBACTER PYLORI 210 -11539237 7000689661 biopolymer transport protein (cl:tolr protein) (db:pir2.dat) D64687 D64687 Helicobacter pylori 210 -11539237 7500958475 hp1340 biopolymer transport protein exbd (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:28888 percent identity: 35.77;) (le:5827) (re:6216) (di:direct) HPAE000635 AE000635 g2314507 Helicobacter pylori 210 -11539237 7502853101 hp1340 biopolymer transport protein exbd (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:28888 percent identity: 35.77;) (le:5827) (re:6216) (di:direct) HPAE000635 AE000635 g2314507 Helicobacter pylori 26695 85962 -11539237

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907172	17740	39896	1182	393

Description

6500735380 tonb:hp1341 siderophore-mediated iron transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP1341 HP1341 Helicobacter pylori 210 -11539238 7502853102 tonb:hp1341 (sr:,campylobacter pylori) (de:tonb protein) (db:swissprot) TONB_HELPY O25899 HELICOBACTER PYLORI 210 -11539238 7000690701 siderophore-mediated iron transport protein (db:pir2.dat) E64687 E64687 Helicobacter pylori 210 -11539238 7500959468 hp1341 siderophore-mediated iron transport protein (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:38752 percent identity: 37.22;) (le:6182) (re:7039) (di:direct) HPAE000635 AE000635 g2314508 Helicobacter pylori 210 -11539238 7502853103 hp1341 siderophore-mediated iron transport protein (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:38752 percent identity: 37.22;) (le:6182) (re:7039) (di:direct) HPAE000635 AE000635 g2314508 Helicobacter pylori 26695 85962 -11539238

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907180	17741	39897	1557	518

Description

6500735381 exbb:hp1445 biopolymer transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP1445 HP1445 Helicobacter pylori 210 -11539239 7502853104 hp1445 (sr:,campylobacter pylori) (de:putative biopolymer transport exbb-like protein 2) (db:swissprot) EXB2_HELPY O25986 HELICOBACTER PYLORI 210 -11539239 7000689442 biopolymer transport protein (cl:biopolymer transport protein) (db:pir2.dat) E64700 E64700 Helicobacter pylori 210 -11539239 7500955512 hp1445 biopolymer transport protein exbb (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to egad:28889 percent identity: 45.45;) (le:10013) (re:10465) (di:direct) HPAE000644 AE000644 g2314617 Helicobacter pylori 210 -11539239 7502853105 hp1445 biopolymer transport protein exbb (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to egad:28889 percent identity: 45.45;) (le:10013) (re:10465) (di:direct) HPAE000644 AE000644 g2314617 Helicobacter pylori 26695 85962 -11539239

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907182	17742	39898	2787	928

Description

6500735382 exbd:hp1446 biopolymer transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP1446 HP1446 Helicobacter pylori 210 -11539240 7502853106 hp1446 (sr:,campylobacter pylori) (de:putative biopolymer transport exbd-like protein 2) (db:swissprot) EXD2_HELPY O25987 HELICOBACTER PYLORI 210 -11539240 7000689662 biopolymer transport protein (cl:tolr protein) (db:pir2.dat) F64700 F64700 Helicobacter pylori 210 -11539240 7500958476 hp1446 biopolymer transport protein exbd (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to egad:28888 percent identity: 36.22;) (le:10476) (re:10877) (di:direct) HPAE000644 AE000644 g2314618 Helicobacter pylori 210 -11539240 7502853107 exbd_3 biopolymer transport protein (db:genpept) (de:helicobacter pylori, strain j99 section 117 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1446) (le:9919) (re:10320) (di:direct) AE001556 AE001556 g4155949 Helicobacter pylori J99 85963 -11539240 7502853108 hp1446 biopolymer transport protein exbd (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to egad:28888 percent identity: 36.22;) (le:10476) (re:10877) (di:direct) HPAE000644 AE000644 g2314618 Helicobacter pylori 26695 85962 -11539240

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907203	17743	39899	1398	466

Description

6500735383 frpb:hp1512 iron-regulated outer membrane protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.7) (db:gtc-helicobacter pylori) HP1512 HP1512 Helicobacter pylori 210 -11539241 7000690491 iron-regulated outer membrane protein (cl:iron-regulated outer membrane protein) (db:pir2.dat) H64708 H64708 Helicobacter pylori 210 -11539241 7500959277 hp1512 iron-regulated outer membrane protein frpb (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:similar to egad:40658 percent identity: 26.59;) (le:4219) (re:6852) (di:direct) HPAE000649 AE000649 g2314692 Helicobacter pylori 210 -11539241 7502853109 hp1512 iron-regulated outer membrane protein frpb (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:similar to egad:40658 percent identity: 26.59;) (le:4219) (re:6852) (di:direct) HPAE000649 AE000649 g2314692 Helicobacter pylori 26695 85962 -11539241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907233	17744	39900	384	127

Description

6500735384 groel:hp0010 chaperone and heat shock protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.4) (db:gtc-helicobacter pylori) HP0010 HP0010 Helicobacter pylori 210 -11539242 64137 groel:hsp60:hspb:hp0010 (sr:,campylobacter pylori) (de:60)) (db:swissprot) CH60_HELPY P42383 HELICOBACTER PYLORI 210 -11539242 7000684802 groel:hspb chaperonin groel:heat shock protein 60:heat shock protein b hspb:urease-associated heat shock protein hsp62 (cl:chaperonin groel) (db:pir2.dat) S36237 B64521 Helicobacter pylori 210 -11539242 7500878596 hp0010 chaperone and heat shock protein groel (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to egad:13101 percent identity: 99.63;) (le:7603) (re:9243) (di:complement) HPAE000523 AE000523 g2313084 Helicobacter pylori 210 -11539242 7502853110 hp0010 chaperone and heat shock protein groel (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to egad:13101 percent identity: 99.63;) (le:7603) (re:9243) (di:complement) HPAE000523 AE000523 g2313084 Helicobacter pylori 26695 85962 -11539242

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907241	17745	39901	348	115

Description

7500878587 groes:groel:hsp10:hspa:hp0011 co-chaperone:10 kd chaperonin:protein cpn10:protein groes:heat shock protein 10 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.4) (db:gtc-helicobacter pylori) HP0011 HP0011 Helicobacter pylori 210 -11539243 64047 groes:hsp10:hspa:hp0011 (sr:,campylobacter pylori) (de:10)) (db:swissprot) CH10_HELPY P48225 HELICOBACTER PYLORI 210 -11539243 7500878586 hp0011 co-chaperone groes (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:similar to egad:32041 percent identity: 99.15;) (le:9268) (re:9624) (di:complement) HPAE000523 AE000523 g2313085 Helicobacter pylori 210 -11539243 7502853111 groes 10kda chaperone (db:genpept) (de:helicobacter pylori, strain j99 section 1 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0011) (le:9423) (re:9779) (di:complement) AE001440 AE001440 g4154503 Helicobacter pylori J99 85963 -11539243 6500735385 hp0011 co-chaperone groes (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:similar to egad:32041 percent identity: 99.15;) (le:9268) (re:9624) (di:complement) HPAE000523 AE000523 g2313085 Helicobacter pylori 26695 85962 -11539243

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907248	17746	39902	5661	1886

Description

6500735386 dnak:hp0109 chaperone and heat shock protein 70 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.4) (db:gtc-helicobacter pylori) HP0109 HP0109 Helicobacter pylori 210 -11539244 7000689348 dnak-type molecular chaperone:heat shock protein 70 (cl:heat shock protein 70) (db:pir2.dat) E64533 E64533 Helicobacter pylori 210 -11539244 7500955122 hp0109 chaperone and heat shock protein 70 dnak (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:similar to egad:30787 percent identity: 63.40;) (le:9028) (re:10890) (di:complement) HPAE000532 AE000532 g2313191 Helicobacter pylori 210 -11539244 7502853112 hp0109 chaperone and heat shock protein 70 dnak (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:similar to egad:30787 percent identity: 63.40;) (le:9028) (re:10890) (di:complement) HPAE000532 AE000532 g2313191 Helicobacter pylori 26695 85962 -11539244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907249	17747	39903	564	187

Description

6500735387 grpe:hp0110 co-chaperone and heat shock protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.4) (db:gtc-helicobacter pylori) HP0110 HP0110 Helicobacter pylori 210 -11539245 5500685303 grpe:hp0110 (sr:,campylobacter pylori) (de:grpe protein) (db:swissprot) GRPE_HELPY P55970 HELICOBACTER PYLORI 210 -11539245 7000685455 co-chaperone and heat shock protein (db:pir2.dat) F64533 F64533 Helicobacter pylori 210 -11539245 7500882749 hp0110 co-chaperone and heat shock protein grpe (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:similar to egad:20561 percent identity: 32.98;) (le:10920) (re:11489) (di:complement) HPAE000532 AE000532 g2313192 Helicobacter pylori 210 -11539245 7502853113 hp0110 co-chaperone and heat shock protein grpe (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:similar to egad:20561 percent identity: 32.98;) (le:10920) (re:11489) (di:complement) HPAE000532 AE000532 g2313192 Helicobacter pylori 26695 85962 -11539245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907265	17748	39904	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907306	17749	39905	357	118

Description

6500735388 htpg:hp0210 chaperone and heat shock protein c62 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.4) (db:gtc-helicobacter pylori) HP0210 HP0210 Helicobacter pylori 210 -11539246 5500685372 htpg:hp0210 (sr:,campylobacter pylori) (de:heat shock protein htpg (high temperature protein g)) (db:swissprot) HTPG_HELPY P56116 HELICOBACTER PYLORI 210 -11539246 7000685568 chaperone and heat shock protein c62.5 (cl:heat shock protein 90) (db:pir2.dat) B64546 B64546 Helicobacter pylori 210 -11539246 7500883601 hp0210 chaperone and heat shock protein c62.5 htpg (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:similar to egad:16078 percent identity: 46.45;) (le:1563) (re:3428) (di:direct) HPAE000541 AE000541 g2313300 Helicobacter pylori 210 -11539246 7502853114 hp0210 chaperone and heat shock protein c62.5 htpg (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:similar to egad:16078 percent identity: 46.45;) (le:1563) (re:3428) (di:direct) HPAE000541 AE000541 g2313300 Helicobacter pylori 26695 85962 -11539246

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907313	17750	39906	468	155

Description

6500735389 cbpa:hp1024 co-chaperone-curved dna binding protein a (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.4) (db:gtc-helicobacter pylori) HP1024 HP1024 Helicobacter pylori 210 -11539247 7000689717 co-chaperone-curved dna binding protein a (cl:dnaj amino-terminal homology) (db:pir2.dat) H64647 H64647 Helicobacter pylori 210 -11539247 7500958524 hp1024 co-chaperone-curved dna binding protein a (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:similar to egad:28238 percent identity: 37.68;) (le:9026) (re:9892) (di:direct) HPAE000610 AE000610 g2314166 Helicobacter pylori 210 -11539247 7502853115 hp1024 co-chaperone-curved dna binding protein a (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:similar to egad:28238 percent identity: 37.68;) (le:9026) (re:9892) (di:direct) HPAE000610 AE000610 g2314166 Helicobacter pylori 26695 85962 -11539247

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907318	17751	39907	1008	335

Description

6500735390 dnaj:hp1332 co-chaperone and heat shock protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.4) (db:gtc-helicobacter pylori) HP1332 HP1332 Helicobacter pylori 210 -11539248 7000689716 co-chaperone and heat shock protein (cl:heat shock protein dnaj:dnaj amino-terminal homology) (db:pir2.dat) D64686 D64686 Helicobacter pylori 210 -11539248 7500958523 hp1332 co-chaperone and heat shock protein dnaj (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:similar to egad:13193 percent identity: 42.66;) (le:11297) (re:12406) (di:complement) HPAE000634 AE000634 g2314497 Helicobacter pylori 210 -11539248 7502853116 hp1332 co-chaperone and heat shock protein dnaj (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:similar to egad:13193 percent identity: 42.66;) (le:11297) (re:12406) (di:complement) HPAE000634 AE000634 g2314497 Helicobacter pylori 26695 85962 -11539248

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907327	17752	39908	393	130

Description

6500735391 ftsh:hp0286 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP0286 HP0286 Helicobacter pylori 210 -11539249 7000689708 cell division protein (cl:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir2.dat) F64555 F64555 Helicobacter pylori 210 -11539249 7500958516 hp0286 cell division protein ftsh (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:similar to egad:18839 percent identity: 41.16;) (le:6526) (re:8178) (di:direct) HPAE000547 AE000547 g2313382 Helicobacter pylori 210 -11539249 7502853117 hp0286 cell division protein ftsh (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:similar to egad:18839 percent identity: 41.16;) (le:6526) (re:8178) (di:direct) HPAE000547 AE000547 g2313382 Helicobacter pylori 26695 85962 -11539249

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907343	17753	39909	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907344	17754	39910	237	79

Description

6500735392 mind:hp0331 cell division inhibitor (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP0331 HP0331 Helicobacter pylori 210 -11539250 7000689420 mind cell division inhibitor mind (cl:cell division inhibitor mind) (db:pir2.dat) C64561 C64561 Helicobacter pylori 210 -11539250 7500955459 hp0331 cell division inhibitor mind (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:similar to egad:13527 percent identity: 50.19;) (le:1254) (re:2060) (di:direct) HPAE000551 AE000551 g2313432 Helicobacter pylori 210 -11539250 7502853118 hp0331 cell division inhibitor mind (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:similar to egad:13527 percent identity: 50.19;) (le:1254) (re:2060) (di:direct) HPAE000551 AE000551 g2313432 Helicobacter pylori 26695 85962 -11539250

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907350	17755	39911	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907365	17756	39912	318	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907380	17757	39913	537	178

Description

GTC ORF with score 116 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.cerevisiae hypothetical 105.9 kd) (le:35939:36599) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907382	17758	39914	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907386	17759	39915	759	252

Description

6500735393 mine:hp0332 cell division topological specificity factor (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP0332 HP0332 Helicobacter pylori 210 -11539251 7000689709 cell division topological specificity factor (db:pir2.dat) D64561 D64561 Helicobacter pylori 210 -11539251 7500958517 hp0332 cell division topological specificity factor (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:similar to egad:13270 percent identity: 33.75;) (le:2057) (re:2290) (di:direct) HPAE000551 AE000551 g2313433 Helicobacter pylori 210 -11539251 7502853119 hp0332 cell division topological specificity factor (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:similar to egad:13270 percent identity: 33.75;) (le:2057) (re:2290) (di:direct) HPAE000551 AE000551 g2313433 Helicobacter pylori 26695 85962 -11539251

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907390	17760	39916	1230	409

Description

6500735394 ftse:hp0748 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP0748 HP0748 Helicobacter pylori 210 -11539252 7000689706 cell division protein (cl:atp-binding cassette homology) (db:pir2.dat) D64613 D64613 Helicobacter pylori 210 -11539252 7500958514 hp0748 cell division protein ftse (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:similar to egad:27936 percent identity: 37.56;) (le:7001) (re:7672) (di:direct) HPAE000587 AE000587 g2313874 Helicobacter pylori 210 -11539252 7502853120 hp0748 cell division protein ftse (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:similar to egad:27936 percent identity: 37.56;) (le:7001) (re:7672) (di:direct) HPAE000587 AE000587 g2313874 Helicobacter pylori 26695 85962 -11539252

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907392	17761	39917	486	162

Description

6500735395 ftsx:hp0749 cell division membrane protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP0749 HP0749 Helicobacter pylori 210 -11539253 7000689702 cell division membrane protein (db:pir2.dat) E64613 E64613 Helicobacter pylori 210 -11539253 7500958512 hp0749 cell division membrane protein ftsx (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:similar to egad:27937 percent identity: 25.75;) (le:7659) (re:8465) (di:direct) HPAE000587 AE000587 g2313875 Helicobacter pylori 210 -11539253 7502853121 hp0749 cell division membrane protein ftsx (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:similar to egad:27937 percent identity: 25.75;) (le:7659) (re:8465) (di:direct) HPAE000587 AE000587 g2313875 Helicobacter pylori 26695 85962 -11539253

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907397	17762	39918	1044	347

Description

6500735396 ftsy:hp0763 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP0763 HP0763 Helicobacter pylori 210 -11539254 7500881854 ftsy:hp0763 (sr:,campylobacter pylori) (de:cell division protein ftsy homolog) (db:swissprot) FTSY_HELPY O25458 HELICOBACTER PYLORI 210 -11539254 7000689705 cell division protein (cl:docking protein) (db:pir2.dat) C64615 C64615 Helicobacter pylori 210 -11539254 7500881856 hp0763 cell division protein ftsy (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:similar to egad:27935 percent identity: 46.64;) (le:8013) (re:8894) (di:direct) HPAE000588 AE000588 g2313887 Helicobacter pylori 210 -11539254 7502853122 hp0763 cell division protein ftsy (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:similar to egad:27935 percent identity: 46.64;) (le:8013) (re:8894) (di:direct) HPAE000588 AE000588 g2313887 Helicobacter pylori 26695 85962 -11539254

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907402	17763	39919	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907403	17764	39920	348	115

Description

6500735397 ftsa:hp0978 cell division protein:cell division protein protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP0978 HP0978 Helicobacter pylori 210 -11539255 7500881805 ftsa:hp0978 (sr:,campylobacter pylori) (de:cell division protein ftsa) (db:swissprot) FTSA_HELPY O25629 HELICOBACTER PYLORI 210 -11539255 7000689703 cell division protein (db:pir2.dat) B64642 B64642 Helicobacter pylori 210 -11539255 7500881807 hp0978 cell division protein ftsa protein (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:similar to egad:35570 percent identity: 31.85;) (le:5969) (re:7447) (di:direct) HPAE000606 AE000606 g2314120 Helicobacter pylori 210 -11539255 7502853123 hp0978 cell division protein ftsa protein (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:similar to egad:35570 percent identity: 31.85;) (le:5969) (re:7447) (di:direct) HPAE000606 AE000606 g2314120 Helicobacter pylori 26695 85962 -11539255

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907405	17765	39921	417	138

Description

6500735398 ftsz:hp0979 cell divison protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP0979 HP0979 Helicobacter pylori 210 -11539256 5500685239 ftsz:hp0979 (sr:,campylobacter pylori) (de:cell division protein ftsz) (db:swissprot) FTSZ_HELPY P56097 HELICOBACTER PYLORI 210 -11539256 7000685328 cell divison protein (cl:cell division protein ftsz) (db:pir2.dat) C64642 C64642 Helicobacter pylori 210 -11539256 7500881878 hp0979 cell divison protein ftsz (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:similar to egad:17529 percent identity: 43.30;) (le:7578) (re:8735) (di:direct) HPAE000606 AE000606 g2314121 Helicobacter pylori 210 -11539256 7502853124 hp0979 cell divison protein ftsz (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:similar to egad:17529 percent identity: 43.30;) (le:7578) (re:8735) (di:direct) HPAE000606 AE000606 g2314121 Helicobacter pylori 26695 85962 -11539256

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907407	17766	39922	753	250

Description

6500735399 ftsh:hp1069 cell division protein:cell division protein homolog (gtcfc:12.8) (ec:3.4.24.-) (keggfc:14.1) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP1069 HP1069 Helicobacter pylori 210 -11539257 1500685758 ftsh:hp1069 (sr:,campylobacter pylori) (ec:3.4.24.-) (de:cell division protein ftsh homolog,) (db:swissprot) FTSH_HELPY P71408 HELICOBACTER PYLORI 210 -11539257 7000685324 cell division protein (cl:cell division protein ftsh:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir2.dat) E64653 E64653 Helicobacter pylori 210 -11539257 7500881824 hp1069 cell division protein ftsh (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:similar to gp:1589774 percent identity: 98.58;) (le:1561) (re:3459) (di:direct) HPAE000614 AE000614 g2314219 Helicobacter pylori 210 -11539257 7502853125 hp1069 cell division protein ftsh (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:similar to gp:1589774 percent identity: 98.58;) (le:1561) (re:3459) (di:direct) HPAE000614 AE000614 g2314219 Helicobacter pylori 26695 85962 -11539257

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907458	17767	39923	534	177

Description

6500735400 ftsk:hp1090 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP1090 HP1090 Helicobacter pylori 210 -11539258 7000689704 cell division protein (db:pir2.dat) B64656 B64656 Helicobacter pylori 210 -11539258 7500958513 hp1090 cell division protein ftsk (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:similar to egad:30442 percent identity: 39.78;) (le:12030) (re:14606) (di:direct) HPAE000615 AE000615 g2314237 Helicobacter pylori 210 -11539258 7502853126 hp1090 cell division protein ftsk (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:similar to egad:30442 percent identity: 39.78;) (le:12030) (re:14606) (di:direct) HPAE000615 AE000615 g2314237 Helicobacter pylori 26695 85962 -11539258

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907462	17768	39924	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907464	17769	39925	624	208

Description

6500735401 fic:hp1159 cell filamentation protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP1159 HP1159 Helicobacter pylori 210 -11539259 7000689710 cell filamentation protein (db:pir2.dat) G64664 G64664 Helicobacter pylori 210 -11539259 7500958518 hp1159 cell filamentation protein fic (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:27990 percent identity: 63.22;) (le:16420) (re:16953) (di:direct) HPAE000621 AE000621 g2314309 Helicobacter pylori 210 -11539259 7502853127 hp1159 cell filamentation protein fic (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:27990 percent identity: 63.22;) (le:16420) (re:16953) (di:direct) HPAE000621 AE000621 g2314309 Helicobacter pylori 26695 85962 -11539259

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907470	17770	39926	246	81

Description

6500735402 ftsi:hp1556 cell division protein (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP1556 HP1556 Helicobacter pylori 210 -11539260 7000689707 cell division protein (db:pir2.dat) D64714 D64714 Helicobacter pylori 210 -11539260 7500958515 hp1556 cell division protein ftsi (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:15720 percent identity: 30.65;) (le:7229) (re:9076) (di:complement) HPAE000653 AE000653 g2314739 Helicobacter pylori 210 -11539260 7502853128 hp1556 cell division protein ftsi (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:15720 percent identity: 30.65;) (le:7229) (re:9076) (di:complement) HPAE000653 AE000653 g2314739 Helicobacter pylori 26695 85962 -11539260

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907471	17771	39927	894	297

Description

6500735403 ftsw:hp1560 cell division protein:cell division protein escherichia coli (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.2) (db:gtc-helicobacter pylori) HP1560 HP1560 Helicobacter pylori 210 -11539261 5500685235 ftsw:hp1560 (sr:,campylobacter pylori) (de:probable cell division protein ftsw) (db:swissprot) FTSW_HELPY P56096 HELICOBACTER PYLORI 210 -11539261 7000685327 cell division protein (db:pir2.dat) H64714 H64714 Helicobacter pylori 210 -11539261 7500881848 hp1560 cell division protein ftsw escherichia coli (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:20048 percent identity: 32.73;) (le:134) (re:1300) (di:direct) HPAE000654 AE000654 g2314744 Helicobacter pylori 210 -11539261 7502853129 hp1560 cell division protein ftsw escherichia coli (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:20048 percent identity: 32.73;) (le:134) (re:1300) (di:direct) HPAE000654 AE000654 g2314744 Helicobacter pylori 26695 85962 -11539261

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907484	17772	39928	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907486	17773	39929	1086	361

Description

6500735404 chev:hp0019 chemotaxis protein chev:chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0019 HP0019 Helicobacter pylori 210 -11539262 7000689397 chemotaxis protein chev homolog 1 (cl:chemotaxis chev protein:response regulator homology) (db:pir2.dat) C64522 C64522 Helicobacter pylori 210 -11539262 7500955344 hp0019 chemotaxis protein chev (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:similar to egad:9880 percent identity: 26.80;) (le:5727) (re:6692) (di:direct) HPAE000524 AE000524 g2313092 Helicobacter pylori 210 -11539262 7502853130 hp0019 chemotaxis protein chev (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:similar to egad:9880 percent identity: 26.80;) (le:5727) (re:6692) (di:direct) HPAE000524 AE000524 g2313092 Helicobacter pylori 26695 85962 -11539262

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907497	17774	39930	225	74

Description

6500735405 tlpc:hp0082 methyl-accepting chemotaxis transducer (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0082 HP0082 Helicobacter pylori 210 -11539263 7000689407 methyl-accepting chemotaxis transducer tlpc (cl:probable methyl-accepting chemotaxis transducer) (db:pir2.dat) B64530 B64530 Helicobacter pylori 210 -11539263 7500955410 hp0082 methyl-accepting chemotaxis transducer tlpc (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:similar to egad:17602 percent identity: 28.21;) (le:411) (re:2432) (di:complement) HPAE000530 AE000530 g2313163 Helicobacter pylori 210 -11539263 7502853131 hp0082 methyl-accepting chemotaxis transducer tlpc (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:similar to egad:17602 percent identity: 28.21;) (le:411) (re:2432) (di:complement) HPAE000530 AE000530 g2313163 Helicobacter pylori 26695 85962 -11539263

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907503	17775	39931	1188	395

Description

6500735406 tlpa:hp0099 methyl-accepting chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0099 HP0099 Helicobacter pylori 210 -11539264 7000689406 methyl-accepting chemotaxis protein tlpa (cl:probable methyl-accepting chemotaxis transducer) (db:pir2.dat) C64532 C64532 Helicobacter pylori 210 -11539264 7500955409 hp0099 methyl-accepting chemotaxis protein tlpa (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:similar to egad:16680 percent identity: 32.81;) (le:7263) (re:9290) (di:direct) HPAE000531 AE000531 g2313179 Helicobacter pylori 210 -11539264 7502853132 hp0099 methyl-accepting chemotaxis protein tlpa (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:similar to egad:16680 percent identity: 32.81;) (le:7263) (re:9290) (di:direct) HPAE000531 AE000531 g2313179 Helicobacter pylori 26695 85962 -11539264

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907507	17776	39932	507	168

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907508	17777	39933	219	72

Description

6500735407 tlpb:hp0103 methyl-accepting chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0103 HP0103 Helicobacter pylori 210 -11539265 7000690517 methyl-accepting chemotaxis protein (db:pir2.dat) G64532 G64532 Helicobacter pylori 210 -11539265 7500959309 hp0103 methyl-accepting chemotaxis protein tlpb (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:similar to egad:15044 percent identity: 30.71;) (le:1691) (re:3388) (di:complement) HPAE000532 AE000532 g2313186 Helicobacter pylori 210 -11539265 7502853133 hp0103 methyl-accepting chemotaxis protein tlpb (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:similar to egad:15044 percent identity: 30.71;) (le:1691) (re:3388) (di:complement) HPAE000532 AE000532 g2313186 Helicobacter pylori 26695 85962 -11539265

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907509	17778	39934	192	63

Description

6500735408 chew:hp0391 purine-binding chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0391 HP0391 Helicobacter pylori 210 -11539266 7000690661 purine-binding chemotaxis protein (cl:chemotaxis chew protein) (db:pir2.dat) G64568 G64568 Helicobacter pylori 210 -11539266 7500959436 hp0391 purine-binding chemotaxis protein chew (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:22082 percent identity: 34.31;) (le:8578) (re:9075) (di:complement) HPAE000555 AE000555 g2313492 Helicobacter pylori 210 -11539266 7502853134 hp0391 purine-binding chemotaxis protein chew (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:22082 percent identity: 34.31;) (le:8578) (re:9075) (di:complement) HPAE000555 AE000555 g2313492 Helicobacter pylori 26695 85962 -11539266

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907510	17779	39935	741	246

Description

6500735409 chea:hp0392 histidine kinase chea:histidine kinase (gtcfc:12.9) (ec:2.7.3.-) (keggfc:14.1) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0392 HP0392 Helicobacter pylori 210 -11539267 7000689988 histidine kinase (cl:response regulator homology) (db:pir2.dat) H64568 H64568 Helicobacter pylori 210 -11539267 7500958767 hp0392 histidine kinase chea (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:38099 percent identity: 41.41;) (le:9072) (re:11483) (di:complement) HPAE000555 AE000555 g2313493 Helicobacter pylori 210 -11539267 7502853135 hp0392 histidine kinase chea (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:38099 percent identity: 41.41;) (le:9072) (re:11483) (di:complement) HPAE000555 AE000555 g2313493 Helicobacter pylori 26695 85962 -11539267

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907514	17780	39936	219	72

Description

6500735410 chev:hp0393 chemotaxis protein chev:chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0393 HP0393 Helicobacter pylori 210 -11539268 7000689711 chemotaxis protein (cl:response regulator homology) (db:pir2.dat) A64569 A64569 Helicobacter pylori 210 -11539268 7500958519 hp0393 chemotaxis protein chev (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:9880 percent identity: 31.66;) (le:11540) (re:12475) (di:complement) HPAE000555 AE000555 g2313494 Helicobacter pylori 210 -11539268 7502853136 hp0393 chemotaxis protein chev (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:9880 percent identity: 31.66;) (le:11540) (re:12475) (di:complement) HPAE000555 AE000555 g2313494 Helicobacter pylori 26695 85962 -11539268

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907520	17781	39937	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907521	17782	39938	1077	358

Description

6500735411 era:hp0517 gtp-binding protein (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0517 HP0517 Helicobacter pylori 210 -11539269 5500685163 era:hp0517 (sr:,campylobacter pylori) (de:gtp-binding protein era homolog) (db:swissprot) ERA_HELPY P56059 HELICOBACTER PYLORI 210 -11539269 7000685181 gtp-binding protein (cl:translation elongation factor tu homology) (db:pir2.dat) E64584 E64584 Helicobacter pylori 210 -11539269 7500881109 hp0517 gtp-binding protein era (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800154 percent identity: 95.57;) (le:2387) (re:3295) (di:direct) HPAE000566 AE000566 g2313632 Helicobacter pylori 210 -11539269 7502853137 hp0517 gtp-binding protein era (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800154 percent identity: 95.57;) (le:2387) (re:3295) (di:direct) HPAE000566 AE000566 g2313632 Helicobacter pylori 26695 85962 -11539269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907539	17783	39939	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907540	17784	39940	543	180

Description

GTC ORF with score 123 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0143.) (nt:unnamed protein product) (le:<1) (re:951) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907541	17785	39941	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907547	17786	39942	243	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907556	17787	39943	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907568	17788	39944	678	225

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907573	17789	39945	951	316

Description

6500735412 hylb:hp0599 hemolysin secretion protein precursor (gtcfc:12.10:12.11) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0599 HP0599 Helicobacter pylori 210 -11539270 7000689986 hemolysin secretion protein precursor (db:pir2.dat) G64594 G64594 Helicobacter pylori 210 -11539270 7500958766 hp0599 hemolysin secretion protein precursor hylb (db:genpept-bct1) (de:helicobacter pylori section 51 of 134 of the complete genome.) (nt:similar to egad:6938 percent identity: 45.39;) (le:7785) (re:9086) (di:complement) HPAE000573 AE000573 g2313716 Helicobacter pylori 210 -11539270 7502853138 hp0599 hemolysin secretion protein precursor hylb (db:genpept) (de:helicobacter pylori 26695 section 51 of 134 of the complete genome.) (nt:similar to egad:6938 percent identity: 45.39;) (le:7785) (re:9086) (di:complement) HPAE000573 AE000573 g2313716 Helicobacter pylori 26695 85962 -11539270

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907577	17790	39946	1026	341

Description

6500735413 chev:hp0616 chemotaxis protein chev:chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP0616 HP0616 Helicobacter pylori 210 -11539271 7000689398 chemotaxis protein chev homolog 2 (cl:chemotaxis chev protein:response regulator homology) (db:pir2.dat) H64596 H64596 Helicobacter pylori 210 -11539271 7500955345 hp0616 chemotaxis protein chev (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:similar to egad:9880 percent identity: 27.94;) (le:2665) (re:3606) (di:direct) HPAE000576 AE000576 g2313738 Helicobacter pylori 210 -11539271 7502853139 hp0616 chemotaxis protein chev (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:similar to egad:9880 percent identity: 27.94;) (le:2665) (re:3606) (di:direct) HPAE000576 AE000576 g2313738 Helicobacter pylori 26695 85962 -11539271

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907583	17791	39947	594	197

Description

GTC ORF with score 137 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907587	17792	39948	1269	422

Description

6500735414 chey:hp1067 chemotaxis protein chey:chemotaxis protein homolog:fragment (gtcfc:12.9) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP1067 HP1067 Helicobacter pylori 210 -11539272 1500687347 chey:hp1067 (sr:,campylobacter pylori) (de:chemotaxis protein chey homolog) (db:swissprot) CHEY_HELPY P71403 HELICOBACTER PYLORI 210 -11539272 7000684811 chemotaxis protein (cl:chemotaxis chey protein:response regulator homology) (db:pir2.dat) C64653 C64653 Helicobacter pylori 210 -11539272 7500878644 hp1067 chemotaxis protein chey (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:similar to gp:1653994 percent identity: 99.19;) (le:176) (re:550) (di:direct) HPAE000614 AE000614 g2314217 Helicobacter pylori 210 -11539272 7502853140 chey chey (fn:chemotaxis response regulator) (db:genpept) (de:helicobacter pylori conserved hypothetical protein (hp1066) gene,partial cds; chey (chey) gene, complete cds; and methyltransferase(prma) gene, partial cds.) (le:769) (re:1143) (di:direct) AF021090 AF021090 g4103138 Helicobacter pylori 210 -11539272 7502853141 hp1067 chemotaxis protein chey (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:similar to gp:1653994 percent identity: 99.19;) (le:176) (re:550) (di:direct) HPAE000614 AE000614 g2314217 Helicobacter pylori 26695 85962 -11539272

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907588	17793	39949	420	139

Description

6500735415 hemolysin tly:hemolysin:tly (gtcfc:12.10:12.11) (keggfc:14.2) (tigrfc:4.1) (db:gtc-helicobacter pylori) HP1086 HP1086 Helicobacter pylori 210 -11539273 7000689985 hemolysin (cl:hemolysin homolog yqxc) (db:pir2.dat) F64655 F64655 Helicobacter pylori 210 -11539273 7500958765 hp1086 hemolysin tly (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:similar to egad:20008 percent identity: 40.17;) (le:6222) (re:6929) (di:direct) HPAE000615 AE000615 g2314234 Helicobacter pylori 210 -11539273 7502853142 hp1086 hemolysin tly (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:similar to egad:20008 percent identity: 40.17;) (le:6222) (re:6929) (di:direct) HPAE000615 AE000615 g2314234 Helicobacter pylori 26695 85962 -11539273

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907589	17794	39950	774	258

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907591	17795	39951	603	200

Description

GTC ORF with score 121 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0252 gene, partial cds.) (nt:similar to plasmodium falciparum glutamic acid-rich) (le:<1) (re:1995) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907621	17796	39952	399	132

Description

6500735416 n-methylhydantoinase (gtcfc:13.10) (keggfc:13.10) (tigrfc:5.3) (db:gtc-helicobacter pylori) HP0696 HP0696 Helicobacter pylori 210 -11539274 7000690538 n-methylhydantoinase (db:pir2.dat) H64606 H64606 Helicobacter pylori 210 -11539274 7500959325 hp0696 n-methylhydantoinase (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:similar to egad:45132 percent identity: 26.92;) (le:10714) (re:13011) (di:direct) HPAE000582 AE000582 g2313819 Helicobacter pylori 210 -11539274 7502853143 hp0696 n-methylhydantoinase (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:similar to egad:45132 percent identity: 26.92;) (le:10714) (re:13011) (di:direct) HPAE000582 AE000582 g2313819 Helicobacter pylori 26695 85962 -11539274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907626	17797	39953	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907629	17798	39954	585	194

Description

6500735417 nspc:hp0020 carboxynorspermidine decarboxylase (gtcfc:13.11) (keggfc:14.2) (tigrfc:5.4) (db:gtc-helicobacter pylori) HP0020 HP0020 Helicobacter pylori 210 -11539275 7000689694 carboxynorspermidine decarboxylase (db:pir2.dat) D64522 D64522 Helicobacter pylori 210 -11539275 7500958505 hp0020 carboxynorspermidine decarboxylase nspc (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:similar to gp:1652682 percent identity: 45.62;) (le:6689) (re:7906) (di:direct) HPAE000524 AE000524 g2313093 Helicobacter pylori 210 -11539275 7502853144 hp0020 carboxynorspermidine decarboxylase nspc (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:similar to gp:1652682 percent identity: 45.62;) (le:6689) (re:7906) (di:direct) HPAE000524 AE000524 g2313093 Helicobacter pylori 26695 85962 -11539275

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907634	17799	39955	585	195

Description

6500735418 virb4 homolog virb4:virb4 homolog:virb4 (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0017 HP0017 Helicobacter pylori 210 -11539276 7000690793 virb4 homolog (db:pir2.dat) A64522 A64522 Helicobacter pylori 210 -11539276 7500959552 hp0017 virb4 homolog virb4 (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:similar to egad:8065 percent identity: 25.23;) (le:1595) (re:3958) (di:direct) HPAE000524 AE000524 g2313091 Helicobacter pylori 210 -11539276 7502853145 hp0017 virb4 homolog virb4 (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:similar to egad:8065 percent identity: 25.23;) (le:1595) (re:3958) (di:direct) HPAE000524 AE000524 g2313091 Helicobacter pylori 26695 85962 -11539276

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907638	17800	39956	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907639	17801	39957	723	240

Description

6500735419 trbi protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0042 HP0042 Helicobacter pylori 210 -11539277 7000690747 trbi protein (db:pir2.dat) B64525 B64525 Helicobacter pylori 210 -11539277 7500959514 hp0042 trbi protein (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:similar to egad:20555 percent identity: 31.38;) (le:2236) (re:2937) (di:direct) HPAE000526 AE000526 g2313117 Helicobacter pylori 210 -11539277 7502853146 hp0042 trbi protein (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:similar to egad:20555 percent identity: 31.38;) (le:2236) (re:2937) (di:direct) HPAE000526 AE000526 g2313117 Helicobacter pylori 26695 85962 -11539277

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907650	17802	39958	885	294

Description

6500735420 dpra:hp0333 dna processing chain a (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0333 HP0333 Helicobacter pylori 210 -11539278 7000689905 dna processing chain a (db:pir2.dat) E64561 E64561 Helicobacter pylori 210 -11539278 7500958701 hp0333 dna processing chain a dpra (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:similar to egad:27998 percent identity: 32.91;) (le:2290) (re:3102) (di:direct) HPAE000551 AE000551 g2313434 Helicobacter pylori 210 -11539278 7502853147 hp0333 dna processing chain a dpra (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:similar to egad:27998 percent identity: 32.91;) (le:2290) (re:3102) (di:direct) HPAE000551 AE000551 g2313434 Helicobacter pylori 26695 85962 -11539278

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907651	17803	39959	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907653	17804	39960	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907670	17805	39961	1074	357

Description

6500735421 virb4 homolog (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0441 HP0441 Helicobacter pylori 210 -11539279 7000690794 virb4 homolog (db:pir2.dat) A64575 A64575 Helicobacter pylori 210 -11539279 7500959553 hp0441 virb4 homolog (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:similar to egad:33799 percent identity: 23.50;) (le:11026) (re:13449) (di:complement) HPAE000559 AE000559 g2313543 Helicobacter pylori 210 -11539279 7502853148 hp0441 virb4 homolog (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:similar to egad:33799 percent identity: 23.50;) (le:11026) (re:13449) (di:complement) HPAE000559 AE000559 g2313543 Helicobacter pylori 26695 85962 -11539279

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907674	17806	39962	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907708	17807	39963	480	159

Description

GTC ORF with score 100 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome 1 bac f12f1 sequence, completesequence.) (nt:similar to fumarylacetoacetate hydrolase, gb|141670) (le:38769:38966:39186) (re:38831:39091:39260) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907718	17808	39964	984	327

Description

6500735422 virb4 homolog virb4:virb4 homolog:virb4 (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0459 HP0459 Helicobacter pylori 210 -11539280 7000690795 virb4 homolog (db:pir2.dat) C64577 C64577 Helicobacter pylori 210 -11539280 7500959554 hp0459 virb4 homolog virb4 (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to egad:8065 percent identity: 25.28;) (le:2178) (re:4754) (di:direct) HPAE000561 AE000561 g2313565 Helicobacter pylori 210 -11539280 7502853149 hp0459 virb4 homolog virb4 (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to egad:8065 percent identity: 25.28;) (le:2178) (re:4754) (di:direct) HPAE000561 AE000561 g2313565 Helicobacter pylori 26695 85962 -11539280

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907722	17809	39965	1569	522

Description

GTC ORF with score 208 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c1827.) (nt:spcc1827.07c, major facilitator superfamily member;) (le:15698:15932:17089) (re:15856:17023:17361) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907725	17810	39966	312	103

Description

6500735423 cag1:hp0520 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0520 HP0520 Helicobacter pylori 210 -11539281 7000689688 cag pathogenicity island protein cag1 (db:pir2.dat) H64584 H64584 Helicobacter pylori 210 -11539281 7500958499 hp0520 cag pathogenicity island protein cag1 (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800157 percent identity: 96.52;) (le:5379) (re:5726) (di:direct) HPAE000566 AE000566 g2313635 Helicobacter pylori 210 -11539281 7502853150 hp0520 cag pathogenicity island protein cag1 (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800157 percent identity: 96.52;) (le:5379) (re:5726) (di:direct) HPAE000566 AE000566 g2313635 Helicobacter pylori 26695 85962 -11539281

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907763	17811	39967	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907765	17812	39968	342	113

Description

6500735424 cag3:hp0522 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0522 HP0522 Helicobacter pylori 210 -11539282 7000689673 cag pathogenicity island protein cag3 (db:pir2.dat) B64585 B64585 Helicobacter pylori 210 -11539282 7500958484 hp0522 cag pathogenicity island protein cag3 (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800159 percent identity: 98.13;) (le:6185) (re:7630) (di:direct) HPAE000566 AE000566 g2313636 Helicobacter pylori 210 -11539282 7502853151 hp0522 cag pathogenicity island protein cag3 (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800159 percent identity: 98.13;) (le:6185) (re:7630) (di:direct) HPAE000566 AE000566 g2313636 Helicobacter pylori 26695 85962 -11539282

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907766	17813	39969	1053	350

Description

6500735425 cag4:hp0523 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0523 HP0523 Helicobacter pylori 210 -11539283 7000689677 cag pathogenicity island protein cag4 (db:pir2.dat) C64585 C64585 Helicobacter pylori 210 -11539283 7500958488 hp0523 cag pathogenicity island protein cag4 (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800160 percent identity: 95.74;) (le:7640) (re:8149) (di:direct) HPAE000566 AE000566 g2313637 Helicobacter pylori 210 -11539283 7502853152 hp0523 cag pathogenicity island protein cag4 (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800160 percent identity: 95.74;) (le:7640) (re:8149) (di:direct) HPAE000566 AE000566 g2313637 Helicobacter pylori 26695 85962 -11539283

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907775	17814	39970	318	105

Description

6500735426 cag5:hp0524 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0524 HP0524 Helicobacter pylori 210 -11539284 7000689680 cag pathogenicity island protein cag5 (db:pir2.dat) D64585 D64585 Helicobacter pylori 210 -11539284 7500958491 hp0524 cag pathogenicity island protein cag5 (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800161 percent identity: 99.06;) (le:8268) (re:10514) (di:complement) HPAE000566 AE000566 g2313638 Helicobacter pylori 210 -11539284 7502853153 hp0524 cag pathogenicity island protein cag5 (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800161 percent identity: 99.06;) (le:8268) (re:10514) (di:complement) HPAE000566 AE000566 g2313638 Helicobacter pylori 26695 85962 -11539284

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907810	17815	39971	471	156

Description

5000696558 virb11 homolog (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0525 HP0525 Helicobacter pylori 210 -11539285 7000690792 virb11 homolog (db:pir2.dat) E64585 E64585 Helicobacter pylori 210 -11539285 7500959551 hp0525 virb11 homolog (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800162 percent identity: 100.00;) (le:10523) (re:11515) (di:complement) HPAE000566 AE000566 g2313639 Helicobacter pylori 210 -11539285 6500735427 hp0525 virb11 homolog (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800162 percent identity: 100.00;) (le:10523) (re:11515) (di:complement) HPAE000566 AE000566 g2313639 Helicobacter pylori 26695 85962 -11539285 243450 orf11 (db:genpept-bct1) (de:h. pylori chromosomal fragment ~38.5kb, complete sequence.) (nt:orf11 - similar to b. pertussis virb11 homolog -) (le:9526) (re:10518) (di:complement) HPAC000108 AC000108 g1800162 Helicobacter pylori 210 -11539285

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907811	17816	39972	1713	570

Description

GTC ORF with score 296 to: (db:genpept-bct1) (de:pseudomonas aeruginosa pyoverdine chromophore biosynthesis genecluster including pvca (pvca), pvcb (pvcb), pvcc (pvcc), and pvcd(pvcd) genes, complete cds, and transcriptional activator ptxr(ptxr) gene, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907830	17817	39973	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907840	17818	39974	351	116

Description

6500735428 cag6:hp0526 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0526 HP0526 Helicobacter pylori 210 -11539286 7000689683 cag pathogenicity island protein cag6 (db:pir2.dat) F64585 F64585 Helicobacter pylori 210 -11539286 7500958494 hp0526 cag pathogenicity island protein cag6 (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800163 percent identity: 97.49;) (le:11520) (re:12119) (di:complement) HPAE000566 AE000566 g2313640 Helicobacter pylori 210 -11539286 7502853154 hp0526 cag pathogenicity island protein cag6 (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800163 percent identity: 97.49;) (le:11520) (re:12119) (di:complement) HPAE000566 AE000566 g2313640 Helicobacter pylori 26695 85962 -11539286

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907846	17819	39975	309	102

Description

6500735429 cag7:hp0527 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0527 HP0527 Helicobacter pylori 210 -11539287 7000689685 cag pathogenicity island protein cag7 (db:pir2.dat) G64585 G64585 Helicobacter pylori 210 -11539287 7500958496 hp0527 cag pathogenicity island protein cag7 (db:genpept-bct1) (de:helicobacter pylori section 45 of 134 of the complete genome.) (nt:similar to gp:1800165 percent identity: 94.57;) (le:99) (re:5882) (di:complement) HPAE000567 AE000567 g2313642 Helicobacter pylori 210 -11539287 7502853155 hp0527 cag pathogenicity island protein cag7 (db:genpept) (de:helicobacter pylori 26695 section 45 of 134 of the complete genome.) (nt:similar to gp:1800165 percent identity: 94.57;) (le:99) (re:5882) (di:complement) HPAE000567 AE000567 g2313642 Helicobacter pylori 26695 85962 -11539287

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907847	17820	39976	609	202

Description

GTC ORF with score 93 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f42g9.) (nt:similarity to a number of different protein with) (le:11542:12744:13093) (re:11775:13044:13409) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907848	17821	39977	609	202

Description

6500735430 cag8:hp0528 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0528 HP0528 Helicobacter pylori 210 -11539288 7000689689 cag pathogenicity island protein cag8 (db:pir2.dat) H64585 H64585 Helicobacter pylori 210 -11539288 7500958500 hp0528 cag pathogenicity island protein cag8 (db:genpept-bct1) (de:helicobacter pylori section 45 of 134 of the complete genome.) (nt:similar to gp:1800166 percent identity: 99.04;) (le:5897) (re:7465) (di:complement) HPAE000567 AE000567 g2313643 Helicobacter pylori 210 -11539288 7502853156 hp0528 cag pathogenicity island protein cag8 (db:genpept) (de:helicobacter pylori 26695 section 45 of 134 of the complete genome.) (nt:similar to gp:1800166 percent identity: 99.04;) (le:5897) (re:7465) (di:complement) HPAE000567 AE000567 g2313643 Helicobacter pylori 26695 85962 -11539288

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907850	17822	39978	315	104

Description

6500735431 cag9:hp0529 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0529 HP0529 Helicobacter pylori 210 -11539289 7000689670 cag pathogenicity island protein cag9 (db:pir2.dat) A64586 A64586 Helicobacter pylori 210 -11539289 7500958481 hp0529 cag pathogenicity island protein cag9 (db:genpept-bct1) (de:helicobacter pylori section 45 of 134 of the complete genome.) (nt:similar to gp:1800167 percent identity: 98.88;) (le:7518) (re:9125) (di:complement) HPAE000567 AE000567 g2313644 Helicobacter pylori 210 -11539289 7502853157 hp0529 cag pathogenicity island protein cag9 (db:genpept) (de:helicobacter pylori 26695 section 45 of 134 of the complete genome.) (nt:similar to gp:1800167 percent identity: 98.88;) (le:7518) (re:9125) (di:complement) HPAE000567 AE000567 g2313644 Helicobacter pylori 26695 85962 -11539289

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907851	17823	39979	243	80

Description

6500735432 cag10:hp0530 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0530 HP0530 Helicobacter pylori 210 -11539290 7000689674 cag pathogenicity island protein cag10 (db:pir2.dat) B64586 B64586 Helicobacter pylori 210 -11539290 7500958485 hp0530 cag pathogenicity island protein cag10 (db:genpept-bct1) (de:helicobacter pylori section 45 of 134 of the complete genome.) (nt:similar to gp:1800168 percent identity: 98.41;) (le:9130) (re:9888) (di:complement) HPAE000567 AE000567 g2313645 Helicobacter pylori 210 -11539290 7502853158 hp0530 cag pathogenicity island protein cag10 (db:genpept) (de:helicobacter pylori 26695 section 45 of 134 of the complete genome.) (nt:similar to gp:1800168 percent identity: 98.41;) (le:9130) (re:9888) (di:complement) HPAE000567 AE000567 g2313645 Helicobacter pylori 26695 85962 -11539290

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907856	17824	39980	501	166

Description

GTC ORF with score 106 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1495.) (nt:similar to saccharomyces cerevisiae zinc/cadmium) (le:154) (re:1317) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907857	17825	39981	225	74

Description

6500735433 cag11:hp0531 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0531 HP0531 Helicobacter pylori 210 -11539291 7000689678 cag pathogenicity island protein cag11 (db:pir2.dat) C64586 C64586 Helicobacter pylori 210 -11539291 7500958489 hp0531 cag pathogenicity island protein cag11 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1800169 percent identity: 97.20;) (le:223) (re:879) (di:direct) HPAE000568 AE000568 g2313647 Helicobacter pylori 210 -11539291 7502853159 hp0531 cag pathogenicity island protein cag11 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1800169 percent identity: 97.20;) (le:223) (re:879) (di:direct) HPAE000568 AE000568 g2313647 Helicobacter pylori 26695 85962 -11539291

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907859	17826	39982	462	153

Description

6500735434 cag12:hp0532 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0532 HP0532 Helicobacter pylori 210 -11539292 5500684957 cagt:cag12:hp0532 (sr:,campylobacter pylori) (de:cag pathogenicity island protein 12 precursor) (db:swissprot) CAGT_HELPY P97245 HELICOBACTER PYLORI 210 -11539292 7000684742 cag pathogenicity island protein cag12 (db:pir2.dat) D64586 D64586 Helicobacter pylori 210 -11539292 7500878109 hp0532 cag pathogenicity island protein cag12 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752681 percent identity: 98.93;) (le:915) (re:1757) (di:direct) HPAE000568 AE000568 g2313648 Helicobacter pylori 210 -11539292 7502853160 hp0532 cag pathogenicity island protein cag12 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752681 percent identity: 98.93;) (le:915) (re:1757) (di:direct) HPAE000568 AE000568 g2313648 Helicobacter pylori 26695 85962 -11539292

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907861	17827	39983	291	97

Description

6500735435 cag13:hp0534 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0534 HP0534 Helicobacter pylori 210 -11539293 5500684956 cags:cag13:hp0534 (sr:,campylobacter pylori) (de:cag pathogenicity island protein 13) (db:swissprot) CAGS_HELPY P97227 HELICOBACTER PYLORI 210 -11539293 7000684741 cag pathogenicity island protein cag13 (db:pir2.dat) F64586 F64586 Helicobacter pylori 210 -11539293 7500878108 hp0534 cag pathogenicity island protein cag13 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752682 percent identity: 97.96;) (le:1968) (re:2558) (di:complement) HPAE000568 AE000568 g2313649 Helicobacter pylori 210 -11539293 7502853161 hp0534 cag pathogenicity island protein cag13 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752682 percent identity: 97.96;) (le:1968) (re:2558) (di:complement) HPAE000568 AE000568 g2313649 Helicobacter pylori 26695 85962 -11539293

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907908	17828	39984	1356	451

Description

6500735436 cag14:hp0535 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0535 HP0535 Helicobacter pylori 210 -11539294 7000689686 cag pathogenicity island protein cag14 (db:pir2.dat) G64586 G64586 Helicobacter pylori 210 -11539294 7500958497 hp0535 cag pathogenicity island protein cag14 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752685 percent identity: 97.62;) (le:2984) (re:3364) (di:complement) HPAE000568 AE000568 g2313650 Helicobacter pylori 210 -11539294 7502853162 hp0535 cag pathogenicity island protein cag14 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752685 percent identity: 97.62;) (le:2984) (re:3364) (di:complement) HPAE000568 AE000568 g2313650 Helicobacter pylori 26695 85962 -11539294

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907919	17829	39985	1131	376

Description

6500735437 cag15:hp0536 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0536 HP0536 Helicobacter pylori 210 -11539295 7000689690 cag pathogenicity island protein cag15 (db:pir2.dat) H64586 H64586 Helicobacter pylori 210 -11539295 7500958501 hp0536 cag pathogenicity island protein cag15 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752687 percent identity: 96.36;) (le:3797) (re:4141) (di:complement) HPAE000568 AE000568 g2313651 Helicobacter pylori 210 -11539295 7502853163 hp0536 cag pathogenicity island protein cag15 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752687 percent identity: 96.36;) (le:3797) (re:4141) (di:complement) HPAE000568 AE000568 g2313651 Helicobacter pylori 26695 85962 -11539295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907939	17830	39986	2112	703

Description

6500735438 cag16:hp0537 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0537 HP0537 Helicobacter pylori 210 -11539296 7000689671 cag pathogenicity island protein cag16 (db:pir2.dat) A64587 A64587 Helicobacter pylori 210 -11539296 7500958482 hp0537 cag pathogenicity island protein cag16 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752689 percent identity: 98.94;) (le:4565) (re:5695) (di:direct) HPAE000568 AE000568 g2313652 Helicobacter pylori 210 -11539296 7502853164 hp0537 cag pathogenicity island protein cag16 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752689 percent identity: 98.94;) (le:4565) (re:5695) (di:direct) HPAE000568 AE000568 g2313652 Helicobacter pylori 26695 85962 -11539296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907940	17831	39987	510	169

Description

6500735439 cag17:hp0538 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0538 HP0538 Helicobacter pylori 210 -11539297 7000689675 cag pathogenicity island protein cag17 (db:pir2.dat) B64587 B64587 Helicobacter pylori 210 -11539297 7500958486 hp0538 cag pathogenicity island protein cag17 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752690 percent identity: 95.27;) (le:5710) (re:6630) (di:direct) HPAE000568 AE000568 g2313653 Helicobacter pylori 210 -11539297 7502853165 hp0538 cag pathogenicity island protein cag17 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752690 percent identity: 95.27;) (le:5710) (re:6630) (di:direct) HPAE000568 AE000568 g2313653 Helicobacter pylori 26695 85962 -11539297

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907941	17832	39988	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907944	17833	39989	1443	480

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907949	17834	39990	552	183

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907974	17835	39991	555	184

Description

GTC ORF with score 201 to: (db:genpept-pln2) (de:emericella nidulans negative-acting regulatory protein (qutr) gene,complete cds; and unknown gene.) (nt:repressor protein; coding region predicted from dna) (le:3826) (re:6531) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907983	17836	39992	633	210

Description

6500735440 cag18:hp0539 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0539 HP0539 Helicobacter pylori 210 -11539298 7000689679 cag pathogenicity island protein cag18 (db:pir2.dat) C64587 C64587 Helicobacter pylori 210 -11539298 7500958490 hp0539 cag pathogenicity island protein cag18 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752691 percent identity: 98.73;) (le:6712) (re:7425) (di:complement) HPAE000568 AE000568 g2313654 Helicobacter pylori 210 -11539298 7502853166 hp0539 cag pathogenicity island protein cag18 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752691 percent identity: 98.73;) (le:6712) (re:7425) (di:complement) HPAE000568 AE000568 g2313654 Helicobacter pylori 26695 85962 -11539298

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501907987	17837	39993	306	101

Description

6500735441 cag19:hp0540 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0540 HP0540 Helicobacter pylori 210 -11539299 7000689681 cag pathogenicity island protein cag19 (db:pir2.dat) D64587 D64587 Helicobacter pylori 210 -11539299 7500958492 hp0540 cag pathogenicity island protein cag19 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752692 percent identity: 99.48;) (le:7422) (re:8567) (di:complement) HPAE000568 AE000568 g2313655 Helicobacter pylori 210 -11539299 7502853167 hp0540 cag pathogenicity island protein cag19 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752692 percent identity: 99.48;) (le:7422) (re:8567) (di:complement) HPAE000568 AE000568 g2313655 Helicobacter pylori 26695 85962 -11539299

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908002	17838	39994	588	195

Description

GTC ORF with score 673 to: (sr:human) (db:genpept-pri2) (de:homo sapiens dna from chromosome 19, cosmid r33485 containingpnorf1, complete sequence.) (nt:human type 1 rna helicase; dps similarity to) (le:891:14661:16425:18756) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908004	17839	39995	435	144

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908020	17840	39996	249	82

Description

GTC ORF with score 133 to: (sr:plasmid ptrab4) (db:genpept-bct1) (de:agrobacterium vitis plasmid ptrab4 putative lysr-type protein(ttua), putative tartrate transport protein (ttub), putativetartrate dehydrogenase (ttuc), putative hydroxypyruvate ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908021	17841	39997	255	84

Description

6500735442 cag20:hp0541 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0541 HP0541 Helicobacter pylori 210 -11539300 7000689682 cag pathogenicity island protein cag20 (db:pir2.dat) E64587 E64587 Helicobacter pylori 210 -11539300 7500958493 hp0541 cag pathogenicity island protein cag20 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752693 percent identity: 97.84;) (le:8578) (re:9690) (di:complement) HPAE000568 AE000568 g2313656 Helicobacter pylori 210 -11539300 7502853168 hp0541 cag pathogenicity island protein cag20 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752693 percent identity: 97.84;) (le:8578) (re:9690) (di:complement) HPAE000568 AE000568 g2313656 Helicobacter pylori 26695 85962 -11539300

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908025	17842	39998	1866	621

Description

6500735443 cag21:hp0542 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0542 HP0542 Helicobacter pylori 210 -11539301 7000689684 cag pathogenicity island protein cag21 (db:pir2.dat) F64587 F64587 Helicobacter pylori 210 -11539301 7500958495 hp0542 cag pathogenicity island protein cag21 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752694 percent identity: 97.89;) (le:9706) (re:10134) (di:complement) HPAE000568 AE000568 g2313657 Helicobacter pylori 210 -11539301 7502853169 hp0542 cag pathogenicity island protein cag21 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752694 percent identity: 97.89;) (le:9706) (re:10134) (di:complement) HPAE000568 AE000568 g2313657 Helicobacter pylori 26695 85962 -11539301

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908033	17843	39999	399	132

Description

6500735444 cag22:hp0543 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0543 HP0543 Helicobacter pylori 210 -11539302 5000696575 (de:(hp0543) (pn:cag pathogenicity island protein:cag22) (gtcfc:13.12) (ec:) (keggfc:11.2) (tigrfc:4.8) (db:gtc-helicobacter pylori)) HP0543 HP0543 Helicobacter pylori 210 10316864

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908039	17844	40000	450	149

Description

6500735445 cag24:hp0545 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0545 HP0545 Helicobacter pylori 210 -11539303 7000689672 pica cag pathogenicity island protein cag24:pica protein (db:pir2.dat) A64588 A64588 Helicobacter pylori 210 -11539303 7500958483 hp0545 cag pathogenicity island protein cag24 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752697 percent identity: 98.54;) (le:13957) (re:14580) (di:complement) HPAE000568 AE000568 g2313660 Helicobacter pylori 210 -11539303 7502853170 hp0545 cag pathogenicity island protein cag24 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752697 percent identity: 98.54;) (le:13957) (re:14580) (di:complement) HPAE000568 AE000568 g2313660 Helicobacter pylori 26695 85962 -11539303

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908043	17845	40001	315	104

Description

6500735446 cag25:hp0546 cag pathogenicity island protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0546 HP0546 Helicobacter pylori 210 -11539304 7000689676 cag pathogenicity island protein cag25 (db:pir2.dat) B64588 B64588 Helicobacter pylori 210 -11539304 7500958487 hp0546 cag pathogenicity island protein cag25 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:similar to gp:1752698 percent identity: 95.65;) (le:14582) (re:14929) (di:complement) HPAE000568 AE000568 g2313661 Helicobacter pylori 210 -11539304 7502853171 hp0546 cag pathogenicity island protein cag25 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:similar to gp:1752698 percent identity: 95.65;) (le:14582) (re:14929) (di:complement) HPAE000568 AE000568 g2313661 Helicobacter pylori 26695 85962 -11539304

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908044	17846	40002	597	198

Description

6500735447 cag26:caga:cai:hp0547 cag pathogenicity island protein:cytotoxicity associated immunodominant antigen:120 kd protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP0547 HP0547 Helicobacter pylori 210 -11539305 5500684989 caga:cai:gag26:hp0547 (sr:,campylobacter pylori) (de:(cag pathogenicity island protein 26)) (db:swissprot) CGA0_HELPY P55980 HELICOBACTER PYLORI 210 -11539305 7000684794 cag pathogenicity island protein cag26 (db:pir2.dat) C64588 C64588 Helicobacter pylori 210 -11539305 7500878565 hp0547 cag pathogenicity island protein cag26 (db:genpept-bct1) (de:helicobacter pylori section 47 of 134 of the complete genome.) (nt:similar to gp:1752700 percent identity: 92.87;) (le:447) (re:4007) (di:direct) HPAE000569 AE000569 g2313664 Helicobacter pylori 210 -11539305 7502853172 hp0547 cag pathogenicity island protein cag26 (db:genpept) (de:helicobacter pylori 26695 section 47 of 134 of the complete genome.) (nt:similar to gp:1752700 percent identity: 92.87;) (le:447) (re:4007) (di:direct) HPAE000569 AE000569 g2313664 Helicobacter pylori 26695 85962 -11539305

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908049	17847	40003	288	95

Description

6500735448 trag:hp1006 conjugal transfer protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP1006 HP1006 Helicobacter pylori 210 -11539306 7000689721 conjugal transfer protein (db:pir2.dat) F64645 F64645 Helicobacter pylori 210 -11539306 7500958528 hp1006 conjugal transfer protein trag (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:similar to egad:40371 percent identity: 27.33;) (le:1036) (re:1569) (di:complement) HPAE000609 AE000609 g2314151 Helicobacter pylori 210 -11539306 7502853173 hp1006 conjugal transfer protein trag (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:similar to egad:40371 percent identity: 27.33;) (le:1036) (re:1569) (di:complement) HPAE000609 AE000609 g2314151 Helicobacter pylori 26695 85962 -11539306

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908075	17848	40004	1533	510

Description

6500735449 competence locus e come3:competence locus e:come3 (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP1361 HP1361 Helicobacter pylori 210 -11539307 7000689720 competence locus e (db:pir2.dat) A64690 A64690 Helicobacter pylori 210 -11539307 7500958527 hp1361 competence locus e come3 (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:20088 percent identity: 26.74;) (le:14500) (re:15753) (di:complement) HPAE000636 AE000636 g2314527 Helicobacter pylori 210 -11539307 7502853174 hp1361 competence locus e come3 (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:20088 percent identity: 26.74;) (le:14500) (re:15753) (di:complement) HPAE000636 AE000636 g2314527 Helicobacter pylori 26695 85962 -11539307

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908080	17849	40005	303	100

Description

6500735450 coml:hp1378 competence lipoprotein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP1378 HP1378 Helicobacter pylori 210 -11539308 7000689719 competence lipoprotein (db:pir2.dat) B64692 B64692 Helicobacter pylori 210 -11539308 7500958526 hp1378 competence lipoprotein coml (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:similar to egad:40678 percent identity: 25.53;) (le:914) (re:1576) (di:direct) HPAE000638 AE000638 g2314548 Helicobacter pylori 210 -11539308 7502853175 hp1378 competence lipoprotein coml (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:similar to egad:40678 percent identity: 25.53;) (le:914) (re:1576) (di:direct) HPAE000638 AE000638 g2314548 Helicobacter pylori 26695 85962 -11539308

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908083	17850	40006	2193	730

Description

6500735451 trbb:hp1421 conjugative transfer regulon protein (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.8) (db:gtc-helicobacter pylori) HP1421 HP1421 Helicobacter pylori 210 -11539309 7000689722 conjugative transfer regulon protein (db:pir2.dat) E64697 E64697 Helicobacter pylori 210 -11539309 7500958529 hp1421 conjugative transfer regulon protein trbb (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to gp:1800162 percent identity: 30.69;) (le:7055) (re:7969) (di:complement) HPAE000642 AE000642 g2314595 Helicobacter pylori 210 -11539309 7502853176 hp1421 conjugative transfer regulon protein trbb (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to gp:1800162 percent identity: 30.69;) (le:7055) (re:7969) (di:complement) HPAE000642 AE000642 g2314595 Helicobacter pylori 26695 85962 -11539309

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908088	17851	40007	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908100	17852	40008	255	84

Description

6500735452 ibpb:hp0280 heat shock protein b (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP0280 HP0280 Helicobacter pylori 210 -11539310 7000689983 heat shock protein b (db:pir2.dat) H64554 H64554 Helicobacter pylori 210 -11539310 7500958763 hp0280 heat shock protein b ibpb (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:similar to egad:10469 percent identity: 27.23;) (le:9434) (re:10420) (di:direct) HPAE000546 AE000546 g2313370 Helicobacter pylori 210 -11539310 7502853177 hp0280 heat shock protein b ibpb (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:similar to egad:10469 percent identity: 27.23;) (le:9434) (re:10420) (di:direct) HPAE000546 AE000546 g2313370 Helicobacter pylori 26695 85962 -11539310

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908117	17853	40009	2208	735

Description

6500735453 vapd:hp0315 virulence associated protein d (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP0315 HP0315 Helicobacter pylori 210 -11539311 5500686147 vapd:hp0315 (sr:,campylobacter pylori) (de:virulence associated protein d) (db:swissprot) VAPD_HELPY O05728 HELICOBACTER PYLORI 210 -11539311 7000686935 virulence associated protein d (cl:virulence-associated protein vapd) (db:pir2.dat) C64559 C64559 Helicobacter pylori 210 -11539311 7500893963 hp0315 virulence associated protein d vapd (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:similar to egad:23165 percent identity: 70.21;) (le:7579) (re:7863) (di:complement) HPAE000549 AE000549 g2313409 Helicobacter pylori 210 -11539311 7502853178 hp0315 virulence associated protein d vapd (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:similar to egad:23165 percent identity: 70.21;) (le:7579) (re:7863) (di:complement) HPAE000549 AE000549 g2313409 Helicobacter pylori 26695 85962 -11539311

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908121	17854	40010	453	150

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908124	17855	40011	657	218

Description

6500735454 mvin:hp0885 virulence factor protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP0885 HP0885 Helicobacter pylori 210 -11539312 7000690797 virulence factor mvin protein (cl:mvin protein) (db:pir2.dat) E64630 E64630 Helicobacter pylori 210 -11539312 7500955346 hp0885 virulence factor mvin protein mvin (db:genpept-bct1) (de:helicobacter pylori section 76 of 134 of the complete genome.) (nt:similar to egad:27987 percent identity: 33.51;) (le:2964) (re:4349) (di:direct) HPAE000598 AE000598 g2314021 Helicobacter pylori 210 -11539312 7502853179 hp0885 virulence factor mvin protein mvin (db:genpept) (de:helicobacter pylori 26695 section 76 of 134 of the complete genome.) (nt:similar to egad:27987 percent identity: 33.51;) (le:2964) (re:4349) (di:direct) HPAE000598 AE000598 g2314021 Helicobacter pylori 26695 85962 -11539312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908125	17856	40012	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908130	17857	40013	393	130

Description

6500735455 htpx:hp0927 heat shock protein htpx:heat shock protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP0927 HP0927 Helicobacter pylori 210 -11539313 7000689982 heat shock protein (cl:heat-shock protein htpx) (db:pir2.dat) G64635 G64635 Helicobacter pylori 210 -11539313 7500955128 hp0927 heat shock protein htpx (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:18140 percent identity: 32.80;) (le:10905) (re:11885) (di:direct) HPAE000602 AE000602 g2314064 Helicobacter pylori 210 -11539313 7502853180 hp0927 heat shock protein htpx (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:18140 percent identity: 32.80;) (le:10905) (re:11885) (di:direct) HPAE000602 AE000602 g2314064 Helicobacter pylori 26695 85962 -11539313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908133	17858	40014	423	140

Description

6500735456 sure:hp0930 stationary-phase survival protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP0930 HP0930 Helicobacter pylori 210 -11539314 7000690719 stationary-phase survival protein (cl:stationary-phase survival protein sure) (db:pir2.dat) B64636 B64636 Helicobacter pylori 210 -11539314 7500959485 hp0930 stationary-phase survival protein sure (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:15808 percent identity: 37.65;) (le:13352) (re:14155) (di:direct) HPAE000602 AE000602 g2314067 Helicobacter pylori 210 -11539314 7502853181 hp0930 stationary-phase survival protein sure (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:15808 percent identity: 37.65;) (le:13352) (re:14155) (di:direct) HPAE000602 AE000602 g2314067 Helicobacter pylori 26695 85962 -11539314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908150	17859	40015	270	89

Description

6500735457 vapd:hp0967 virulence associated protein d (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP0967 HP0967 Helicobacter pylori 210 -11539315 7000690796 virulence associated protein d (db:pir2.dat) G64640 G64640 Helicobacter pylori 210 -11539315 7500959555 hp0967 virulence associated protein d vapd (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:similar to egad:29086 percent identity: 28.89;) (le:6089) (re:6376) (di:complement) HPAE000605 AE000605 g2314106 Helicobacter pylori 210 -11539315 7502853182 hp0967 virulence associated protein d vapd (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:similar to egad:29086 percent identity: 28.89;) (le:6089) (re:6376) (di:complement) HPAE000605 AE000605 g2314106 Helicobacter pylori 26695 85962 -11539315

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908192	17860	40016	525	174

Description

GTC ORF with score 97 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid r02c2.) (nt:similar to serine/threonine-protein kinases) (le:15406:16033:16521:17024) (re:15901:16246:16676:17387) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908198	17861	40017	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908207	17862	40018	486	161

Description

6500735458 nccb:hp0970 nickel-cobalt-cadmium resistance protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP0970 HP0970 Helicobacter pylori 210 -11539316 7000690555 nickel-cobalt-cadmium resistance protein (db:pir2.dat) B64641 B64641 Helicobacter pylori 210 -11539316 7500959342 hp0970 nickel-cobalt-cadmium resistance protein nccb (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:similar to egad:42735 percent identity: 21.13;) (le:9802) (re:10881) (di:complement) HPAE000605 AE000605 g2314108 Helicobacter pylori 210 -11539316 7502853183 hp0970 nickel-cobalt-cadmium resistance protein nccb (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:similar to egad:42735 percent identity: 21.13;) (le:9802) (re:10881) (di:complement) HPAE000605 AE000605 g2314108 Helicobacter pylori 26695 85962 -11539316

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908211	17863	40019	576	191

Description

6500735459 inva:hp1228 invasion protein inva:invasion protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP1228 HP1228 Helicobacter pylori 210 -11539317 7000690481 invasion protein (cl:mutt domain homology) (db:pir2.dat) D64673 D64673 Helicobacter pylori 210 -11539317 7500959267 hp1228 invasion protein inva (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to egad:14214 percent identity: 38.21;) (le:3142) (re:3609) (di:direct) HPAE000628 AE000628 g2314391 Helicobacter pylori 210 -11539317 7502853184 hp1228 invasion protein inva (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to egad:14214 percent identity: 38.21;) (le:3142) (re:3609) (di:direct) HPAE000628 AE000628 g2314391 Helicobacter pylori 26695 85962 -11539317

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908212	17864	40020	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908223	17865	40021	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908225	17866	40022	681	226

Description

6500735460 vacb:hp1248 virulence associated protein homolog (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP1248 HP1248 Helicobacter pylori 210 -11539318 5500686146 vacb:hp1248 (sr:,campylobacter pylori) (de:vacb protein homolog) (db:swissprot) VACB_HELPY P56123 HELICOBACTER PYLORI 210 -11539318 7000686933 virulence associated protein homolog (db:pir2.dat) H64675 H64675 Helicobacter pylori 210 -11539318 7500893950 hp1248 virulence associated protein homolog vacb (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:similar to egad:24912 percent identity: 36.03;) (le:2603) (re:4537) (di:complement) HPAE000630 AE000630 g2314413 Helicobacter pylori 210 -11539318 7502853185 hp1248 virulence associated protein homolog vacb (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:similar to egad:24912 percent identity: 36.03;) (le:2603) (re:4537) (di:complement) HPAE000630 AE000630 g2314413 Helicobacter pylori 26695 85962 -11539318

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908273	17867	40023	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908280	17868	40024	1056	351

Description

6500735461 smpb:hp1444 small protein smpb:small protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP1444 HP1444 Helicobacter pylori 210 -11539319 7500891747 smpb:hp1444 (sr:,campylobacter pylori) (de:small protein b homolog) (db:swissprot) SMPB_HELPY O25985 HELICOBACTER PYLORI 210 -11539319 7000690710 small protein (cl:small protein smpb) (db:pir2.dat) D64700 D64700 Helicobacter pylori 210 -11539319 7500891749 hp1444 small protein smpb (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to egad:28004 percent identity: 42.11;) (le:9552) (re:10010) (di:direct) HPAE000644 AE000644 g2314616 Helicobacter pylori 210 -11539319 7502853186 hp1444 small protein smpb (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to egad:28004 percent identity: 42.11;) (le:9552) (re:10010) (di:direct) HPAE000644 AE000644 g2314616 Helicobacter pylori 26695 85962 -11539319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908281	17869	40025	2907	968

Description

6500735462 gerc2 protein gerc2:gerc2 protein:gerc2 (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP1483 HP1483 Helicobacter pylori 210 -11539320 7000689959 gerc2 protein (cl:spore germination protein c2:bioc homology) (db:pir2.dat) C64705 C64705 Helicobacter pylori 210 -11539320 7500958747 hp1483 gerc2 protein gerc2 (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:12212 percent identity: 33.33;) (le:18555) (re:19295) (di:complement) HPAE000647 AE000647 g2314655 Helicobacter pylori 210 -11539320 7502853187 hp1483 gerc2 protein gerc2 (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:12212 percent identity: 33.33;) (le:18555) (re:19295) (di:complement) HPAE000647 AE000647 g2314655 Helicobacter pylori 26695 85962 -11539320

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908284	17870	40026	783	260

Description

6500735463 ctc:hp1496 general stress protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.2) (db:gtc-helicobacter pylori) HP1496 HP1496 Helicobacter pylori 210 -11539321 5500685859 rply:hp1496 (sr:,campylobacter pylori) (de:probable 50s ribosomal protein l25) (db:swissprot) RL25_HELPY P56078 HELICOBACTER PYLORI 210 -11539321 7000686373 general stress protein (db:pir2.dat) H64706 H64706 Helicobacter pylori 210 -11539321 7500890122 hp1496 general stress protein ctc (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:13734 percent identity: 26.47;) (le:5070) (re:5606) (di:direct) HPAE000648 AE000648 g2314675 Helicobacter pylori 210 -11539321 7502853188 hp1496 general stress protein ctc (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:13734 percent identity: 26.47;) (le:5070) (re:5606) (di:direct) HPAE000648 AE000648 g2314675 Helicobacter pylori 26695 85962 -11539321

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908308	17871	40027	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908309	17872	40028	477	158

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908320	17873	40029	447	148

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908322	17874	40030	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908323	17875	40031	579	192

Description

6500735464 mtrc:hp0606 membrane fusion protein (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.4) (db:gtc-helicobacter pylori) HP0606 HP0606 Helicobacter pylori 210 -11539322 7000690513 membrane fusion protein (db:pir2.dat) F64595 F64595 Helicobacter pylori 210 -11539322 7500959306 hp0606 membrane fusion protein mtrc (db:genpept-bct1) (de:helicobacter pylori section 52 of 134 of the complete genome.) (nt:similar to egad:29377 percent identity: 24.21;) (le:5573) (re:6277) (di:direct) HPAE000574 AE000574 g2313725 Helicobacter pylori 210 -11539322 7502853189 hp0606 membrane fusion protein mtrc (db:genpept) (de:helicobacter pylori 26695 section 52 of 134 of the complete genome.) (nt:similar to egad:29377 percent identity: 24.21;) (le:5573) (re:6277) (di:direct) HPAE000574 AE000574 g2313725 Helicobacter pylori 26695 85962 -11539322

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908336	17876	40032	591	196

Description

6500735465 mda66:hp0630 modulator of drug activity (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.4) (db:gtc-helicobacter pylori) HP0630 HP0630 Helicobacter pylori 210 -11539323 7000690521 modulator of drug activity (db:pir2.dat) F64598 F64598 Helicobacter pylori 210 -11539323 7500959312 hp0630 modulator of drug activity mda66 (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:similar to egad:29270 percent identity: 62.30;) (le:5694) (re:6278) (di:complement) HPAE000577 AE000577 g2313748 Helicobacter pylori 210 -11539323 7502853190 hp0630 modulator of drug activity mda66 (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:similar to egad:29270 percent identity: 62.30;) (le:5694) (re:6278) (di:complement) HPAE000577 AE000577 g2313748 Helicobacter pylori 26695 85962 -11539323

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908337	17877	40033	513	170

Description

6500735466 tetracycline resistance protein teta:putative:tetracycline resistance protein teta:p:putative (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.4) (db:gtc-helicobacter pylori) HP1165 HP1165 Helicobacter pylori 210 -11539324 7000690723 tetracycline resistance protein teta p homolog (db:pir2.dat) E64665 E64665 Helicobacter pylori 210 -11539324 7500959489 hp1165 tetracycline resistance protein teta p (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:similar to egad:22986 percent identity: 26.96;) (le:3042) (re:4202) (di:complement) HPAE000622 AE000622 g2314322 Helicobacter pylori 210 -11539324 7502853191 hp1165 tetracycline resistance protein teta p (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:similar to egad:22986 percent identity: 26.96;) (le:3042) (re:4202) (di:complement) HPAE000622 AE000622 g2314322 Helicobacter pylori 26695 85962 -11539324

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908338	17878	40034	1182	393

Description

6500735467 ksga:hp1431 16s rrna:adenosine-n6-dimethyltransferase:16s rrna:adenosine-n6:n6--dimethyltransferase (gtcfc:13.3) (keggfc:14.2) (tigrfc:14.4) (db:gtc-helicobacter pylori) HP1431 HP1431 Helicobacter pylori 210 -11539325 7000689059 16s rrna (cl:rrna (adenine-n6-)-methyltransferase) (db:pir2.dat) G64698 G64698 Helicobacter pylori 210 -11539325 7500953972 hp1431 16s rrna adenosine-n6:n6--dimethyltransferase (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:similar to egad:29184 percent identity: 35.50;) (le:6534) (re:7349) (di:complement) HPAE000643 AE000643 g2314603 Helicobacter pylori 210 -11539325 7502853192 hp1431 16s rrna adenosine-n6:n6--dimethyltransferase (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:similar to egad:29184 percent identity: 35.50;) (le:6534) (re:7349) (di:complement) HPAE000643 AE000643 g2314603 Helicobacter pylori 26695 85962 -11539325

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908349	17879	40035	729	242

Description

GTC ORF with score 421 to: (fn:catalyzes hydroxylation at c-15 of) (db:genpept-pln1) (de:fusarium sporotrichioides isotrichodermin c-15 hydroxylase (tri11)gene, complete cds.) (nt:cytochrome p450 monooxygenase) (le:189:286:1132:1526:1757) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908350	17880	40036	492	163

Description

6500735468 transposase-like protein:ps3is (gtcfc:13.5) (keggfc:14.2) (tigrfc:14.5) (db:gtc-helicobacter pylori) HP0413 HP0413 Helicobacter pylori 210 -11539326 7500975631 hp0413 transposase-like protein:ps3is (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to egad:42030 percent identity: 33.61;) (le:4512) (re:5318) (di:complement) HPAE000557 AE000557 g2313517 Helicobacter pylori 210 -11539326 7502853193 hp0413 transposase-like protein:ps3is (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to egad:42030 percent identity: 33.61;) (le:4512) (re:5318) (di:complement) HPAE000557 AE000557 g2313517 Helicobacter pylori 26695 85962 -11539326

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908383	17881	40037	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908388	17882	40038	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908390	17883	40039	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908415	17884	40040	528	175

Description

GTC ORF with score 111 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908422	17885	40041	1125	374

Description

6500735469 is200 insertion sequence from sara17 (gtcfc:13.5) (keggfc:14.2) (tigrfc:14.5) (db:gtc-helicobacter pylori) HP0414 HP0414 Helicobacter pylori 210 -11539327 7000689466 hypothetical protein sara17 (cl:conserved hypothetical protein 4 (insertion sequence ish1.8)) (db:pir2.dat) F64571 F64571 Helicobacter pylori 210 -11539327 7500955761 hp0414 is200 insertion sequence from sara17 (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to egad:14951 percent identity: 33.91;) (le:5356) (re:5772) (di:direct) HPAE000557 AE000557 g2313518 Helicobacter pylori 210 -11539327 7500955762 hp1008 is200 insertion sequence from sara17 (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:similar to egad:14951 percent identity: 33.91;) (le:2982) (re:3398) (di:direct) HPAE000609 AE000609 g2314152 Helicobacter pylori 210 -11539327 7502853194 hp0414 is200 insertion sequence from sara17 (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to egad:14951 percent identity: 33.91;) (le:5356) (re:5772) (di:direct) HPAE000557 AE000557 g2313518 Helicobacter pylori 26695 85962 -11539327 7502853195 hp1008 is200 insertion sequence from sara17 (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:similar to egad:14951 percent identity: 33.91;) (le:2982) (re:3398) (di:direct) HPAE000609 AE000609 g2314152 Helicobacter pylori 26695 85962 -11539327

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908426	17886	40042	1383	460

Description

6500735470 tnpa:hp0437 is605 transposase (gtcfc:13.5) (keggfc:14.2) (tigrfc:14.5) (db:gtc-helicobacter pylori) HP0437 HP0437 Helicobacter pylori 210 -11539328 7000690493 is605 transposase tnpa (db:pir2.dat) D64643 D64643 Helicobacter pylori 210 -11539328 7500959281 hp0437 is605 transposase tnpa (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:6023) (re:6451) (di:complement) HPAE000559 AE000559 g2313540 Helicobacter pylori 210 -11539328 7500959282 hp0988 is605 transposase tnpa (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:5732) (re:6160) (di:complement) HPAE000607 AE000607 g2314127 Helicobacter pylori 210 -11539328 7500959283 hp0998 is605 transposase tnpa (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:5708) (re:6136) (di:direct) HPAE000608 AE000608 g2314142 Helicobacter pylori 210 -11539328 7500959284 hp1096 is605 transposase tnpa (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:4561) (re:4989) (di:direct) HPAE000616 AE000616 g2314246 Helicobacter pylori 210 -11539328 7500959285 hp1535 is605 transposase tnpa (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:8557) (re:8985) (di:direct) HPAE000651 AE000651 g2314714 Helicobacter pylori 210 -11539328 7502853196 hp0437 is605 transposase tnpa (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:6023) (re:6451) (di:complement) HPAE000559 AE000559 g2313540 Helicobacter pylori 26695 85962 -11539328 7502853197 hp0988 is605 transposase tnpa (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:5732) (re:6160) (di:complement) HPAE000607 AE000607 g2314127 Helicobacter pylori 26695 85962 -11539328 7502853198 hp0998 is605 transposase tnpa (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:5708) (re:6136) (di:direct) HPAE000608 AE000608 g2314142 Helicobacter pylori 26695 85962 -11539328 7502853199 hp1096 is605 transposase tnpa (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:4561) (re:4989) (di:direct) HPAE000616 AE000616 g2314246 Helicobacter pylori 26695 85962 -11539328 7502853200 hp1535 is605 transposase tnpa (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:similar to gp:1800172 percent identity: 97.18;) (le:8557) (re:8985) (di:direct) HPAE000651 AE000651 g2314714 Helicobacter pylori 26695 85962 -11539328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908435	17887	40043	561	186

Description

6500735471 tnpb:hp0438 is605 transposase (gtcfc:13.5) (keggfc:14.2) (tigrfc:14.5) (db:gtc-helicobacter pylori) HP0438 HP0438 Helicobacter pylori 210 -11539329 7000690492 is605 transposase (db:pir2.dat) E64644 E64644 Helicobacter pylori 210 -11539329 7500959278 hp0438 is605 transposase tnpb (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:6521) (re:7804) (di:direct) HPAE000559 AE000559 g2313541 Helicobacter pylori 210 -11539329 7500959279 hp0997 is605 transposase tnpb (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:4355) (re:5638) (di:complement) HPAE000608 AE000608 g2314141 Helicobacter pylori 210 -11539329 7500959280 hp1095 is605 transposase tnpb (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:3208) (re:4491) (di:complement) HPAE000616 AE000616 g2314245 Helicobacter pylori 210 -11539329 7502853201 hp0438 is605 transposase tnpb (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:6521) (re:7804) (di:direct) HPAE000559 AE000559 g2313541 Helicobacter pylori 26695 85962 -11539329 7502853202 hp0997 is605 transposase tnpb (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:4355) (re:5638) (di:complement) HPAE000608 AE000608 g2314141 Helicobacter pylori 26695 85962 -11539329 7502853203 hp1095 is605 transposase tnpb (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:3208) (re:4491) (di:complement) HPAE000616 AE000616 g2314245 Helicobacter pylori 26695 85962 -11539329

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908437	17888	40044	3180	1059

Description

6500735472 tnpb:hp0989 is605 transposase (gtcfc:13.5) (keggfc:14.2) (tigrfc:14.5) (db:gtc-helicobacter pylori) HP0989 HP0989 Helicobacter pylori 210 -11539330 7000690494 is605 transposase tnpb (db:pir2.dat) E64643 E64643 Helicobacter pylori 210 -11539330 7500959286 hp0989 is605 transposase tnpb (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:6230) (re:7513) (di:direct) HPAE000607 AE000607 g2314128 Helicobacter pylori 210 -11539330 7500959287 hp1534 is605 transposase tnpb (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:7204) (re:8487) (di:complement) HPAE000651 AE000651 g2314713 Helicobacter pylori 210 -11539330 7502853204 hp0989 is605 transposase tnpb (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:6230) (re:7513) (di:direct) HPAE000607 AE000607 g2314128 Helicobacter pylori 26695 85962 -11539330 7502853205 hp1534 is605 transposase tnpb (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:similar to gp:1800173 percent identity: 93.35;) (le:7204) (re:8487) (di:complement) HPAE000651 AE000651 g2314713 Helicobacter pylori 26695 85962 -11539330

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908439	17889	40045	1326	442

Description

6500735473 plasmid replication-partition related protein (gtcfc:13.6) (keggfc:14.2) (tigrfc:4.5) (db:gtc-helicobacter pylori) HP1138 HP1138 Helicobacter pylori 210 -11539331 7000690628 plasmid replication-partition related protein (cl:bacillus subtilis transport protein spo0j) (db:pir2.dat) B64662 B64662 Helicobacter pylori 210 -11539331 7500959408 hp1138 plasmid replication-partition related protein (db:genpept-bct1) (de:helicobacter pylori section 98 of 134 of the complete genome.) (nt:similar to egad:14311 percent identity: 40.43;) (le:86) (re:958) (di:complement) HPAE000620 AE000620 g2314294 Helicobacter pylori 210 -11539331 7502853206 hp1138 plasmid replication-partition related protein (db:genpept) (de:helicobacter pylori 26695 section 98 of 134 of the complete genome.) (nt:similar to egad:14311 percent identity: 40.43;) (le:86) (re:958) (di:complement) HPAE000620 AE000620 g2314294 Helicobacter pylori 26695 85962 -11539331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908454	17890	40046	252	83

Description

6500735474 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0007 HP0007 Helicobacter pylori 210 -11539332 7000690003 hypothetical protein hp0007 (db:pir2.dat) G64520 G64520 Helicobacter pylori 210 -11539332 7500958782 hp0007 h. pylori predicted coding region hp0007 (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4697) (re:4768) (di:direct) HPAE000523 AE000523 g2313088 Helicobacter pylori 210 -11539332 7502853207 hp0007 h. pylori predicted coding region hp0007 (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4697) (re:4768) (di:direct) HPAE000523 AE000523 g2313088 Helicobacter pylori 26695 85962 -11539332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908457	17891	40047	351	116

Description

GTC ORF with score 189 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t32f6 genomic sequence,complete sequence.) (nt:unknown protein) (le:57064:57317:57519) (re:57237:57402:57688) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908463	17892	40048	1956	651

Description

6500735475 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0008 HP0008 Helicobacter pylori 210 -11539333 7000690004 hypothetical protein hp0008 (db:pir2.dat) H64520 H64520 Helicobacter pylori 210 -11539333 7500958783 hp0008 h. pylori predicted coding region hp0008 (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4937) (re:5020) (di:direct) HPAE000523 AE000523 g2313089 Helicobacter pylori 210 -11539333 7502853208 hp0008 h. pylori predicted coding region hp0008 (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4937) (re:5020) (di:direct) HPAE000523 AE000523 g2313089 Helicobacter pylori 26695 85962 -11539333

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908464	17893	40049	414	137

Description

6500735476 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0013 HP0013 Helicobacter pylori 210 -11539334 7000689644 argininosuccinate synthase (db:pir2.dat) E64521 E64521 Helicobacter pylori 210 -11539334 7500958461 hp0013 h. pylori predicted coding region hp0013 (db:genpept-bct1) (de:helicobacter pylori section 1 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11587) (re:12639) (di:direct) HPAE000523 AE000523 g2313087 Helicobacter pylori 210 -11539334 7502853209 hp0013 h. pylori predicted coding region hp0013 (db:genpept) (de:helicobacter pylori 26695 section 1 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11587) (re:12639) (di:direct) HPAE000523 AE000523 g2313087 Helicobacter pylori 26695 85962 -11539334

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908471	17894	40050	1119	372

Description

6500735477 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0014 HP0014 Helicobacter pylori 210 -11539335 7000690005 hypothetical protein hp0014 (db:pir2.dat) F64521 F64521 Helicobacter pylori 210 -11539335 7500958784 hp0014 h. pylori predicted coding region hp0014 (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:75) (re:902) (di:direct) HPAE000524 AE000524 g2313095 Helicobacter pylori 210 -11539335 7502853210 hp0014 h. pylori predicted coding region hp0014 (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:75) (re:902) (di:direct) HPAE000524 AE000524 g2313095 Helicobacter pylori 26695 85962 -11539335

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908478	17895	40051	189	62

Description

GTC ORF with score 125 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t32f6 genomic sequence,complete sequence.) (nt:unknown protein) (le:57064:57317:57519) (re:57237:57402:57688) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908494	17896	40052	342	113

Description

6500735478 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0015 HP0015 Helicobacter pylori 210 -11539336 7000690006 hypothetical protein hp0015 (db:pir2.dat) G64521 G64521 Helicobacter pylori 210 -11539336 7500958785 hp0015 h. pylori predicted coding region hp0015 (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1049) (re:1330) (di:direct) HPAE000524 AE000524 g2313096 Helicobacter pylori 210 -11539336 7502853211 hp0015 h. pylori predicted coding region hp0015 (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1049) (re:1330) (di:direct) HPAE000524 AE000524 g2313096 Helicobacter pylori 26695 85962 -11539336

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908497	17897	40053	402	133

Description

6500735479 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0016 HP0016 Helicobacter pylori 210 -11539337 7000690007 hypothetical protein hp0016 (db:pir2.dat) H64521 H64521 Helicobacter pylori 210 -11539337 7500958786 hp0016 h. pylori predicted coding region hp0016 (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1330) (re:1593) (di:direct) HPAE000524 AE000524 g2313097 Helicobacter pylori 210 -11539337 7502853212 hp0016 h. pylori predicted coding region hp0016 (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1330) (re:1593) (di:direct) HPAE000524 AE000524 g2313097 Helicobacter pylori 26695 85962 -11539337

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908513	17898	40054	204	67

Description

6500735480 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0018 HP0018 Helicobacter pylori 210 -11539338 7000690008 hypothetical protein hp0018 (db:pir2.dat) B64522 B64522 Helicobacter pylori 210 -11539338 7500958787 hp0018 h. pylori predicted coding region hp0018 (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4210) (re:5619) (di:direct) HPAE000524 AE000524 g2313098 Helicobacter pylori 210 -11539338 7502853213 hp0018 h. pylori predicted coding region hp0018 (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4210) (re:5619) (di:direct) HPAE000524 AE000524 g2313098 Helicobacter pylori 26695 85962 -11539338

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908514	17899	40055	1107	368

Description

6500735481 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0021 HP0021 Helicobacter pylori 210 -11539339 7000690009 hypothetical protein hp0021 (db:pir2.dat) E64522 E64522 Helicobacter pylori 210 -11539339 7500958788 hp0021 h. pylori predicted coding region hp0021 (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7916) (re:8488) (di:complement) HPAE000524 AE000524 g2313099 Helicobacter pylori 210 -11539339 7502853214 hp0021 h. pylori predicted coding region hp0021 (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7916) (re:8488) (di:complement) HPAE000524 AE000524 g2313099 Helicobacter pylori 26695 85962 -11539339

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908517	17900	40056	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908519	17901	40057	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908520	17902	40058	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908522	17903	40059	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908525	17904	40060	207	68

Description

6500735482 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0023 HP0023 Helicobacter pylori 210 -11539340 7000690010 hypothetical protein hp0023 (db:pir2.dat) G64522 G64522 Helicobacter pylori 210 -11539340 7500958789 hp0023 h. pylori predicted coding region hp0023 (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10120) (re:10239) (di:direct) HPAE000524 AE000524 g2313100 Helicobacter pylori 210 -11539340 7502853215 hp0023 h. pylori predicted coding region hp0023 (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10120) (re:10239) (di:direct) HPAE000524 AE000524 g2313100 Helicobacter pylori 26695 85962 -11539340

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908529	17905	40061	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908532	17906	40062	219	72

Description

GTC ORF with score 125 to: (sr:rhizobium meliloti (strain 1021) dna) (db:genpept-bct1) (de:rhizobium meliloti 1021 ribosomal protein s20 (rps20), enoyl coahydratase (fadb1), dnaa, orfx, genes, complete cds, and orfy,formamidopyrimidine-dna glycosylase ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908537	17907	40063	372	123

Description

6500735483 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0024 HP0024 Helicobacter pylori 210 -11539341 7000690011 hypothetical protein hp0024 (db:pir2.dat) H64522 H64522 Helicobacter pylori 210 -11539341 7500958790 hp0024 h. pylori predicted coding region hp0024 (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10250) (re:10342) (di:direct) HPAE000524 AE000524 g2313101 Helicobacter pylori 210 -11539341 7502853216 hp0024 h. pylori predicted coding region hp0024 (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10250) (re:10342) (di:direct) HPAE000524 AE000524 g2313101 Helicobacter pylori 26695 85962 -11539341

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908538	17908	40064	297	98

Description

GTC ORF with score 141 to: (sr:rhizobium meliloti (strain 1021) dna) (db:genpept-bct1) (de:rhizobium meliloti 1021 ribosomal protein s20 (rps20), enoyl coahydratase (fadb1), dnaa, orfx, genes, complete cds, and orfy,formamidopyrimidine-dna glycosylase ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908543	17909	40065	813	270

Description

6500735484 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0030 HP0030 Helicobacter pylori 210 -11539342 7000690012 hypothetical protein hp0030 (db:pir2.dat) F64523 F64523 Helicobacter pylori 210 -11539342 7500958791 hp0030 h. pylori predicted coding region hp0030 (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6942) (re:8723) (di:complement) HPAE000525 AE000525 g2313113 Helicobacter pylori 210 -11539342 7502853217 hp0030 h. pylori predicted coding region hp0030 (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6942) (re:8723) (di:complement) HPAE000525 AE000525 g2313113 Helicobacter pylori 26695 85962 -11539342

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908563	17910	40066	1290	429

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908566	17911	40067	639	212

Description

7500958793 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0031 HP0031 Helicobacter pylori 210 -11539343 7000690013 hypothetical protein hp0031 (db:pir2.dat) G64523 G64523 Helicobacter pylori 210 -11539343 7500958792 hp0031 h. pylori predicted coding region hp0031 (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8832) (re:9245) (di:direct) HPAE000525 AE000525 g2313114 Helicobacter pylori 210 -11539343 7502853218 jhp0027 putative (db:genpept) (de:helicobacter pylori, strain j99 section 3 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0031) (le:8912) (re:9325) (di:direct) AE001442 AE001442 g4154532 Helicobacter pylori J99 85963 -11539343 6500735485 hp0031 h. pylori predicted coding region hp0031 (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8832) (re:9245) (di:direct) HPAE000525 AE000525 g2313114 Helicobacter pylori 26695 85962 -11539343

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908570	17912	40068	399	132

Description

6500735486 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0036 HP0036 Helicobacter pylori 210 -11539344 7000690014 hypothetical protein hp0036 (db:pir2.dat) D64524 D64524 Helicobacter pylori 210 -11539344 7500958794 hp0036 h. pylori predicted coding region hp0036 (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12415) (re:13419) (di:direct) HPAE000525 AE000525 g2313115 Helicobacter pylori 210 -11539344 7502853219 hp0036 h. pylori predicted coding region hp0036 (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12415) (re:13419) (di:direct) HPAE000525 AE000525 g2313115 Helicobacter pylori 26695 85962 -11539344

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908582	17913	40069	660	219

Description

6500735487 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0038 HP0038 Helicobacter pylori 210 -11539345 7000690015 hypothetical protein hp0038 (db:pir2.dat) F64524 F64524 Helicobacter pylori 210 -11539345 7500958795 hp0038 h. pylori predicted coding region hp0038 (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:94) (re:831) (di:direct) HPAE000526 AE000526 g2313125 Helicobacter pylori 210 -11539345 7502853220 hp0038 h. pylori predicted coding region hp0038 (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:94) (re:831) (di:direct) HPAE000526 AE000526 g2313125 Helicobacter pylori 26695 85962 -11539345

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908585	17914	40070	498	165

Description

6500735488 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0039 HP0039 Helicobacter pylori 210 -11539346 7000690016 hypothetical protein hp0039 (db:pir2.dat) G64524 G64524 Helicobacter pylori 210 -11539346 7500958796 hp0039 h. pylori predicted coding region hp0039 (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:828) (re:1100) (di:direct) HPAE000526 AE000526 g2313126 Helicobacter pylori 210 -11539346 7502853221 hp0039 h. pylori predicted coding region hp0039 (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:828) (re:1100) (di:direct) HPAE000526 AE000526 g2313126 Helicobacter pylori 26695 85962 -11539346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908598	17915	40071	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908604	17916	40072	246	81

Description

GTC ORF with score 156 to: (de:(yhr051w) (pn:cytochrome c oxidase polypeptide vi precursor:cytochrome c oxidase subunit vi) (gn:cox6) (gtcfc:2.1) (ec:1.9.3.1) (cox6_yeast) (keggfc:2.1) (sgdfc:2.5.0:9.7.0) (db:gtc-saccharomyces cerevisiae))

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908607	17917	40073	2622	873

Description

GTC ORF with score 205 to: (fn:required for gamma-tubulin ring function and) (sr:african clawed frog) (db:genpept-vrt) (de:xenopus laevis gamma-tubulin interacting protein mrna, completecds.) (nt:xgrip109) (le:118) (re:2838) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908611	17918	40074	570	189

Description

6500735489 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0040 HP0040 Helicobacter pylori 210 -11539347 7000690017 hypothetical protein hp0040 (db:pir2.dat) H64524 H64524 Helicobacter pylori 210 -11539347 7500958797 hp0040 h. pylori predicted coding region hp0040 (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1066) (re:1809) (di:direct) HPAE000526 AE000526 g2313127 Helicobacter pylori 210 -11539347 7502853222 hp0040 h. pylori predicted coding region hp0040 (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1066) (re:1809) (di:direct) HPAE000526 AE000526 g2313127 Helicobacter pylori 26695 85962 -11539347

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908612	17919	40075	516	171

Description

6500735490 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0041 HP0041 Helicobacter pylori 210 -11539348 7000690018 hypothetical protein hp0041 (db:pir2.dat) A64525 A64525 Helicobacter pylori 210 -11539348 7500958798 hp0041 h. pylori predicted coding region hp0041 (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1802) (re:2173) (di:direct) HPAE000526 AE000526 g2313128 Helicobacter pylori 210 -11539348 7502853223 hp0041 h. pylori predicted coding region hp0041 (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1802) (re:2173) (di:direct) HPAE000526 AE000526 g2313128 Helicobacter pylori 26695 85962 -11539348

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908625	17920	40076	2757	918

Description

6500735491 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0046 HP0046 Helicobacter pylori 210 -11539349 7000690019 hypothetical protein hp0046 (db:pir2.dat) F64525 F64525 Helicobacter pylori 210 -11539349 7500958799 hp0046 h. pylori predicted coding region hp0046 (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6655) (re:6792) (di:direct) HPAE000526 AE000526 g2313130 Helicobacter pylori 210 -11539349 7502853224 hp0046 h. pylori predicted coding region hp0046 (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6655) (re:6792) (di:direct) HPAE000526 AE000526 g2313130 Helicobacter pylori 26695 85962 -11539349

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908629	17921	40077	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908645	17922	40078	657	218

Description

6500735492 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0049 HP0049 Helicobacter pylori 210 -11539350 7000690020 hypothetical protein hp0049 (db:pir2.dat) A64526 A64526 Helicobacter pylori 210 -11539350 7500958800 hp0049 h. pylori predicted coding region hp0049 (db:genpept-bct1) (de:helicobacter pylori section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10647) (re:11639) (di:complement) HPAE000526 AE000526 g2313129 Helicobacter pylori 210 -11539350 7502853225 hp0049 h. pylori predicted coding region hp0049 (db:genpept) (de:helicobacter pylori 26695 section 4 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10647) (re:11639) (di:complement) HPAE000526 AE000526 g2313129 Helicobacter pylori 26695 85962 -11539350

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908651	17923	40079	2001	666

Description

6500735493 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0052 HP0052 Helicobacter pylori 210 -11539351 7000690021 hypothetical protein hp0052 (db:pir2.dat) D64526 D64526 Helicobacter pylori 210 -11539351 7500958801 hp0052 h. pylori predicted coding region hp0052 (db:genpept-bct1) (de:helicobacter pylori section 5 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:118) (re:1110) (di:complement) HPAE000527 AE000527 g2313135 Helicobacter pylori 210 -11539351 7502853226 hp0052 h. pylori predicted coding region hp0052 (db:genpept) (de:helicobacter pylori 26695 section 5 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:118) (re:1110) (di:complement) HPAE000527 AE000527 g2313135 Helicobacter pylori 26695 85962 -11539351

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908664	17924	40080	351	116

Description

6500735494 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0053 HP0053 Helicobacter pylori 210 -11539352 7000690022 hypothetical protein hp0053 (db:pir2.dat) E64526 E64526 Helicobacter pylori 210 -11539352 7500958802 hp0053 h. pylori predicted coding region hp0053 (db:genpept-bct1) (de:helicobacter pylori section 5 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1305) (re:2564) (di:complement) HPAE000527 AE000527 g2313136 Helicobacter pylori 210 -11539352 7502853227 hp0053 h. pylori predicted coding region hp0053 (db:genpept) (de:helicobacter pylori 26695 section 5 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1305) (re:2564) (di:complement) HPAE000527 AE000527 g2313136 Helicobacter pylori 26695 85962 -11539352

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908665	17925	40081	720	239

Description

GTC ORF with score 245 to: (fn:cellular receptor for hepatitis a virus in) (sr:african green monkey) (db:genpept-pri3) (de:cercopithecus aethiops hepatitis a virus cellular receptor 1 shortform (havcr-1) mrna, complete cds.) (nt:mucin-like class i ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908671	17926	40082	675	224

Description

6500735495 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0057 HP0057 Helicobacter pylori 210 -11539353 7000690023 hypothetical protein hp0057 (db:pir2.dat) A64527 A64527 Helicobacter pylori 210 -11539353 7500958803 hp0057 h. pylori predicted coding region hp0057 (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:191) (re:400) (di:direct) HPAE000528 AE000528 g2313144 Helicobacter pylori 210 -11539353 7502853228 hp0057 h. pylori predicted coding region hp0057 (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:191) (re:400) (di:direct) HPAE000528 AE000528 g2313144 Helicobacter pylori 26695 85962 -11539353

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908681	17927	40083	606	201

Description

6500735496 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0059 HP0059 Helicobacter pylori 210 -11539354 7000690508 m protein (db:pir2.dat) C64527 C64527 Helicobacter pylori 210 -11539354 7500959301 hp0059 h. pylori predicted coding region hp0059 (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1717) (re:2571) (di:direct) HPAE000528 AE000528 g2313145 Helicobacter pylori 210 -11539354 7502853229 hp0059 h. pylori predicted coding region hp0059 (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1717) (re:2571) (di:direct) HPAE000528 AE000528 g2313145 Helicobacter pylori 26695 85962 -11539354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908688	17928	40084	777	258

Description

6500735497 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0060 HP0060 Helicobacter pylori 210 -11539355 7000690024 hypothetical protein hp0060 (db:pir2.dat) D64527 D64527 Helicobacter pylori 210 -11539355 7500958804 hp0060 h. pylori predicted coding region hp0060 (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2588) (re:5029) (di:direct) HPAE000528 AE000528 g2313146 Helicobacter pylori 210 -11539355 7502853230 hp0060 h. pylori predicted coding region hp0060 (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2588) (re:5029) (di:direct) HPAE000528 AE000528 g2313146 Helicobacter pylori 26695 85962 -11539355

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908725	17929	40085	543	180

Description

6500735498 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0061 HP0061 Helicobacter pylori 210 -11539356 7000690025 hypothetical protein hp0061 (db:pir2.dat) E64527 E64527 Helicobacter pylori 210 -11539356 7500958805 hp0061 h. pylori predicted coding region hp0061 (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5026) (re:5595) (di:direct) HPAE000528 AE000528 g2313147 Helicobacter pylori 210 -11539356 7502853231 hp0061 h. pylori predicted coding region hp0061 (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5026) (re:5595) (di:direct) HPAE000528 AE000528 g2313147 Helicobacter pylori 26695 85962 -11539356

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908728	17930	40086	333	110

Description

6500735499 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0062 HP0062 Helicobacter pylori 210 -11539357 7000690026 hypothetical protein hp0062 (db:pir2.dat) F64527 F64527 Helicobacter pylori 210 -11539357 7500958806 hp0062 h. pylori predicted coding region hp0062 (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5611) (re:5871) (di:direct) HPAE000528 AE000528 g2313148 Helicobacter pylori 210 -11539357 7502853232 hp0062 h. pylori predicted coding region hp0062 (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5611) (re:5871) (di:direct) HPAE000528 AE000528 g2313148 Helicobacter pylori 26695 85962 -11539357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908731	17931	40087	1515	504

Description

GTC ORF with score 119 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908754	17932	40088	990	329

Description

6500735500 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0063 HP0063 Helicobacter pylori 210 -11539358 7000690027 hypothetical protein hp0063 (db:pir2.dat) G64527 G64527 Helicobacter pylori 210 -11539358 7500958807 hp0063 h. pylori predicted coding region hp0063 (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5882) (re:7372) (di:direct) HPAE000528 AE000528 g2313149 Helicobacter pylori 210 -11539358 7502853233 hp0063 h. pylori predicted coding region hp0063 (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5882) (re:7372) (di:direct) HPAE000528 AE000528 g2313149 Helicobacter pylori 26695 85962 -11539358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908763	17933	40089	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908764	17934	40090	240	79

Description

6500735501 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0064 HP0064 Helicobacter pylori 210 -11539359 7000690028 hypothetical protein hp0064 (db:pir2.dat) H64527 H64527 Helicobacter pylori 210 -11539359 7500958808 hp0064 h. pylori predicted coding region hp0064 (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7342) (re:7761) (di:direct) HPAE000528 AE000528 g2313150 Helicobacter pylori 210 -11539359 7502853234 hp0064 h. pylori predicted coding region hp0064 (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7342) (re:7761) (di:direct) HPAE000528 AE000528 g2313150 Helicobacter pylori 26695 85962 -11539359

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908771	17935	40091	618	205

Description

6500735502 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0065 HP0065 Helicobacter pylori 210 -11539360 7000690029 hypothetical protein hp0065 (db:pir2.dat) A64528 A64528 Helicobacter pylori 210 -11539360 7500958809 hp0065 h. pylori predicted coding region hp0065 (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7763) (re:8116) (di:direct) HPAE000528 AE000528 g2313151 Helicobacter pylori 210 -11539360 7502853235 hp0065 h. pylori predicted coding region hp0065 (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7763) (re:8116) (di:direct) HPAE000528 AE000528 g2313151 Helicobacter pylori 26695 85962 -11539360

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908782	17936	40092	1227	408

Description

GTC ORF with score 109 to: (sr:human nalm6 and hela cells) (db:genpept-pri1) (de:e2f-4=transcription factor (human, nalm6 and hela cells, mrna, 1539nt).) (nt:transcription factor; this sequence comes from fig.) (le:55) (re:1305) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908797	17937	40093	993	330

Description

6500735503 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0080 HP0080 Helicobacter pylori 210 -11539361 7000690031 hypothetical protein hp0080 (db:pir2.dat) H64529 H64529 Helicobacter pylori 210 -11539361 7500958811 hp0080 h. pylori predicted coding region hp0080 (db:genpept-bct1) (de:helicobacter pylori section 7 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8959) (re:10740) (di:direct) HPAE000529 AE000529 g2313161 Helicobacter pylori 210 -11539361 7502853236 hp0080 h. pylori predicted coding region hp0080 (db:genpept) (de:helicobacter pylori 26695 section 7 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8959) (re:10740) (di:direct) HPAE000529 AE000529 g2313161 Helicobacter pylori 26695 85962 -11539361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908803	17938	40094	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908804	17939	40095	657	218

Description

6500735504 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0081 HP0081 Helicobacter pylori 210 -11539362 7000690032 hypothetical protein hp0081 (db:pir2.dat) A64530 A64530 Helicobacter pylori 210 -11539362 7500958812 hp0081 h. pylori predicted coding region hp0081 (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:165) (re:287) (di:direct) HPAE000530 AE000530 g2313171 Helicobacter pylori 210 -11539362 7502853237 hp0081 h. pylori predicted coding region hp0081 (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:165) (re:287) (di:direct) HPAE000530 AE000530 g2313171 Helicobacter pylori 26695 85962 -11539362

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908805	17940	40096	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908818	17941	40097	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908836	17942	40098	582	193

Description

GTC ORF with score 116 to: (fn:binds to orip to permit replication of the) (db:genpept-vrl) (de:herpesvirus papio brrf2 homolog gene, partial cds, ebna1, bkrf2homolog and bkrf3 homolog genes, complete cds, and bkrf4 homologgene, partial cds.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908850	17943	40099	297	98

Description

7500958814 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0085 HP0085 Helicobacter pylori 210 -11539363 7000690033 hypothetical protein hp0085 (db:pir2.dat) E64530 E64530 Helicobacter pylori 210 -11539363 7500958813 hp0085 h. pylori predicted coding region hp0085 (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3712) (re:3900) (di:complement) HPAE000530 AE000530 g2313172 Helicobacter pylori 210 -11539363 7502853238 jhp0078 putative (db:genpept) (de:helicobacter pylori, strain j99 section 8 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0085) (le:1269) (re:1457) (di:complement) AE001447 AE001447 g4154588 Helicobacter pylori J99 85963 -11539363 6500735505 hp0085 h. pylori predicted coding region hp0085 (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3712) (re:3900) (di:complement) HPAE000530 AE000530 g2313172 Helicobacter pylori 26695 85962 -11539363

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908851	17944	40100	360	119

Description

6500735506 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0087 HP0087 Helicobacter pylori 210 -11539364 7000690034 hypothetical protein hp0087 (db:pir2.dat) G64530 G64530 Helicobacter pylori 210 -11539364 7500958815 hp0087 h. pylori predicted coding region hp0087 (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5313) (re:6686) (di:complement) HPAE000530 AE000530 g2313170 Helicobacter pylori 210 -11539364 7502853239 hp0087 h. pylori predicted coding region hp0087 (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5313) (re:6686) (di:complement) HPAE000530 AE000530 g2313170 Helicobacter pylori 26695 85962 -11539364

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908852	17945	40101	945	314

Description

6500735507 pfs protein:pfs (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0089 HP0089 Helicobacter pylori 210 -11539365 7500887919 pfs:hp0089 (sr:,campylobacter pylori) (ec:3.2.2.16:3.2.2.9) (de:nucleosidase, (mta/sah nucleosidase) (p46)) (db:swissprot) PFS_HELPY O24915 HELICOBACTER PYLORI 210 -11539365 7000690616 pfs protein (cl:escherichia coli pfs protein) (db:pir2.dat) A64531 A64531 Helicobacter pylori 210 -11539365 7500887921 hp0089 pfs protein pfs (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:similar to egad:28227 percent identity: 34.50;) (le:8946) (re:9641) (di:complement) HPAE000530 AE000530 g2313168 Helicobacter pylori 210 -11539365 7502853240 hp0089 pfs protein pfs (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:similar to egad:28227 percent identity: 34.50;) (le:8946) (re:9641) (di:complement) HPAE000530 AE000530 g2313168 Helicobacter pylori 26695 85962 -11539365

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908887	17946	40102	678	225

Description

6500735508 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0093 HP0093 Helicobacter pylori 210 -11539366 7000690035 hypothetical protein hp0093 (db:pir2.dat) E64531 E64531 Helicobacter pylori 210 -11539366 7500958816 hp0093 h. pylori predicted coding region hp0093 (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2074) (re:2406) (di:complement) HPAE000531 AE000531 g2313181 Helicobacter pylori 210 -11539366 7502853241 hp0093 h. pylori predicted coding region hp0093 (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2074) (re:2406) (di:complement) HPAE000531 AE000531 g2313181 Helicobacter pylori 26695 85962 -11539366

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908888	17947	40103	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908915	17948	40104	513	170

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908922	17949	40105	219	72

Description

GTC ORF with score 101 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0414.) (nt:unnamed protein product) (le:<1) (re:1074) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908923	17950	40106	645	214

Description

6500735509 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0095 HP0095 Helicobacter pylori 210 -11539367 7000690036 hypothetical protein hp0095 (db:pir2.dat) G64531 G64531 Helicobacter pylori 210 -11539367 7500958817 hp0095 h. pylori predicted coding region hp0095 (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3077) (re:3607) (di:complement) HPAE000531 AE000531 g2313182 Helicobacter pylori 210 -11539367 7502853242 hp0095 h. pylori predicted coding region hp0095 (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3077) (re:3607) (di:complement) HPAE000531 AE000531 g2313182 Helicobacter pylori 26695 85962 -11539367

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908928	17951	40107	327	108

Description

6500735510 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0097 HP0097 Helicobacter pylori 210 -11539368 7000690037 hypothetical protein hp0097 (db:pir2.dat) A64532 A64532 Helicobacter pylori 210 -11539368 7500958818 hp0097 h. pylori predicted coding region hp0097 (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4781) (re:5494) (di:complement) HPAE000531 AE000531 g2313183 Helicobacter pylori 210 -11539368 7502853243 hp0097 h. pylori predicted coding region hp0097 (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4781) (re:5494) (di:complement) HPAE000531 AE000531 g2313183 Helicobacter pylori 26695 85962 -11539368

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908930	17952	40108	186	61

Description

GTC ORF with score 99 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0414.) (nt:unnamed protein product) (le:<1) (re:1074) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908931	17953	40109	411	136

Description

6500735511 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0101 HP0101 Helicobacter pylori 210 -11539369 7000690038 hypothetical protein hp0101 (db:pir2.dat) E64532 E64532 Helicobacter pylori 210 -11539369 7500958819 hp0101 h. pylori predicted coding region hp0101 (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:137) (re:898) (di:direct) HPAE000532 AE000532 g2313193 Helicobacter pylori 210 -11539369 7502853244 hp0101 h. pylori predicted coding region hp0101 (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:137) (re:898) (di:direct) HPAE000532 AE000532 g2313193 Helicobacter pylori 26695 85962 -11539369

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908932	17954	40110	243	80

Description

6500735512 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0108 HP0108 Helicobacter pylori 210 -11539370 7000690039 hypothetical protein hp0108 (db:pir2.dat) D64533 D64533 Helicobacter pylori 210 -11539370 7500958820 hp0108 h. pylori predicted coding region hp0108 (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8125) (re:8685) (di:direct) HPAE000532 AE000532 g2313194 Helicobacter pylori 210 -11539370 7502853245 hp0108 h. pylori predicted coding region hp0108 (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8125) (re:8685) (di:direct) HPAE000532 AE000532 g2313194 Helicobacter pylori 26695 85962 -11539370

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908938	17955	40111	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908963	17956	40112	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908965	17957	40113	735	244

Description

6500735513 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0111 HP0111 Helicobacter pylori 210 -11539371 7000690040 hypothetical protein hp0111 (db:pir2.dat) G64533 G64533 Helicobacter pylori 210 -11539371 7500958821 hp0111 h. pylori predicted coding region hp0111 (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11489) (re:12319) (di:complement) HPAE000532 AE000532 g2313195 Helicobacter pylori 210 -11539371 7502853246 hp0111 h. pylori predicted coding region hp0111 (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11489) (re:12319) (di:complement) HPAE000532 AE000532 g2313195 Helicobacter pylori 26695 85962 -11539371

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908966	17958	40114	345	114

Description

6500735514 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0112 HP0112 Helicobacter pylori 210 -11539372 7000690041 hypothetical protein hp0112 (db:pir2.dat) H64533 H64533 Helicobacter pylori 210 -11539372 7500958822 hp0112 h. pylori predicted coding region hp0112 (db:genpept-bct1) (de:helicobacter pylori section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:194) (re:889) (di:direct) HPAE000533 AE000533 g2313200 Helicobacter pylori 210 -11539372 7502853247 hp0112 h. pylori predicted coding region hp0112 (db:genpept) (de:helicobacter pylori 26695 section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:194) (re:889) (di:direct) HPAE000533 AE000533 g2313200 Helicobacter pylori 26695 85962 -11539372

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908967	17959	40115	1215	404

Description

6500735515 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0113 HP0113 Helicobacter pylori 210 -11539373 7000690042 hypothetical protein hp0113 (db:pir2.dat) A64534 A64534 Helicobacter pylori 210 -11539373 7500958823 hp0113 h. pylori predicted coding region hp0113 (db:genpept-bct1) (de:helicobacter pylori section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:910) (re:1206) (di:direct) HPAE000533 AE000533 g2313201 Helicobacter pylori 210 -11539373 7502853248 hp0113 h. pylori predicted coding region hp0113 (db:genpept) (de:helicobacter pylori 26695 section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:910) (re:1206) (di:direct) HPAE000533 AE000533 g2313201 Helicobacter pylori 26695 85962 -11539373

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908968	17960	40116	246	81

Description

6500735516 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0114 HP0114 Helicobacter pylori 210 -11539374 7000690043 hypothetical protein hp0114 (db:pir2.dat) B64534 B64534 Helicobacter pylori 210 -11539374 7500958824 hp0114 h. pylori predicted coding region hp0114 (db:genpept-bct1) (de:helicobacter pylori section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1216) (re:3102) (di:complement) HPAE000533 AE000533 g2313202 Helicobacter pylori 210 -11539374 7502853249 hp0114 h. pylori predicted coding region hp0114 (db:genpept) (de:helicobacter pylori 26695 section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1216) (re:3102) (di:complement) HPAE000533 AE000533 g2313202 Helicobacter pylori 26695 85962 -11539374

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908977	17961	40117	390	129

Description

6500735517 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0118 HP0118 Helicobacter pylori 210 -11539375 7000690044 hypothetical protein hp0118 (db:pir2.dat) F64534 F64534 Helicobacter pylori 210 -11539375 7500958825 hp0118 h. pylori predicted coding region hp0118 (db:genpept-bct1) (de:helicobacter pylori section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8145) (re:9332) (di:complement) HPAE000533 AE000533 g2313203 Helicobacter pylori 210 -11539375 7502853250 hp0118 h. pylori predicted coding region hp0118 (db:genpept) (de:helicobacter pylori 26695 section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8145) (re:9332) (di:complement) HPAE000533 AE000533 g2313203 Helicobacter pylori 26695 85962 -11539375

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908978	17962	40118	438	145

Description

6500735518 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0119 HP0119 Helicobacter pylori 210 -11539376 7000690045 hypothetical protein hp0119 (db:pir2.dat) G64534 G64534 Helicobacter pylori 210 -11539376 7500958826 hp0119 h. pylori predicted coding region hp0119 (db:genpept-bct1) (de:helicobacter pylori section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9597) (re:10982) (di:complement) HPAE000533 AE000533 g2313204 Helicobacter pylori 210 -11539376 7502853251 hp0119 h. pylori predicted coding region hp0119 (db:genpept) (de:helicobacter pylori 26695 section 11 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9597) (re:10982) (di:complement) HPAE000533 AE000533 g2313204 Helicobacter pylori 26695 85962 -11539376

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908980	17963	40119	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908987	17964	40120	384	127

Description

6500735519 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0120 HP0120 Helicobacter pylori 210 -11539377 7000690046 hypothetical protein hp0120 (db:pir2.dat) H64534 H64534 Helicobacter pylori 210 -11539377 7500958827 hp0120 h. pylori predicted coding region hp0120 (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:173) (re:1369) (di:complement) HPAE000534 AE000534 g2313211 Helicobacter pylori 210 -11539377 7502853252 hp0120 h. pylori predicted coding region hp0120 (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:173) (re:1369) (di:complement) HPAE000534 AE000534 g2313211 Helicobacter pylori 26695 85962 -11539377

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908988	17965	40121	867	288

Description

6500735520 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0122 HP0122 Helicobacter pylori 210 -11539378 7000690047 hypothetical protein hp0122 (db:pir2.dat) B64535 B64535 Helicobacter pylori 210 -11539378 7500958828 hp0122 h. pylori predicted coding region hp0122 (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4091) (re:4222) (di:direct) HPAE000534 AE000534 g2313215 Helicobacter pylori 210 -11539378 7502853253 jhp0112 putative (db:genpept) (de:helicobacter pylori, strain j99 section 11 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0122) (le:7349) (re:7480) (di:direct) AE001450 AE001450 g4154620 Helicobacter pylori J99 85963 -11539378 7502853254 hp0122 h. pylori predicted coding region hp0122 (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4091) (re:4222) (di:direct) HPAE000534 AE000534 g2313215 Helicobacter pylori 26695 85962 -11539378

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501908991	17966	40122	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909013	17967	40123	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909014	17968	40124	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909044	17969	40125	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909052	17970	40126	312	103

Description

6500735521 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0128 HP0128 Helicobacter pylori 210 -11539379 7000690048 hypothetical protein hp0128 (db:pir2.dat) H64535 H64535 Helicobacter pylori 210 -11539379 7500958829 hp0128 h. pylori predicted coding region hp0128 (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8439) (re:8564) (di:direct) HPAE000534 AE000534 g2313216 Helicobacter pylori 210 -11539379 7502853255 hp0128 h. pylori predicted coding region hp0128 (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8439) (re:8564) (di:direct) HPAE000534 AE000534 g2313216 Helicobacter pylori 26695 85962 -11539379

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909059	17971	40127	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909061	17972	40128	711	236

Description

6500735522 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0129 HP0129 Helicobacter pylori 210 -11539380 7000690049 hypothetical protein hp0129 (db:pir2.dat) A64536 A64536 Helicobacter pylori 210 -11539380 7500958830 hp0129 h. pylori predicted coding region hp0129 (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8737) (re:9162) (di:direct) HPAE000534 AE000534 g2313213 Helicobacter pylori 210 -11539380 7502853256 hp0129 h. pylori predicted coding region hp0129 (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8737) (re:9162) (di:direct) HPAE000534 AE000534 g2313213 Helicobacter pylori 26695 85962 -11539380

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909065	17973	40129	1509	502

Description

6500735523 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0130 HP0130 Helicobacter pylori 210 -11539381 7000690050 hypothetical protein hp0130 (db:pir2.dat) B64536 B64536 Helicobacter pylori 210 -11539381 7500958831 hp0130 h. pylori predicted coding region hp0130 (db:genpept-bct1) (de:helicobacter pylori section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9573) (re:10433) (di:direct) HPAE000534 AE000534 g2313214 Helicobacter pylori 210 -11539381 7502853257 hp0130 h. pylori predicted coding region hp0130 (db:genpept) (de:helicobacter pylori 26695 section 12 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9573) (re:10433) (di:direct) HPAE000534 AE000534 g2313214 Helicobacter pylori 26695 85962 -11539381

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909081	17974	40130	552	183

Description

6500735524 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0131 HP0131 Helicobacter pylori 210 -11539382 7000690051 hypothetical protein hp0131 (db:pir2.dat) C64536 C64536 Helicobacter pylori 210 -11539382 7500958832 hp0131 h. pylori predicted coding region hp0131 (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:388) (re:489) (di:direct) HPAE000535 AE000535 g2313229 Helicobacter pylori 210 -11539382 7502853258 hp0131 h. pylori predicted coding region hp0131 (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:388) (re:489) (di:direct) HPAE000535 AE000535 g2313229 Helicobacter pylori 26695 85962 -11539382

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909101	17975	40131	873	290

Description

7500958834 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0135 HP0135 Helicobacter pylori 210 -11539383 7000690052 hypothetical protein hp0135 (db:pir2.dat) G64536 G64536 Helicobacter pylori 210 -11539383 7500958833 hp0135 h. pylori predicted coding region hp0135 (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4804) (re:4938) (di:direct) HPAE000535 AE000535 g2313228 Helicobacter pylori 210 -11539383 7502853259 jhp0123 putative (db:genpept) (de:helicobacter pylori, strain j99 section 12 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0135) (le:8727) (re:8861) (di:direct) AE001451 AE001451 g4154630 Helicobacter pylori J99 85963 -11539383 6500735525 hp0135 h. pylori predicted coding region hp0135 (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4804) (re:4938) (di:direct) HPAE000535 AE000535 g2313228 Helicobacter pylori 26695 85962 -11539383

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909121	17976	40132	1146	381

Description

6500735526 bacterioferritin comigratory protein:bcp (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0136 HP0136 Helicobacter pylori 210 -11539384 5500684933 bcp:hp0136 (sr:,campylobacter pylori) (de:bacterioferritin comigratory protein homolog) (db:swissprot) BCP_HELPY P55979 HELICOBACTER PYLORI 210 -11539384 7000684690 bacterioferritin comigratory protein (cl:bacterioferritin comigratory protein:alkyl hydroperoxidase c22 protein homology) (db:pir2.dat) H64536 H64536 Helicobacter pylori 210 -11539384 7500877729 hp0136 bacterioferritin comigratory protein bcp (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:similar to egad:18740 percent identity: 35.53;) (le:5173) (re:5631) (di:complement) HPAE000535 AE000535 g2313221 Helicobacter pylori 210 -11539384 7502853260 hp0136 bacterioferritin comigratory protein bcp (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:similar to egad:18740 percent identity: 35.53;) (le:5173) (re:5631) (di:complement) HPAE000535 AE000535 g2313221 Helicobacter pylori 26695 85962 -11539384

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909122	17977	40133	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909133	17978	40134	195	64

Description

6500735527 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0137 HP0137 Helicobacter pylori 210 -11539385 7000690053 hypothetical protein hp0137 (db:pir2.dat) A64537 A64537 Helicobacter pylori 210 -11539385 7500958835 hp0137 h. pylori predicted coding region hp0137 (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5641) (re:6276) (di:complement) HPAE000535 AE000535 g2313227 Helicobacter pylori 210 -11539385 7502853261 hp0137 h. pylori predicted coding region hp0137 (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5641) (re:6276) (di:complement) HPAE000535 AE000535 g2313227 Helicobacter pylori 26695 85962 -11539385

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909134	17979	40135	963	320

Description

6500735528 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0148 HP0148 Helicobacter pylori 210 -11539386 7000690054 hypothetical protein hp0148 (db:pir2.dat) D64538 D64538 Helicobacter pylori 210 -11539386 7500958836 hp0148 h. pylori predicted coding region hp0148 (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3411) (re:3617) (di:direct) HPAE000536 AE000536 g2313246 Helicobacter pylori 210 -11539386 7502853262 hp0148 h. pylori predicted coding region hp0148 (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3411) (re:3617) (di:direct) HPAE000536 AE000536 g2313246 Helicobacter pylori 26695 85962 -11539386

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909138	17980	40136	450	149

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909139	17981	40137	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909140	17982	40138	684	227

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909155	17983	40139	240	79

Description

GTC ORF with score 170 to: (fn:converts phenylacetaldehyde to phenylacetic) (db:genpept-bct1) (de:pseudomonas sp. vlb120 styrene degradation genes includinghistidine kinase (stdsc) gene, partial cds; and transcriptionalactivator (stdr), styrene ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909185	17984	40140	513	170

Description

6500735529 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0149 HP0149 Helicobacter pylori 210 -11539387 7000690055 hypothetical protein hp0149 (db:pir2.dat) E64538 E64538 Helicobacter pylori 210 -11539387 7500958837 hp0149 h. pylori predicted coding region hp0149 (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3718) (re:4302) (di:direct) HPAE000536 AE000536 g2313240 Helicobacter pylori 210 -11539387 7502853263 hp0149 h. pylori predicted coding region hp0149 (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3718) (re:4302) (di:direct) HPAE000536 AE000536 g2313240 Helicobacter pylori 26695 85962 -11539387

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909198	17985	40141	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909215	17986	40142	345	114

Description

6500735530 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0150 HP0150 Helicobacter pylori 210 -11539388 7000690056 hypothetical protein hp0150 (db:pir2.dat) F64538 F64538 Helicobacter pylori 210 -11539388 7500958838 hp0150 h. pylori predicted coding region hp0150 (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4315) (re:4905) (di:direct) HPAE000536 AE000536 g2313241 Helicobacter pylori 210 -11539388 7502853264 hp0150 h. pylori predicted coding region hp0150 (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4315) (re:4905) (di:direct) HPAE000536 AE000536 g2313241 Helicobacter pylori 26695 85962 -11539388

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909216	17987	40143	198	65

Description

6500735531 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0152 HP0152 Helicobacter pylori 210 -11539389 7000690057 hypothetical protein hp0152 (cl:hypothetical protein hp0152) (db:pir2.dat) H64538 H64538 Helicobacter pylori 210 -11539389 7500958839 hp0152 h. pylori predicted coding region hp0152 (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5747) (re:6610) (di:complement) HPAE000536 AE000536 g2313242 Helicobacter pylori 210 -11539389 7502853265 hp0152 h. pylori predicted coding region hp0152 (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5747) (re:6610) (di:complement) HPAE000536 AE000536 g2313242 Helicobacter pylori 26695 85962 -11539389

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909226	17988	40144	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909229	17989	40145	183	60

Description

GTC ORF with score 186 to: (fn:catalyzes hydroxylation at c-15 of) (db:genpept-pln1) (de:fusarium sporotrichioides isotrichodermin c-15 hydroxylase (tri11)gene, complete cds.) (nt:cytochrome p450 monooxygenase) (le:189:286:1132:1526:1757) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909234	17990	40146	258	85

Description

GTC ORF with score 189 to: (db:genpept-pln2) (de:emericella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj),(stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909238	17991	40147	192	63

Description

GTC ORF with score 129 to: (fn:catalyzes hydroxylation at c-15 of) (db:genpept-pln1) (de:fusarium sporotrichioides isotrichodermin c-15 hydroxylase (tri11)gene, complete cds.) (nt:cytochrome p450 monooxygenase) (le:189:286:1132:1526:1757) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909239	17992	40148	276	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909245	17993	40149	690	229

Description

GTC ORF with score 302 to: (fn:catalyzes hydroxylation at c-15 of) (db:genpept-pln1) (de:fusarium sporotrichioides isotrichodermin c-15 hydroxylase (tri11)gene, complete cds.) (nt:cytochrome p450 monooxygenase) (le:189:286:1132:1526:1757) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909246	17994	40150	378	125

Description

GTC ORF with score 242 to: (fn:catalyzes hydroxylation at c-15 of) (db:genpept-pln1) (de:fusarium sporotrichioides isotrichodermin c-15 hydroxylase (tri11)gene, complete cds.) (nt:cytochrome p450 monooxygenase) (le:189:286:1132:1526:1757) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909249	17995	40151	1590	529

Description

6500735532 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0155 HP0155 Helicobacter pylori 210 -11539390 7000690058 hypothetical protein hp0155 (db:pir2.dat) C64539 C64539 Helicobacter pylori 210 -11539390 7500958840 hp0155 h. pylori predicted coding region hp0155 (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9037) (re:9312) (di:direct) HPAE000536 AE000536 g2313243 Helicobacter pylori 210 -11539390 7502853266 hp0155 h. pylori predicted coding region hp0155 (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9037) (re:9312) (di:direct) HPAE000536 AE000536 g2313243 Helicobacter pylori 26695 85962 -11539390

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909256	17996	40152	1071	356

Description

6500735533 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0156 HP0156 Helicobacter pylori 210 -11539391 7000690059 hypothetical protein hp0156 (db:pir2.dat) D64539 D64539 Helicobacter pylori 210 -11539391 7500958841 hp0156 h. pylori predicted coding region hp0156 (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9324) (re:9926) (di:direct) HPAE000536 AE000536 g2313244 Helicobacter pylori 210 -11539391 7502853267 hp0156 h. pylori predicted coding region hp0156 (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9324) (re:9926) (di:direct) HPAE000536 AE000536 g2313244 Helicobacter pylori 26695 85962 -11539391

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909257	17997	40153	507	168

Description

6500735534 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0158 HP0158 Helicobacter pylori 210 -11539392 7000690060 hypothetical protein hp0158 (db:pir2.dat) F64539 F64539 Helicobacter pylori 210 -11539392 7500958842 hp0158 h. pylori predicted coding region hp0158 (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10441) (re:11397) (di:direct) HPAE000536 AE000536 g2313245 Helicobacter pylori 210 -11539392 7502853268 hp0158 h. pylori predicted coding region hp0158 (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10441) (re:11397) (di:direct) HPAE000536 AE000536 g2313245 Helicobacter pylori 26695 85962 -11539392

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909269	17998	40154	360	119

Description

6500735535 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0161 HP0161 Helicobacter pylori 210 -11539393 7000690061 hypothetical protein hp0161 (db:pir2.dat) A64540 A64540 Helicobacter pylori 210 -11539393 7500958843 hp0161 h. pylori predicted coding region hp0161 (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1369) (re:1479) (di:direct) HPAE000537 AE000537 g2313262 Helicobacter pylori 210 -11539393 7502853269 hp0161 h. pylori predicted coding region hp0161 (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1369) (re:1479) (di:direct) HPAE000537 AE000537 g2313262 Helicobacter pylori 26695 85962 -11539393

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909271	17999	40155	300	99

Description

6500735536 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0165 HP0165 Helicobacter pylori 210 -11539394 7000690062 hypothetical protein hp0165 (db:pir2.dat) E64540 E64540 Helicobacter pylori 210 -11539394 7500958844 hp0165 h. pylori predicted coding region hp0165 (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4455) (re:4976) (di:complement) HPAE000537 AE000537 g2313257 Helicobacter pylori 210 -11539394 7502853270 hp0165 h. pylori predicted coding region hp0165 (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4455) (re:4976) (di:complement) HPAE000537 AE000537 g2313257 Helicobacter pylori 26695 85962 -11539394

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909291	18000	40156	648	215

Description

6500735537 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0167 HP0167 Helicobacter pylori 210 -11539395 7000690063 hypothetical protein hp0167 (db:pir2.dat) G64540 G64540 Helicobacter pylori 210 -11539395 7500958845 hp0167 h. pylori predicted coding region hp0167 (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5915) (re:6388) (di:complement) HPAE000537 AE000537 g2313258 Helicobacter pylori 210 -11539395 7502853271 hp0167 h. pylori predicted coding region hp0167 (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5915) (re:6388) (di:complement) HPAE000537 AE000537 g2313258 Helicobacter pylori 26695 85962 -11539395

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909292	18001	40157	243	80

Description

6500735538 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0168 HP0168 Helicobacter pylori 210 -11539396 7000690064 hypothetical protein hp0168 (db:pir2.dat) H64540 H64540 Helicobacter pylori 210 -11539396 7500958846 hp0168 h. pylori predicted coding region hp0168 (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6367) (re:6630) (di:complement) HPAE000537 AE000537 g2313259 Helicobacter pylori 210 -11539396 7502853272 hp0168 h. pylori predicted coding region hp0168 (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6367) (re:6630) (di:complement) HPAE000537 AE000537 g2313259 Helicobacter pylori 26695 85962 -11539396

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909301	18002	40158	339	112

Description

6500735539 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0170 HP0170 Helicobacter pylori 210 -11539397 7000690065 hypothetical protein hp0170 (db:pir2.dat) B64541 B64541 Helicobacter pylori 210 -11539397 7500958847 hp0170 h. pylori predicted coding region hp0170 (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7948) (re:8709) (di:complement) HPAE000537 AE000537 g2313260 Helicobacter pylori 210 -11539397 7502853273 hp0170 h. pylori predicted coding region hp0170 (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7948) (re:8709) (di:complement) HPAE000537 AE000537 g2313260 Helicobacter pylori 26695 85962 -11539397

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909308	18003	40159	462	153

Description

6500735540 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0174 HP0174 Helicobacter pylori 210 -11539398 7000690066 hypothetical protein hp0174 (db:pir2.dat) F64541 F64541 Helicobacter pylori 210 -11539398 7500958848 hp0174 h. pylori predicted coding region hp0174 (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11882) (re:12658) (di:complement) HPAE000537 AE000537 g2313261 Helicobacter pylori 210 -11539398 7502853274 hp0174 h. pylori predicted coding region hp0174 (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11882) (re:12658) (di:complement) HPAE000537 AE000537 g2313261 Helicobacter pylori 26695 85962 -11539398

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909315	18004	40160	345	114

Description

6500735541 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0181 HP0181 Helicobacter pylori 210 -11539399 7000690067 hypothetical protein hp0181 (db:pir2.dat) E64542 E64542 Helicobacter pylori 210 -11539399 7500958849 hp0181 h. pylori predicted coding region hp0181 (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6378) (re:7052) (di:direct) HPAE000538 AE000538 g2313272 Helicobacter pylori 210 -11539399 7502853275 hp0181 h. pylori predicted coding region hp0181 (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6378) (re:7052) (di:direct) HPAE000538 AE000538 g2313272 Helicobacter pylori 26695 85962 -11539399

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909317	18005	40161	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909334	18006	40162	561	186

Description

6500735542 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0184 HP0184 Helicobacter pylori 210 -11539400 7000690068 hypothetical protein hp0184 (db:pir2.dat) H64542 H64542 Helicobacter pylori 210 -11539400 7500958850 hp0184 h. pylori predicted coding region hp0184 (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9828) (re:10370) (di:direct) HPAE000538 AE000538 g2313273 Helicobacter pylori 210 -11539400 7502853276 hp0184 h. pylori predicted coding region hp0184 (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9828) (re:10370) (di:direct) HPAE000538 AE000538 g2313273 Helicobacter pylori 26695 85962 -11539400

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909336	18007	40163	471	156

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909350	18008	40164	885	294

Description

6500735543 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0185 HP0185 Helicobacter pylori 210 -11539401 7000690069 hypothetical protein hp0185 (db:pir2.dat) A64543 A64543 Helicobacter pylori 210 -11539401 7500958851 hp0185 h. pylori predicted coding region hp0185 (db:genpept-bct1) (de:helicobacter pylori section 16 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10392) (re:11195) (di:direct) HPAE000538 AE000538 g2313274 Helicobacter pylori 210 -11539401 7502853277 hp0185 h. pylori predicted coding region hp0185 (db:genpept) (de:helicobacter pylori 26695 section 16 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10392) (re:11195) (di:direct) HPAE000538 AE000538 g2313274 Helicobacter pylori 26695 85962 -11539401

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909351	18009	40165	1401	466

Description

6500735544 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0186 HP0186 Helicobacter pylori 210 -11539402 7000690070 hypothetical protein hp0186 (db:pir2.dat) B64543 B64543 Helicobacter pylori 210 -11539402 7500958852 hp0186 h. pylori predicted coding region hp0186 (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:228) (re:1442) (di:complement) HPAE000539 AE000539 g2313284 Helicobacter pylori 210 -11539402 7502853278 hp0186 h. pylori predicted coding region hp0186 (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:228) (re:1442) (di:complement) HPAE000539 AE000539 g2313284 Helicobacter pylori 26695 85962 -11539402

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909352	18010	40166	900	299

Description

6500735545 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0187 HP0187 Helicobacter pylori 210 -11539403 7000690071 hypothetical protein hp0187 (db:pir2.dat) C64543 C64543 Helicobacter pylori 210 -11539403 7500958853 hp0187 h. pylori predicted coding region hp0187 (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1469) (re:1756) (di:complement) HPAE000539 AE000539 g2313285 Helicobacter pylori 210 -11539403 7502853279 hp0187 h. pylori predicted coding region hp0187 (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1469) (re:1756) (di:complement) HPAE000539 AE000539 g2313285 Helicobacter pylori 26695 85962 -11539403

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909353	18011	40167	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909372	18012	40168	333	110

Description

6500735546 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0188 HP0188 Helicobacter pylori 210 -11539404 7000690072 hypothetical protein hp0188 (db:pir2.dat) D64543 D64543 Helicobacter pylori 210 -11539404 7500958854 hp0188 h. pylori predicted coding region hp0188 (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1817) (re:1918) (di:complement) HPAE000539 AE000539 g2313286 Helicobacter pylori 210 -11539404 7502853280 hp0188 h. pylori predicted coding region hp0188 (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1817) (re:1918) (di:complement) HPAE000539 AE000539 g2313286 Helicobacter pylori 26695 85962 -11539404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909393	18013	40169	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909399	18014	40170	204	67

Description

6500735547 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0199 HP0199 Helicobacter pylori 210 -11539405 7000690073 hypothetical protein hp0199 (db:pir2.dat) G64544 G64544 Helicobacter pylori 210 -11539405 7500958855 hp0199 h. pylori predicted coding region hp0199 (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1726) (re:2082) (di:direct) HPAE000540 AE000540 g2313294 Helicobacter pylori 210 -11539405 7502853281 hp0199 h. pylori predicted coding region hp0199 (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1726) (re:2082) (di:direct) HPAE000540 AE000540 g2313294 Helicobacter pylori 26695 85962 -11539405

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909406	18015	40171	1227	408

Description

6500735548 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0203 HP0203 Helicobacter pylori 210 -11539406 7000690074 hypothetical protein hp0203 (db:pir2.dat) C64545 C64545 Helicobacter pylori 210 -11539406 7500958856 hp0203 h. pylori predicted coding region hp0203 (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4377) (re:4652) (di:direct) HPAE000540 AE000540 g2313295 Helicobacter pylori 210 -11539406 7502853282 hp0203 h. pylori predicted coding region hp0203 (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4377) (re:4652) (di:direct) HPAE000540 AE000540 g2313295 Helicobacter pylori 26695 85962 -11539406

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909422	18016	40172	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909425	18017	40173	297	98

Description

6500735549 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0204 HP0204 Helicobacter pylori 210 -11539407 7000690075 hypothetical protein hp0204 (db:pir2.dat) D64545 D64545 Helicobacter pylori 210 -11539407 7500958857 hp0204 h. pylori predicted coding region hp0204 (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5311) (re:5694) (di:complement) HPAE000540 AE000540 g2313296 Helicobacter pylori 210 -11539407 7502853283 hp0204 h. pylori predicted coding region hp0204 (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5311) (re:5694) (di:complement) HPAE000540 AE000540 g2313296 Helicobacter pylori 26695 85962 -11539407

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909431	18018	40174	681	226

Description

6500735550 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0205 HP0205 Helicobacter pylori 210 -11539408 7000690076 hypothetical protein hp0205 (db:pir2.dat) E64545 E64545 Helicobacter pylori 210 -11539408 7500958858 hp0205 h. pylori predicted coding region hp0205 (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5710) (re:8091) (di:complement) HPAE000540 AE000540 g2313297 Helicobacter pylori 210 -11539408 7502853284 hp0205 h. pylori predicted coding region hp0205 (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5710) (re:8091) (di:complement) HPAE000540 AE000540 g2313297 Helicobacter pylori 26695 85962 -11539408

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909439	18019	40175	318	105

Description

6500735551 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0206 HP0206 Helicobacter pylori 210 -11539409 7000690077 hypothetical protein hp0206 (db:pir2.dat) F64545 F64545 Helicobacter pylori 210 -11539409 7500958859 hp0206 h. pylori predicted coding region hp0206 (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8295) (re:8621) (di:complement) HPAE000540 AE000540 g2313298 Helicobacter pylori 210 -11539409 7502853285 hp0206 h. pylori predicted coding region hp0206 (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8295) (re:8621) (di:complement) HPAE000540 AE000540 g2313298 Helicobacter pylori 26695 85962 -11539409

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909470	18020	40176	417	138

Description

6500735552 atp-binding protein:mpr (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0207 HP0207 Helicobacter pylori 210 -11539410 7500885884 mrp:hp0207 (sr:,campylobacter pylori) (de:mrp protein homolog) (db:swissprot) MRP_HELPY O24999 HELICOBACTER PYLORI 210 -11539410 7000689651 atp-binding protein (cl:conserved probable membrane protein yil003w) (db:pir2.dat) G64545 G64545 Helicobacter pylori 210 -11539410 7500885886 hp0207 atp-binding protein mpr (db:genpept-bct1) (de:helicobacter pylori section 18 of 134 of the complete genome.) (nt:similar to egad:10837 percent identity: 38.94;) (le:8586) (re:9824) (di:direct) HPAE000540 AE000540 g2313292 Helicobacter pylori 210 -11539410 7502853286 hp0207 atp-binding protein mpr (db:genpept) (de:helicobacter pylori 26695 section 18 of 134 of the complete genome.) (nt:similar to egad:10837 percent identity: 38.94;) (le:8586) (re:9824) (di:direct) HPAE000540 AE000540 g2313292 Helicobacter pylori 26695 85962 -11539410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909472	18021	40177	1395	464

Description

6500735553 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0209 HP0209 Helicobacter pylori 210 -11539411 7000690078 hypothetical protein hp0209 (db:pir2.dat) A64546 A64546 Helicobacter pylori 210 -11539411 7500958860 hp0209 h. pylori predicted coding region hp0209 (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:107) (re:1459) (di:direct) HPAE000541 AE000541 g2313307 Helicobacter pylori 210 -11539411 7502853287 hp0209 h. pylori predicted coding region hp0209 (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:107) (re:1459) (di:direct) HPAE000541 AE000541 g2313307 Helicobacter pylori 26695 85962 -11539411

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909473	18022	40178	1329	442

Description

GTC ORF with score 130 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid zc449.) (nt:coded for by c. elegans cdna yk61e11.3; coded for) (le:30120:30310:30457) (re:30261:30413:31468) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909475	18023	40179	204	67

Description

6500735554 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0217 HP0217 Helicobacter pylori 210 -11539412 7000690079 hypothetical protein hp0217 (db:pir2.dat) A64547 A64547 Helicobacter pylori 210 -11539412 7500958861 hp0217 h. pylori predicted coding region hp0217 (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:contingency gene.; hypothetical protein; identified) (le:11211) (re:12353) (di:direct) HPAE000541 AE000541 g2313308 Helicobacter pylori 210 -11539412 7502853288 hp0217 h. pylori predicted coding region hp0217 (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:contingency gene.; hypothetical protein; identified) (le:11211) (re:12353) (di:direct) HPAE000541 AE000541 g2313308 Helicobacter pylori 26695 85962 -11539412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909483	18024	40180	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909487	18025	40181	1776	591

Description

6500735555 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0218 HP0218 Helicobacter pylori 210 -11539413 7000690080 hypothetical protein hp0218 (db:pir2.dat) B64547 B64547 Helicobacter pylori 210 -11539413 7500958862 hp0218 h. pylori predicted coding region hp0218 (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12369) (re:12920) (di:complement) HPAE000541 AE000541 g2313309 Helicobacter pylori 210 -11539413 7502853289 hp0218 h. pylori predicted coding region hp0218 (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12369) (re:12920) (di:complement) HPAE000541 AE000541 g2313309 Helicobacter pylori 26695 85962 -11539413

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909491	18026	40182	183	60

Description

6500735556 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0219 HP0219 Helicobacter pylori 210 -11539414 7000690081 hypothetical protein hp0219 (db:pir2.dat) C64547 C64547 Helicobacter pylori 210 -11539414 7500958863 hp0219 h. pylori predicted coding region hp0219 (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:94) (re:573) (di:direct) HPAE000542 AE000542 g2313318 Helicobacter pylori 210 -11539414 7502853290 hp0219 h. pylori predicted coding region hp0219 (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:94) (re:573) (di:direct) HPAE000542 AE000542 g2313318 Helicobacter pylori 26695 85962 -11539414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909506	18027	40183	327	108

Description

6500735557 nifu-like protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0221 HP0221 Helicobacter pylori 210 -11539415 7000690559 nifu-like protein (cl:helicobacter nitrogen fixation protein:nitrogen fixation protein homology) (db:pir2.dat) E64547 E64547 Helicobacter pylori 210 -11539415 7500953961 hp0221 nifu-like protein (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:similar to egad:42702 percent identity: 37.33;) (le:1932) (re:2912) (di:direct) HPAE000542 AE000542 g2313312 Helicobacter pylori 210 -11539415 7502853291 hp0221 nifu-like protein (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:similar to egad:42702 percent identity: 37.33;) (le:1932) (re:2912) (di:direct) HPAE000542 AE000542 g2313312 Helicobacter pylori 26695 85962 -11539415

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909511	18028	40184	285	94

Description

6500735558 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0222 HP0222 Helicobacter pylori 210 -11539416 7000690082 hypothetical protein hp0222 (db:pir2.dat) F64547 F64547 Helicobacter pylori 210 -11539416 7500958864 hp0222 h. pylori predicted coding region hp0222 (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3059) (re:3280) (di:direct) HPAE000542 AE000542 g2313319 Helicobacter pylori 210 -11539416 7502853292 hp0222 h. pylori predicted coding region hp0222 (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3059) (re:3280) (di:direct) HPAE000542 AE000542 g2313319 Helicobacter pylori 26695 85962 -11539416

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909533	18029	40185	201	66

Description

6500735559 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0225 HP0225 Helicobacter pylori 210 -11539417 7000690083 hypothetical protein hp0225 (db:pir2.dat) A64548 A64548 Helicobacter pylori 210 -11539417 7500958865 hp0225 h. pylori predicted coding region hp0225 (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5989) (re:6057) (di:direct) HPAE000542 AE000542 g2313320 Helicobacter pylori 210 -11539417 7502853293 hp0225 h. pylori predicted coding region hp0225 (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5989) (re:6057) (di:direct) HPAE000542 AE000542 g2313320 Helicobacter pylori 26695 85962 -11539417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909542	18030	40186	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909547	18031	40187	285	94

Description

6500735560 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0231 HP0231 Helicobacter pylori 210 -11539418 7000690084 hypothetical protein hp0231 (db:pir2.dat) G64548 G64548 Helicobacter pylori 210 -11539418 7500958866 hp0231 h. pylori predicted coding region hp0231 (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2580) (re:3377) (di:direct) HPAE000543 AE000543 g2313333 Helicobacter pylori 210 -11539418 7502853294 hp0231 h. pylori predicted coding region hp0231 (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2580) (re:3377) (di:direct) HPAE000543 AE000543 g2313333 Helicobacter pylori 26695 85962 -11539418

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909552	18032	40188	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909559	18033	40189	474	157

Description

6500735561 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0236 HP0236 Helicobacter pylori 210 -11539419 7000690085 hypothetical protein hp0236 (db:pir2.dat) D64549 D64549 Helicobacter pylori 210 -11539419 7500958867 hp0236 h. pylori predicted coding region hp0236 (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7645) (re:8016) (di:complement) HPAE000543 AE000543 g2313334 Helicobacter pylori 210 -11539419 7502853295 hp0236 h. pylori predicted coding region hp0236 (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7645) (re:8016) (di:complement) HPAE000543 AE000543 g2313334 Helicobacter pylori 26695 85962 -11539419

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909583	18034	40190	1485	494

Description

6500735562 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0241 HP0241 Helicobacter pylori 210 -11539420 7000690086 hypothetical protein hp0241 (db:pir2.dat) A64550 A64550 Helicobacter pylori 210 -11539420 7500958868 hp0241 h. pylori predicted coding region hp0241 (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12966) (re:13361) (di:complement) HPAE000543 AE000543 g2313335 Helicobacter pylori 210 -11539420 7502853296 hp0241 h. pylori predicted coding region hp0241 (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12966) (re:13361) (di:complement) HPAE000543 AE000543 g2313335 Helicobacter pylori 26695 85962 -11539420

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909588	18035	40191	423	140

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909589	18036	40192	783	260

Description

6500735563 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0242 HP0242 Helicobacter pylori 210 -11539421 7000690087 hypothetical protein hp0242 (db:pir2.dat) B64550 B64550 Helicobacter pylori 210 -11539421 7500958869 hp0242 h. pylori predicted coding region hp0242 (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13354) (re:13638) (di:complement) HPAE000543 AE000543 g2313336 Helicobacter pylori 210 -11539421 7502853297 hp0242 h. pylori predicted coding region hp0242 (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13354) (re:13638) (di:complement) HPAE000543 AE000543 g2313336 Helicobacter pylori 26695 85962 -11539421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909604	18037	40193	573	190

Description

7500958871 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0245 HP0245 Helicobacter pylori 210 -11539422 7000690088 hypothetical protein hp0245 (db:pir2.dat) E64550 E64550 Helicobacter pylori 210 -11539422 7500958870 hp0245 h. pylori predicted coding region hp0245 (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1275) (re:1592) (di:complement) HPAE000544 AE000544 g2313346 Helicobacter pylori 210 -11539422 7502853298 jhp0230 putative (db:genpept) (de:helicobacter pylori, strain j99 section 22 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0245) (le:1277) (re:1594) (di:complement) AE001461 AE001461 g4154756 Helicobacter pylori J99 85963 -11539422 6500735564 hp0245 h. pylori predicted coding region hp0245 (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1275) (re:1592) (di:complement) HPAE000544 AE000544 g2313346 Helicobacter pylori 26695 85962 -11539422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909607	18038	40194	759	252

Description

6500735565 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0249 HP0249 Helicobacter pylori 210 -11539423 7000690089 hypothetical protein hp0249 (db:pir2.dat) A64551 A64551 Helicobacter pylori 210 -11539423 7500958872 hp0249 h. pylori predicted coding region hp0249 (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5400) (re:5939) (di:direct) HPAE000544 AE000544 g2313347 Helicobacter pylori 210 -11539423 7502853299 hp0249 h. pylori predicted coding region hp0249 (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5400) (re:5939) (di:direct) HPAE000544 AE000544 g2313347 Helicobacter pylori 26695 85962 -11539423

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909608	18039	40195	606	201

Description

6500735566 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0253 HP0253 Helicobacter pylori 210 -11539424 7000690090 hypothetical protein hp0253 (db:pir2.dat) E64551 E64551 Helicobacter pylori 210 -11539424 7500958873 hp0253 h. pylori predicted coding region hp0253 (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10416) (re:10532) (di:direct) HPAE000544 AE000544 g2313348 Helicobacter pylori 210 -11539424 7502853300 hp0253 h. pylori predicted coding region hp0253 (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10416) (re:10532) (di:direct) HPAE000544 AE000544 g2313348 Helicobacter pylori 26695 85962 -11539424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909619	18040	40196	1932	643

Description

6500735567 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0256 HP0256 Helicobacter pylori 210 -11539425 7000690091 hypothetical protein hp0256 (db:pir2.dat) H64551 H64551 Helicobacter pylori 210 -11539425 7500958874 hp0256 h. pylori predicted coding region hp0256 (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1312) (re:1740) (di:direct) HPAE000545 AE000545 g2313360 Helicobacter pylori 210 -11539425 7502853301 hp0256 h. pylori predicted coding region hp0256 (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1312) (re:1740) (di:direct) HPAE000545 AE000545 g2313360 Helicobacter pylori 26695 85962 -11539425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909633	18041	40197	1365	454

Description

6500735568 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0261 HP0261 Helicobacter pylori 210 -11539426 7000690092 hypothetical protein hp0261 (db:pir2.dat) E64552 E64552 Helicobacter pylori 210 -11539426 7500958875 hp0261 h. pylori predicted coding region hp0261 (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5896) (re:6294) (di:complement) HPAE000545 AE000545 g2313361 Helicobacter pylori 210 -11539426 7502853302 hp0261 h. pylori predicted coding region hp0261 (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5896) (re:6294) (di:complement) HPAE000545 AE000545 g2313361 Helicobacter pylori 26695 85962 -11539426

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909642	18042	40198	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909664	18043	40199	552	183

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909672	18044	40200	1158	385

Description

6500735569 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0262 HP0262 Helicobacter pylori 210 -11539427 7500894993 hp0262 (sr:,campylobacter pylori) (de:hypothetical protein hp0262) (db:swissprot) Y262_HELPY O25042 HELICOBACTER PYLORI 210 -11539427 7000690093 hypothetical protein hp0262 (db:pir2.dat) F64552 F64552 Helicobacter pylori 210 -11539427 7500894995 hp0262 h. pylori predicted coding region hp0262 (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6452) (re:7054) (di:direct) HPAE000545 AE000545 g2313362 Helicobacter pylori 210 -11539427 7502853303 hp0262 h. pylori predicted coding region hp0262 (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6452) (re:7054) (di:direct) HPAE000545 AE000545 g2313362 Helicobacter pylori 26695 85962 -11539427

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909685	18045	40201	717	239

Description

6500735570 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0268 HP0268 Helicobacter pylori 210 -11539428 7000690094 hypothetical protein hp0268 (db:pir2.dat) D64553 D64553 Helicobacter pylori 210 -11539428 7500958876 hp0268 h. pylori predicted coding region hp0268 (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:61) (re:303) (di:direct) HPAE000546 AE000546 g2313371 Helicobacter pylori 210 -11539428 7502853304 hp0268 h. pylori predicted coding region hp0268 (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:61) (re:303) (di:direct) HPAE000546 AE000546 g2313371 Helicobacter pylori 26695 85962 -11539428

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909713	18046	40202	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909727	18047	40203	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909728	18048	40204	420	139

Description

6500735571 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0270 HP0270 Helicobacter pylori 210 -11539429 7000690095 hypothetical protein hp0270 (db:pir2.dat) F64553 F64553 Helicobacter pylori 210 -11539429 7500958877 hp0270 h. pylori predicted coding region hp0270 (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1831) (re:2319) (di:direct) HPAE000546 AE000546 g2313372 Helicobacter pylori 210 -11539429 7502853305 hp0270 h. pylori predicted coding region hp0270 (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1831) (re:2319) (di:direct) HPAE000546 AE000546 g2313372 Helicobacter pylori 26695 85962 -11539429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909729	18049	40205	186	61

Description

6500735572 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0271 HP0271 Helicobacter pylori 210 -11539430 7000690096 hypothetical protein hp0271 (db:pir2.dat) G64553 G64553 Helicobacter pylori 210 -11539430 7500958878 hp0271 h. pylori predicted coding region hp0271 (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2312) (re:3295) (di:direct) HPAE000546 AE000546 g2313373 Helicobacter pylori 210 -11539430 7502853306 hp0271 h. pylori predicted coding region hp0271 (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2312) (re:3295) (di:direct) HPAE000546 AE000546 g2313373 Helicobacter pylori 26695 85962 -11539430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909733	18050	40206	732	243

Description

6500735573 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0272 HP0272 Helicobacter pylori 210 -11539431 7000690097 hypothetical protein hp0272 (db:pir2.dat) H64553 H64553 Helicobacter pylori 210 -11539431 7500958879 hp0272 h. pylori predicted coding region hp0272 (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3285) (re:3818) (di:direct) HPAE000546 AE000546 g2313374 Helicobacter pylori 210 -11539431 7502853307 hp0272 h. pylori predicted coding region hp0272 (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3285) (re:3818) (di:direct) HPAE000546 AE000546 g2313374 Helicobacter pylori 26695 85962 -11539431

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909738	18051	40207	1152	383

Description

6500735574 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0273 HP0273 Helicobacter pylori 210 -11539432 7000690098 hypothetical protein hp0273 (db:pir2.dat) A64554 A64554 Helicobacter pylori 210 -11539432 7500958880 hp0273 h. pylori predicted coding region hp0273 (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3815) (re:4354) (di:direct) HPAE000546 AE000546 g2313375 Helicobacter pylori 210 -11539432 7502853308 hp0273 h. pylori predicted coding region hp0273 (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3815) (re:4354) (di:direct) HPAE000546 AE000546 g2313375 Helicobacter pylori 26695 85962 -11539432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909740	18052	40208	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909742	18053	40209	567	188

Description

6500735575 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0276 HP0276 Helicobacter pylori 210 -11539433 7000690099 hypothetical protein hp0276 (db:pir2.dat) D64554 D64554 Helicobacter pylori 210 -11539433 7500958881 hp0276 h. pylori predicted coding region hp0276 (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6086) (re:6643) (di:direct) HPAE000546 AE000546 g2313376 Helicobacter pylori 210 -11539433 7502853309 hp0276 h. pylori predicted coding region hp0276 (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6086) (re:6643) (di:direct) HPAE000546 AE000546 g2313376 Helicobacter pylori 26695 85962 -11539433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909743	18054	40210	597	198

Description

6500735576 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0282 HP0282 Helicobacter pylori 210 -11539434 7000690100 hypothetical protein hp0282 (db:pir2.dat) B64555 B64555 Helicobacter pylori 210 -11539434 7500958882 hp0282 h. pylori predicted coding region hp0282 (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1246) (re:2688) (di:direct) HPAE000547 AE000547 g2313386 Helicobacter pylori 210 -11539434 7502853310 hp0282 h. pylori predicted coding region hp0282 (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1246) (re:2688) (di:direct) HPAE000547 AE000547 g2313386 Helicobacter pylori 26695 85962 -11539434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909744	18055	40211	1704	567

Description

6500735577 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0287 HP0287 Helicobacter pylori 210 -11539435 7000690101 hypothetical protein hp0287 (db:pir2.dat) G64555 G64555 Helicobacter pylori 210 -11539435 7500958883 hp0287 h. pylori predicted coding region hp0287 (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8181) (re:8699) (di:direct) HPAE000547 AE000547 g2313387 Helicobacter pylori 210 -11539435 7502853311 hp0287 h. pylori predicted coding region hp0287 (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8181) (re:8699) (di:direct) HPAE000547 AE000547 g2313387 Helicobacter pylori 26695 85962 -11539435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909767	18056	40212	261	87

Description

6500735578 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0288 HP0288 Helicobacter pylori 210 -11539436 7000690102 hypothetical protein hp0288 (db:pir2.dat) H64555 H64555 Helicobacter pylori 210 -11539436 7500958884 hp0288 h. pylori predicted coding region hp0288 (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8712) (re:9185) (di:direct) HPAE000547 AE000547 g2313388 Helicobacter pylori 210 -11539436 7502853312 hp0288 h. pylori predicted coding region hp0288 (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8712) (re:9185) (di:direct) HPAE000547 AE000547 g2313388 Helicobacter pylori 26695 85962 -11539436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909772	18057	40213	1848	615

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909809	18058	40214	1560	519

Description

6500735579 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0291 HP0291 Helicobacter pylori 210 -11539437 7000690103 hypothetical protein hp0291 (db:pir2.dat) C64556 C64556 Helicobacter pylori 210 -11539437 7500958885 hp0291 h. pylori predicted coding region hp0291 (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:19203) (re:19493) (di:direct) HPAE000547 AE000547 g2313389 Helicobacter pylori 210 -11539437 7502853313 hp0291 h. pylori predicted coding region hp0291 (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:19203) (re:19493) (di:direct) HPAE000547 AE000547 g2313389 Helicobacter pylori 26695 85962 -11539437

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909822	18059	40215	987	328

Description

6500735580 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0292 HP0292 Helicobacter pylori 210 -11539438 7000690104 hypothetical protein hp0292 (db:pir2.dat) D64556 D64556 Helicobacter pylori 210 -11539438 7500958886 hp0292 h. pylori predicted coding region hp0292 (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:19506) (re:20378) (di:direct) HPAE000547 AE000547 g2313390 Helicobacter pylori 210 -11539438 7502853314 hp0292 h. pylori predicted coding region hp0292 (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:19506) (re:20378) (di:direct) HPAE000547 AE000547 g2313390 Helicobacter pylori 26695 85962 -11539438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909832	18060	40216	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909837	18061	40217	606	201

Description

6500735581 gtp-binding protein:obg (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0303 HP0303 Helicobacter pylori 210 -11539439 7500895091 hp0303 (sr:,campylobacter pylori) (de:probable gtp-binding protein hp0303) (db:swissprot) Y303_HELPY O25074 HELICOBACTER PYLORI 210 -11539439 7000689977 gtp-binding protein obg (cl:gtp-binding protein obg:translation elongation factor tu homology) (db:pir1.dat) G64557 G64557 Helicobacter pylori 210 -11539439 7500895093 hp0303 gtp-binding protein obg (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:similar to egad:14915 percent identity: 48.17;) (le:9908) (re:10990) (di:direct) HPAE000548 AE000548 g2313401 Helicobacter pylori 210 -11539439 7502853315 hp0303 gtp-binding protein obg (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:similar to egad:14915 percent identity: 48.17;) (le:9908) (re:10990) (di:direct) HPAE000548 AE000548 g2313401 Helicobacter pylori 26695 85962 -11539439

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909845	18062	40218	285	94

Description

GTC ORF with score 216 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.cerevisiae chromosome xv reading frame) (le:20330:20746)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909846	18063	40219	249	82

Description

6500735582 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0304 HP0304 Helicobacter pylori 210 -11539440 7000690105 hypothetical protein hp0304 (db:pir2.dat) H64557 H64557 Helicobacter pylori 210 -11539440 7500958887 hp0304 h. pylori predicted coding region hp0304 (db:genpept-bct1) (de:helicobacter pylori section 26 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11032) (re:12021) (di:direct) HPAE000548 AE000548 g2313402 Helicobacter pylori 210 -11539440 7502853316 hp0304 h. pylori predicted coding region hp0304 (db:genpept) (de:helicobacter pylori 26695 section 26 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11032) (re:12021) (di:direct) HPAE000548 AE000548 g2313402 Helicobacter pylori 26695 85962 -11539440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909847	18064	40220	216	71

Description

6500735583 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0305 HP0305 Helicobacter pylori 210 -11539441 7000690106 hypothetical protein hp0305 (db:pir2.dat) A64558 A64558 Helicobacter pylori 210 -11539441 7500958888 hp0305 h. pylori predicted coding region hp0305 (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:152) (re:706) (di:direct) HPAE000549 AE000549 g2313411 Helicobacter pylori 210 -11539441 7502853317 hp0305 h. pylori predicted coding region hp0305 (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:152) (re:706) (di:direct) HPAE000549 AE000549 g2313411 Helicobacter pylori 26695 85962 -11539441

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909860	18065	40221	756	251

Description

6500735584 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0307 HP0307 Helicobacter pylori 210 -11539442 7000690107 hypothetical protein hp0307 (db:pir2.dat) C64558 C64558 Helicobacter pylori 210 -11539442 7500958889 hp0307 h. pylori predicted coding region hp0307 (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2005) (re:2277) (di:direct) HPAE000549 AE000549 g2313412 Helicobacter pylori 210 -11539442 7502853318 hp0307 h. pylori predicted coding region hp0307 (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2005) (re:2277) (di:direct) HPAE000549 AE000549 g2313412 Helicobacter pylori 26695 85962 -11539442

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909870	18066	40222	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909871	18067	40223	990	329

Description

6500735585 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0308 HP0308 Helicobacter pylori 210 -11539443 7000690108 hypothetical protein hp0308 (db:pir2.dat) D64558 D64558 Helicobacter pylori 210 -11539443 7500958890 hp0308 h. pylori predicted coding region hp0308 (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2293) (re:2697) (di:direct) HPAE000549 AE000549 g2313413 Helicobacter pylori 210 -11539443 7502853319 hp0308 h. pylori predicted coding region hp0308 (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2293) (re:2697) (di:direct) HPAE000549 AE000549 g2313413 Helicobacter pylori 26695 85962 -11539443

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909884	18068	40224	603	200

Description

6500735586 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0311 HP0311 Helicobacter pylori 210 -11539444 7000690109 hypothetical protein hp0311 (db:pir2.dat) G64558 G64558 Helicobacter pylori 210 -11539444 7500958891 hp0311 h. pylori predicted coding region hp0311 (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4599) (re:4967) (di:direct) HPAE000549 AE000549 g2313414 Helicobacter pylori 210 -11539444 7502853320 hp0311 h. pylori predicted coding region hp0311 (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4599) (re:4967) (di:direct) HPAE000549 AE000549 g2313414 Helicobacter pylori 26695 85962 -11539444

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909892	18069	40225	516	171

Description

6500735587 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0314 HP0314 Helicobacter pylori 210 -11539445 7000690110 hypothetical protein hp0314 (db:pir2.dat) B64559 B64559 Helicobacter pylori 210 -11539445 7500958892 hp0314 h. pylori predicted coding region hp0314 (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7444) (re:7563) (di:direct) HPAE000549 AE000549 g2313416 Helicobacter pylori 210 -11539445 7502853321 hp0314 h. pylori predicted coding region hp0314 (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7444) (re:7563) (di:direct) HPAE000549 AE000549 g2313416 Helicobacter pylori 26695 85962 -11539445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909893	18070	40226	240	79

Description

6500735588 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0316 HP0316 Helicobacter pylori 210 -11539446 7000690111 hypothetical protein hp0316 (db:pir2.dat) D64559 D64559 Helicobacter pylori 210 -11539446 7500958893 hp0316 h. pylori predicted coding region hp0316 (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7844) (re:8236) (di:complement) HPAE000549 AE000549 g2313415 Helicobacter pylori 210 -11539446 7502853322 hp0316 h. pylori predicted coding region hp0316 (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7844) (re:8236) (di:complement) HPAE000549 AE000549 g2313415 Helicobacter pylori 26695 85962 -11539446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909898	18071	40227	639	212

Description

GTC ORF with score 152 to: (sr:human) (db:genpept) (de:homo sapiens s164 gene, partial cds; ps1 and hypothetical proteingenes, complete cds; and s171 gene, partial cds.) (nt:unknown; intron-exon boundaries defined by ests) (le:<1465:5979:14890:17363) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909901	18072	40228	297	98

Description

6500735589 poly e-rich protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0322 HP0322 Helicobacter pylori 210 -11539447 7000690630 poly e-rich protein (db:pir2.dat) B64560 B64560 Helicobacter pylori 210 -11539447 7500959410 hp0322 poly e-rich protein (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to gp:632549 percent identity: 28.74;) (le:3547) (re:5064) (di:complement) HPAE000550 AE000550 g2313421 Helicobacter pylori 210 -11539447 7502853323 hp0322 poly e-rich protein (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to gp:632549 percent identity: 28.74;) (le:3547) (re:5064) (di:complement) HPAE000550 AE000550 g2313421 Helicobacter pylori 26695 85962 -11539447

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909905	18073	40229	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909914	18074	40230	501	166

Description

6500735590 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0335 HP0335 Helicobacter pylori 210 -11539448 7000690112 hypothetical protein hp0335 (db:pir2.dat) G64561 G64561 Helicobacter pylori 210 -11539448 7500958894 hp0335 h. pylori predicted coding region hp0335 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3789) (re:3977) (di:direct) HPAE000551 AE000551 g2313439 Helicobacter pylori 210 -11539448 7502853324 hp0335 h. pylori predicted coding region hp0335 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3789) (re:3977) (di:direct) HPAE000551 AE000551 g2313439 Helicobacter pylori 26695 85962 -11539448

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909920	18075	40231	528	175

Description

GTC ORF with score 507 to: (de:(yal012w) (pn:gamma-cystathionase:cystathionine gamma-lyase) (gn:cyi1:str1:fun35:cys3) (gtcfc:2.6:5.4:6.4) (ec:4.4.1.1) (cys3_yeast) (keggfc:2.5:5.4:6.4) (sgdfc:1.1.1:9.2.0) (db:gtc-saccharomyces cerevisiae))

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909921	18076	40232	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909926	18077	40233	582	193

Description

GTC ORF with score 583 to: (de:(yal012w) (pn:gamma-cystathionase:cystathionine gamma-lyase) (gn:cyi1:str1:fun35:cys3) (gtcfc:2.6:5.4:6.4) (ec:4.4.1.1) (cys3_yeast) (keggfc:2.5:5.4:6.4) (sgdfc:1.1.1:9.2.0) (db:gtc-saccharomyces cerevisiae))

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909934	18078	40234	651	216

Description

6500735591 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0336 HP0336 Helicobacter pylori 210 -11539449 7000690480 invalid gene (db:pir2.dat) H64561 H64561 Helicobacter pylori 210 -11539449 7500959266 hp0336 h. pylori predicted coding region hp0336 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3919) (re:4335) (di:direct) HPAE000551 AE000551 g2313440 Helicobacter pylori 210 -11539449 7502853325 hp0336 h. pylori predicted coding region hp0336 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3919) (re:4335) (di:direct) HPAE000551 AE000551 g2313440 Helicobacter pylori 26695 85962 -11539449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909947	18079	40235	501	166

Description

6500735592 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0337 HP0337 Helicobacter pylori 210 -11539450 7000690113 hypothetical protein hp0337 (db:pir2.dat) A64562 A64562 Helicobacter pylori 210 -11539450 7500958895 hp0337 h. pylori predicted coding region hp0337 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4462) (re:4767) (di:direct) HPAE000551 AE000551 g2313441 Helicobacter pylori 210 -11539450 7502853326 hp0337 h. pylori predicted coding region hp0337 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4462) (re:4767) (di:direct) HPAE000551 AE000551 g2313441 Helicobacter pylori 26695 85962 -11539450

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909955	18080	40236	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909956	18081	40237	924	307

Description

6500735593 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0338 HP0338 Helicobacter pylori 210 -11539451 7000690114 hypothetical protein hp0338 (db:pir2.dat) B64562 B64562 Helicobacter pylori 210 -11539451 7500958896 hp0338 h. pylori predicted coding region hp0338 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4751) (re:5317) (di:direct) HPAE000551 AE000551 g2313442 Helicobacter pylori 210 -11539451 7502853327 hp0338 h. pylori predicted coding region hp0338 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4751) (re:5317) (di:direct) HPAE000551 AE000551 g2313442 Helicobacter pylori 26695 85962 -11539451

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909984	18082	40238	1062	353

Description

6500735594 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0339 HP0339 Helicobacter pylori 210 -11539452 7000690115 hypothetical protein hp0339 (cl:phage t4 lysozyme homology) (db:pir2.dat) C64562 C64562 Helicobacter pylori 210 -11539452 7500958897 hp0339 h. pylori predicted coding region hp0339 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5375) (re:5725) (di:direct) HPAE000551 AE000551 g2313443 Helicobacter pylori 210 -11539452 7502853328 hp0339 h. pylori predicted coding region hp0339 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5375) (re:5725) (di:direct) HPAE000551 AE000551 g2313443 Helicobacter pylori 26695 85962 -11539452

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501909998	18083	40239	1188	395

Description

6500735595 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0340 HP0340 Helicobacter pylori 210 -11539453 7000690116 hypothetical protein hp0340 (db:pir2.dat) D64562 D64562 Helicobacter pylori 210 -11539453 7500958898 hp0340 h. pylori predicted coding region hp0340 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5713) (re:5979) (di:direct) HPAE000551 AE000551 g2313444 Helicobacter pylori 210 -11539453 7502853329 hp0340 h. pylori predicted coding region hp0340 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5713) (re:5979) (di:direct) HPAE000551 AE000551 g2313444 Helicobacter pylori 26695 85962 -11539453

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910000	18084	40240	567	188

Description

6500735596 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0341 HP0341 Helicobacter pylori 210 -11539454 7000690117 hypothetical protein hp0341 (db:pir2.dat) E64562 E64562 Helicobacter pylori 210 -11539454 7500958899 hp0341 h. pylori predicted coding region hp0341 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5991) (re:6086) (di:direct) HPAE000551 AE000551 g2313450 Helicobacter pylori 210 -11539454 7502853330 hp0341 h. pylori predicted coding region hp0341 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5991) (re:6086) (di:direct) HPAE000551 AE000551 g2313450 Helicobacter pylori 26695 85962 -11539454

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910011	18085	40241	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910015	18086	40242	222	73

Description

6500735597 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0342 HP0342 Helicobacter pylori 210 -11539455 7000690118 hypothetical protein hp0342 (db:pir2.dat) F64562 F64562 Helicobacter pylori 210 -11539455 7500958900 hp0342 h. pylori predicted coding region hp0342 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6279) (re:6671) (di:direct) HPAE000551 AE000551 g2313445 Helicobacter pylori 210 -11539455 7502853331 hp0342 h. pylori predicted coding region hp0342 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6279) (re:6671) (di:direct) HPAE000551 AE000551 g2313445 Helicobacter pylori 26695 85962 -11539455

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910017	18087	40243	504	167

Description

6500735598 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0343 HP0343 Helicobacter pylori 210 -11539456 7000690119 hypothetical protein hp0343 (db:pir2.dat) G64562 G64562 Helicobacter pylori 210 -11539456 7500958901 hp0343 h. pylori predicted coding region hp0343 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6671) (re:7093) (di:direct) HPAE000551 AE000551 g2313446 Helicobacter pylori 210 -11539456 7502853332 hp0343 h. pylori predicted coding region hp0343 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6671) (re:7093) (di:direct) HPAE000551 AE000551 g2313446 Helicobacter pylori 26695 85962 -11539456

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910032	18088	40244	720	239

Description

6500735599 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0344 HP0344 Helicobacter pylori 210 -11539457 7000690120 hypothetical protein hp0344 (db:pir2.dat) H64562 H64562 Helicobacter pylori 210 -11539457 7500958902 hp0344 h. pylori predicted coding region hp0344 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6993) (re:7457) (di:direct) HPAE000551 AE000551 g2313447 Helicobacter pylori 210 -11539457 7502853333 hp0344 h. pylori predicted coding region hp0344 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6993) (re:7457) (di:direct) HPAE000551 AE000551 g2313447 Helicobacter pylori 26695 85962 -11539457

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910036	18089	40245	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910039	18090	40246	312	103

Description

6500735600 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0345 HP0345 Helicobacter pylori 210 -11539458 7000690121 hypothetical protein hp0345 (db:pir2.dat) A64563 A64563 Helicobacter pylori 210 -11539458 7500958903 hp0345 h. pylori predicted coding region hp0345 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7447) (re:7782) (di:direct) HPAE000551 AE000551 g2313448 Helicobacter pylori 210 -11539458 7502853334 hp0345 h. pylori predicted coding region hp0345 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7447) (re:7782) (di:direct) HPAE000551 AE000551 g2313448 Helicobacter pylori 26695 85962 -11539458

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910041	18091	40247	1176	391

Description

GTC ORF with score 127 to: (sr:pisum sativum (strain alaska) (clone: na481-5) (clone library) (db:genpept-pln1) (de:pisum sativum l. (clone na-481-5) mrna, complete cds.) (nt:protein localized in the nucleoli of pea nuclei;) (le:75) (re:1910) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910050	18092	40248	375	124

Description

6500735601 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0346 HP0346 Helicobacter pylori 210 -11539459 7000690122 hypothetical protein hp0346 (db:pir2.dat) B64563 B64563 Helicobacter pylori 210 -11539459 7500958904 hp0346 h. pylori predicted coding region hp0346 (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7902) (re:8684) (di:direct) HPAE000551 AE000551 g2313449 Helicobacter pylori 210 -11539459 7502853335 hp0346 h. pylori predicted coding region hp0346 (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7902) (re:8684) (di:direct) HPAE000551 AE000551 g2313449 Helicobacter pylori 26695 85962 -11539459

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910059	18093	40249	2187	728

Description

6500735602 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0350 HP0350 Helicobacter pylori 210 -11539460 7000690123 hypothetical protein hp0350 (db:pir2.dat) F64563 F64563 Helicobacter pylori 210 -11539460 7500958905 hp0350 h. pylori predicted coding region hp0350 (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:160) (re:828) (di:direct) HPAE000552 AE000552 g2313458 Helicobacter pylori 210 -11539460 7502853336 hp0350 h. pylori predicted coding region hp0350 (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:160) (re:828) (di:direct) HPAE000552 AE000552 g2313458 Helicobacter pylori 26695 85962 -11539460

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910084	18094	40250	357	118

Description

6500735603 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0356 HP0356 Helicobacter pylori 210 -11539461 7000690124 hypothetical protein hp0356 (db:pir2.dat) D64564 D64564 Helicobacter pylori 210 -11539461 7500958906 hp0356 h. pylori predicted coding region hp0356 (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8060) (re:8818) (di:direct) HPAE000552 AE000552 g2313459 Helicobacter pylori 210 -11539461 7502853337 hp0356 h. pylori predicted coding region hp0356 (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8060) (re:8818) (di:direct) HPAE000552 AE000552 g2313459 Helicobacter pylori 26695 85962 -11539461

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910090	18095	40251	636	211

Description

6500735604 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0358 HP0358 Helicobacter pylori 210 -11539462 7000690125 hypothetical protein hp0358 (db:pir2.dat) F64564 F64564 Helicobacter pylori 210 -11539462 7500958907 hp0358 h. pylori predicted coding region hp0358 (db:genpept-bct1) (de:helicobacter pylori section 30 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9737) (re:11272) (di:complement) HPAE000552 AE000552 g2313460 Helicobacter pylori 210 -11539462 7502853338 hp0358 h. pylori predicted coding region hp0358 (db:genpept) (de:helicobacter pylori 26695 section 30 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9737) (re:11272) (di:complement) HPAE000552 AE000552 g2313460 Helicobacter pylori 26695 85962 -11539462

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910100	18096	40252	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910121	18097	40253	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910131	18098	40254	594	197

Description

6500735605 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0359 HP0359 Helicobacter pylori 210 -11539463 7000690126 hypothetical protein hp0359 (db:pir2.dat) G64564 G64564 Helicobacter pylori 210 -11539463 7500958908 hp0359 h. pylori predicted coding region hp0359 (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:250) (re:315) (di:direct) HPAE000553 AE000553 g2313473 Helicobacter pylori 210 -11539463 7502853339 hp0359 h. pylori predicted coding region hp0359 (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:250) (re:315) (di:direct) HPAE000553 AE000553 g2313473 Helicobacter pylori 26695 85962 -11539463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910136	18099	40255	558	185

Description

6500735606 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0365 HP0365 Helicobacter pylori 210 -11539464 7000690127 hypothetical protein hp0365 (db:pir2.dat) E64565 E64565 Helicobacter pylori 210 -11539464 7500958909 hp0365 h. pylori predicted coding region hp0365 (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5207) (re:5299) (di:direct) HPAE000553 AE000553 g2313474 Helicobacter pylori 210 -11539464 7502853340 hp0365 h. pylori predicted coding region hp0365 (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5207) (re:5299) (di:direct) HPAE000553 AE000553 g2313474 Helicobacter pylori 26695 85962 -11539464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910138	18100	40256	552	184

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910153	18101	40257	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910154	18102	40258	441	146

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910160	18103	40259	960	319

Description

6500735607 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0367 HP0367 Helicobacter pylori 210 -11539465 7000690128 hypothetical protein hp0367 (db:pir2.dat) G64565 G64565 Helicobacter pylori 210 -11539465 7500958910 hp0367 h. pylori predicted coding region hp0367 (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6446) (re:7054) (di:complement) HPAE000553 AE000553 g2313470 Helicobacter pylori 210 -11539465 7502853341 hp0367 h. pylori predicted coding region hp0367 (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6446) (re:7054) (di:complement) HPAE000553 AE000553 g2313470 Helicobacter pylori 26695 85962 -11539465

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910164	18104	40260	585	194

Description

6500735608 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0368 HP0368 Helicobacter pylori 210 -11539466 7000690129 hypothetical protein hp0368 (db:pir2.dat) H64565 H64565 Helicobacter pylori 210 -11539466 7500958911 hp0368 h. pylori predicted coding region hp0368 (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7147) (re:7548) (di:complement) HPAE000553 AE000553 g2313471 Helicobacter pylori 210 -11539466 7502853342 hp0368 h. pylori predicted coding region hp0368 (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7147) (re:7548) (di:complement) HPAE000553 AE000553 g2313471 Helicobacter pylori 26695 85962 -11539466

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910175	18105	40261	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910186	18106	40262	876	291

Description

6500735609 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0369 HP0369 Helicobacter pylori 210 -11539467 7000690130 hypothetical protein hp0369 (db:pir2.dat) A64566 A64566 Helicobacter pylori 210 -11539467 7500958912 hp0369 h. pylori predicted coding region hp0369 (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7694) (re:8404) (di:complement) HPAE000553 AE000553 g2313472 Helicobacter pylori 210 -11539467 7502853343 hp0369 h. pylori predicted coding region hp0369 (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7694) (re:8404) (di:complement) HPAE000553 AE000553 g2313472 Helicobacter pylori 26695 85962 -11539467

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910189	18107	40263	297	98

Description

6500735610 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0375 HP0375 Helicobacter pylori 210 -11539468 7000690131 hypothetical protein hp0375 (db:pir2.dat) G64566 G64566 Helicobacter pylori 210 -11539468 7500958913 hp0375 h. pylori predicted coding region hp0375 (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3630) (re:4061) (di:complement) HPAE000554 AE000554 g2313484 Helicobacter pylori 210 -11539468 7502853344 hp0375 h. pylori predicted coding region hp0375 (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3630) (re:4061) (di:complement) HPAE000554 AE000554 g2313484 Helicobacter pylori 26695 85962 -11539468

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910190	18108	40264	333	110

Description

6500735611 dsbc:hp0377 thiol:disulfide interchange protein:putative (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0377 HP0377 Helicobacter pylori 210 -11539469 7000690727 thiol:disulfide interchange protein (db:pir2.dat) A64567 A64567 Helicobacter pylori 210 -11539469 7500959493 hp0377 thiol:disulfide interchange protein dsbc (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:similar to egad:16596 percent identity: 26.45;) (le:5198) (re:5863) (di:direct) HPAE000554 AE000554 g2313480 Helicobacter pylori 210 -11539469 7502853345 hp0377 thiol:disulfide interchange protein dsbc (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:similar to egad:16596 percent identity: 26.45;) (le:5198) (re:5863) (di:direct) HPAE000554 AE000554 g2313480 Helicobacter pylori 26695 85962 -11539469

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910194	18109	40265	483	160

Description

6500735612 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0383 HP0383 Helicobacter pylori 210 -11539470 7000690132 hypothetical protein hp0383 (db:pir2.dat) G64567 G64567 Helicobacter pylori 210 -11539470 7500958914 hp0383 h. pylori predicted coding region hp0383 (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2296) (re:2820) (di:direct) HPAE000555 AE000555 g2313499 Helicobacter pylori 210 -11539470 7502853346 hp0383 h. pylori predicted coding region hp0383 (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2296) (re:2820) (di:direct) HPAE000555 AE000555 g2313499 Helicobacter pylori 26695 85962 -11539470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910197	18110	40266	576	191

Description

6500735613 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0384 HP0384 Helicobacter pylori 210 -11539471 7000690133 hypothetical protein hp0384 (db:pir2.dat) H64567 H64567 Helicobacter pylori 210 -11539471 7500958915 hp0384 h. pylori predicted coding region hp0384 (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2863) (re:3615) (di:complement) HPAE000555 AE000555 g2313500 Helicobacter pylori 210 -11539471 7502853347 hp0384 h. pylori predicted coding region hp0384 (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2863) (re:3615) (di:complement) HPAE000555 AE000555 g2313500 Helicobacter pylori 26695 85962 -11539471

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910228	18111	40267	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910235	18112	40268	222	73

Description

6500735614 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0385 HP0385 Helicobacter pylori 210 -11539472 7000690134 hypothetical protein hp0385 (db:pir2.dat) A64568 A64568 Helicobacter pylori 210 -11539472 7500958916 hp0385 h. pylori predicted coding region hp0385 (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3815) (re:4045) (di:direct) HPAE000555 AE000555 g2313501 Helicobacter pylori 210 -11539472 7502853348 hp0385 h. pylori predicted coding region hp0385 (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3815) (re:4045) (di:direct) HPAE000555 AE000555 g2313501 Helicobacter pylori 26695 85962 -11539472

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910242	18113	40269	252	83

Description

7500958918 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0386 HP0386 Helicobacter pylori 210 -11539473 7000690135 hypothetical protein hp0386 (db:pir2.dat) B64568 B64568 Helicobacter pylori 210 -11539473 7500958917 hp0386 h. pylori predicted coding region hp0386 (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4058) (re:4294) (di:direct) HPAE000555 AE000555 g2313504 Helicobacter pylori 210 -11539473 7502853349 jhp0995 putative (db:genpept) (de:helicobacter pylori, strain j99 section 89 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0386) (le:4187) (re:4423) (di:complement) AE001528 AE001528 g4155587 Helicobacter pylori J99 85963 -11539473 6500735615 hp0386 h. pylori predicted coding region hp0386 (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4058) (re:4294) (di:direct) HPAE000555 AE000555 g2313504 Helicobacter pylori 26695 85962 -11539473

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910251	18114	40270	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910253	18115	40271	294	97

Description

6500735616 tagd:hp0390 adhesin-thiol peroxidase (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0390 HP0390 Helicobacter pylori 210 -11539474 7000689620 adhesin-thiol peroxidase (cl:thiol peroxidase) (db:pir2.dat) F64568 F64568 Helicobacter pylori 210 -11539474 7500958439 hp0390 adhesin-thiol peroxidase tagd (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:27918 percent identity: 38.27;) (le:7823) (re:8323) (di:direct) HPAE000555 AE000555 g2313491 Helicobacter pylori 210 -11539474 7502853350 hp0390 adhesin-thiol peroxidase tagd (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:27918 percent identity: 38.27;) (le:7823) (re:8323) (di:direct) HPAE000555 AE000555 g2313491 Helicobacter pylori 26695 85962 -11539474

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910254	18116	40272	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910255	18117	40273	663	220

Description

6500735617 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0394 HP0394 Helicobacter pylori 210 -11539475 7000690136 probable phosphoesterase:hp0394 (cl:unassigned probable phosphoesterases:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) B64569 B64569 Helicobacter pylori 210 -11539475 7500954184 hp0394 h. pylori predicted coding region hp0394 (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12479) (re:13237) (di:complement) HPAE000555 AE000555 g2313502 Helicobacter pylori 210 -11539475 7502853351 hp0394 h. pylori predicted coding region hp0394 (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12479) (re:13237) (di:complement) HPAE000555 AE000555 g2313502 Helicobacter pylori 26695 85962 -11539475

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910270	18118	40274	348	115

Description

6500735618 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0398 HP0398 Helicobacter pylori 210 -11539476 7000690137 hypothetical protein hp0398 (db:pir2.dat) F64569 F64569 Helicobacter pylori 210 -11539476 7500958919 hp0398 h. pylori predicted coding region hp0398 (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:17380) (re:17928) (di:complement) HPAE000555 AE000555 g2313503 Helicobacter pylori 210 -11539476 7502853352 hp0398 h. pylori predicted coding region hp0398 (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:17380) (re:17928) (di:complement) HPAE000555 AE000555 g2313503 Helicobacter pylori 26695 85962 -11539476

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910275	18119	40275	1128	375

Description

6500735619 nifs-like protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0405 HP0405 Helicobacter pylori 210 -11539477 7000690558 nifs-like protein (db:pir2.dat) E64570 E64570 Helicobacter pylori 210 -11539477 7500959344 hp0405 nifs-like protein (db:genpept-bct1) (de:helicobacter pylori section 34 of 134 of the complete genome.) (nt:similar to egad:22166 percent identity: 27.31;) (le:5904) (re:7226) (di:direct) HPAE000556 AE000556 g2313511 Helicobacter pylori 210 -11539477 7502853353 hp0405 nifs-like protein (db:genpept) (de:helicobacter pylori 26695 section 34 of 134 of the complete genome.) (nt:similar to egad:22166 percent identity: 27.31;) (le:5904) (re:7226) (di:direct) HPAE000556 AE000556 g2313511 Helicobacter pylori 26695 85962 -11539477

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910277	18120	40276	237	78

Description

6500735620 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0406 HP0406 Helicobacter pylori 210 -11539478 7000690520 mismatch-repair recognition (db:pir2.dat) F64570 F64570 Helicobacter pylori 210 -11539478 7500959311 hp0406 h. pylori predicted coding region hp0406 (db:genpept-bct1) (de:helicobacter pylori section 34 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7252) (re:7842) (di:direct) HPAE000556 AE000556 g2313513 Helicobacter pylori 210 -11539478 7502853354 hp0406 h. pylori predicted coding region hp0406 (db:genpept) (de:helicobacter pylori 26695 section 34 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7252) (re:7842) (di:direct) HPAE000556 AE000556 g2313513 Helicobacter pylori 26695 85962 -11539478

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910278	18121	40277	876	291

Description

6500735621 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0408 HP0408 Helicobacter pylori 210 -11539479 7000690138 hypothetical protein hp0408 (db:pir2.dat) H64570 H64570 Helicobacter pylori 210 -11539479 7500958920 hp0408 h. pylori predicted coding region hp0408 (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:113) (re:601) (di:direct) HPAE000557 AE000557 g2313525 Helicobacter pylori 210 -11539479 7502853355 hp0408 h. pylori predicted coding region hp0408 (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:113) (re:601) (di:direct) HPAE000557 AE000557 g2313525 Helicobacter pylori 26695 85962 -11539479

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910279	18122	40278	375	124

Description

6500735622 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0411 HP0411 Helicobacter pylori 210 -11539480 7000690139 hypothetical protein hp0411 (db:pir2.dat) C64571 C64571 Helicobacter pylori 210 -11539480 7500958921 hp0411 h. pylori predicted coding region hp0411 (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3068) (re:3385) (di:direct) HPAE000557 AE000557 g2313526 Helicobacter pylori 210 -11539480 7502853356 hp0411 h. pylori predicted coding region hp0411 (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3068) (re:3385) (di:direct) HPAE000557 AE000557 g2313526 Helicobacter pylori 26695 85962 -11539480

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910281	18123	40279	306	101

Description

6500735623 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0412 HP0412 Helicobacter pylori 210 -11539481 7000690140 hypothetical protein hp0412 (db:pir2.dat) D64571 D64571 Helicobacter pylori 210 -11539481 7500958922 hp0412 h. pylori predicted coding region hp0412 (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3635) (re:3733) (di:direct) HPAE000557 AE000557 g2313529 Helicobacter pylori 210 -11539481 7502853357 hp0412 h. pylori predicted coding region hp0412 (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3635) (re:3733) (di:direct) HPAE000557 AE000557 g2313529 Helicobacter pylori 26695 85962 -11539481

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910284	18124	40280	381	126

Description

6500735624 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0418 HP0418 Helicobacter pylori 210 -11539482 7000690141 hypothetical protein hp0418 (db:pir2.dat) B64572 B64572 Helicobacter pylori 210 -11539482 7500958923 hp0418 h. pylori predicted coding region hp0418 (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11332) (re:12339) (di:direct) HPAE000557 AE000557 g2313527 Helicobacter pylori 210 -11539482 7502853358 hp0418 h. pylori predicted coding region hp0418 (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11332) (re:12339) (di:direct) HPAE000557 AE000557 g2313527 Helicobacter pylori 26695 85962 -11539482

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910288	18125	40281	441	146

Description

6500735625 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0420 HP0420 Helicobacter pylori 210 -11539483 7000690142 hypothetical protein hp0420 (db:pir2.dat) D64572 D64572 Helicobacter pylori 210 -11539483 7500958924 hp0420 h. pylori predicted coding region hp0420 (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13145) (re:13573) (di:direct) HPAE000557 AE000557 g2313528 Helicobacter pylori 210 -11539483 7502853359 hp0420 h. pylori predicted coding region hp0420 (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13145) (re:13573) (di:direct) HPAE000557 AE000557 g2313528 Helicobacter pylori 26695 85962 -11539483

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910289	18126	40282	366	121

Description

6500735626 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0423 HP0423 Helicobacter pylori 210 -11539484 7500975632 hp0423 h. pylori predicted coding region hp0423 (db:genpept-bct1) (de:helicobacter pylori section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:87) (re:1013) (di:complement) HPAE000558 AE000558 g2313531 Helicobacter pylori 210 -11539484 7500975633 hp1412 h. pylori predicted coding region hp1412 (db:genpept-bct1) (de:helicobacter pylori section 119 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9805) (re:10731) (di:direct) HPAE000641 AE000641 g2314585 Helicobacter pylori 210 -11539484 7502853360 hp0423 h. pylori predicted coding region hp0423 (db:genpept) (de:helicobacter pylori 26695 section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:87) (re:1013) (di:complement) HPAE000558 AE000558 g2313531 Helicobacter pylori 26695 85962 -11539484 7502853361 hp1412 h. pylori predicted coding region hp1412 (db:genpept) (de:helicobacter pylori 26695 section 119 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9805) (re:10731) (di:direct) HPAE000641 AE000641 g2314585 Helicobacter pylori 26695 85962 -11539484

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910323	18127	40283	936	311

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910324	18128	40284	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910325	18129	40285	1764	587

Description

6500735627 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0424 HP0424 Helicobacter pylori 210 -11539485 7000690144 hypothetical protein hp0424/hp1411 (db:pir2.dat) C64696 C64696 Helicobacter pylori 210 -11539485 7500958925 hp0424 h. pylori predicted coding region hp0424 (db:genpept-bct1) (de:helicobacter pylori section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1129) (re:2988) (di:complement) HPAE000558 AE000558 g2313532 Helicobacter pylori 210 -11539485 7500958926 hp1411 h. pylori predicted coding region hp1411 (db:genpept-bct1) (de:helicobacter pylori section 119 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7830) (re:9689) (di:direct) HPAE000641 AE000641 g2314584 Helicobacter pylori 210 -11539485 7502853362 hp0424 h. pylori predicted coding region hp0424 (db:genpept) (de:helicobacter pylori 26695 section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1129) (re:2988) (di:complement) HPAE000558 AE000558 g2313532 Helicobacter pylori 26695 85962 -11539485 7502853363 hp1411 h. pylori predicted coding region hp1411 (db:genpept) (de:helicobacter pylori 26695 section 119 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7830) (re:9689) (di:direct) HPAE000641 AE000641 g2314584 Helicobacter pylori 26695 85962 -11539485

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910326	18130	40286	1020	339

Description

6500735628 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0425 HP0425 Helicobacter pylori 210 -11539486 7000690145 hypothetical protein hp0425 (db:pir2.dat) A64573 A64573 Helicobacter pylori 210 -11539486 7500958927 hp0425 h. pylori predicted coding region hp0425 (db:genpept-bct1) (de:helicobacter pylori section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3030) (re:4283) (di:complement) HPAE000558 AE000558 g2313533 Helicobacter pylori 210 -11539486 7502853364 hp0425 h. pylori predicted coding region hp0425 (db:genpept) (de:helicobacter pylori 26695 section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3030) (re:4283) (di:complement) HPAE000558 AE000558 g2313533 Helicobacter pylori 26695 85962 -11539486

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910327	18131	40287	885	294

Description

6500735629 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0426 HP0426 Helicobacter pylori 210 -11539487 7000690146 hypothetical protein hp0426/hp1409 (db:pir2.dat) A64696 A64696 Helicobacter pylori 210 -11539487 7500958928 hp0426 h. pylori predicted coding region hp0426 (db:genpept-bct1) (de:helicobacter pylori section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4324) (re:6060) (di:complement) HPAE000558 AE000558 g2313534 Helicobacter pylori 210 -11539487 7500958929 hp1409 h. pylori predicted coding region hp1409 (db:genpept-bct1) (de:helicobacter pylori section 119 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4757) (re:6493) (di:direct) HPAE000641 AE000641 g2314583 Helicobacter pylori 210 -11539487 7502853365 hp0426 h. pylori predicted coding region hp0426 (db:genpept) (de:helicobacter pylori 26695 section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4324) (re:6060) (di:complement) HPAE000558 AE000558 g2313534 Helicobacter pylori 26695 85962 -11539487 7502853366 hp1409 h. pylori predicted coding region hp1409 (db:genpept) (de:helicobacter pylori 26695 section 119 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4757) (re:6493) (di:direct) HPAE000641 AE000641 g2314583 Helicobacter pylori 26695 85962 -11539487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910329	18132	40288	243	80

Description

6500735630 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0427 HP0427 Helicobacter pylori 210 -11539488 7000690147 hypothetical protein hp0427/hp1408 (db:pir2.dat) C64573 C64573 Helicobacter pylori 210 -11539488 7500958930 hp0427 h. pylori predicted coding region hp0427 (db:genpept-bct1) (de:helicobacter pylori section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6110) (re:6445) (di:complement) HPAE000558 AE000558 g2313535 Helicobacter pylori 210 -11539488 7500958931 hp1408 h. pylori predicted coding region hp1408 (db:genpept-bct1) (de:helicobacter pylori section 119 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4372) (re:4707) (di:direct) HPAE000641 AE000641 g2314582 Helicobacter pylori 210 -11539488 7502853367 hp0427 h. pylori predicted coding region hp0427 (db:genpept) (de:helicobacter pylori 26695 section 36 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6110) (re:6445) (di:complement) HPAE000558 AE000558 g2313535 Helicobacter pylori 26695 85962 -11539488 7502853368 hp1408 h. pylori predicted coding region hp1408 (db:genpept) (de:helicobacter pylori 26695 section 119 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4372) (re:4707) (di:direct) HPAE000641 AE000641 g2314582 Helicobacter pylori 26695 85962 -11539488

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910342	18133	40289	732	243

Description

6500735631 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0429 HP0429 Helicobacter pylori 210 -11539489 7000690148 hypothetical protein hp0429 (db:pir2.dat) E64573 E64573 Helicobacter pylori 210 -11539489 7500958932 hp0429 h. pylori predicted coding region hp0429 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1525) (re:1563) (di:direct) HPAE000559 AE000559 g2313552 Helicobacter pylori 210 -11539489 7502853369 hp0429 h. pylori predicted coding region hp0429 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1525) (re:1563) (di:direct) HPAE000559 AE000559 g2313552 Helicobacter pylori 26695 85962 -11539489

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910354	18134	40290	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910378	18135	40291	684	227

Description

6500735632 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0430 HP0430 Helicobacter pylori 210 -11539490 7000690149 hypothetical protein hp0430 (db:pir2.dat) F64573 F64573 Helicobacter pylori 210 -11539490 7500958933 hp0430 h. pylori predicted coding region hp0430 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1649) (re:1816) (di:direct) HPAE000559 AE000559 g2313553 Helicobacter pylori 210 -11539490 7502853370 hp0430 h. pylori predicted coding region hp0430 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1649) (re:1816) (di:direct) HPAE000559 AE000559 g2313553 Helicobacter pylori 26695 85962 -11539490

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910385	18136	40292	1011	337

Description

6500735633 protein phosphatase 2c homolog:ptc1 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0431 HP0431 Helicobacter pylori 210 -11539491 7000690652 protein phosphatase 2c homolog (db:pir2.dat) G64573 G64573 Helicobacter pylori 210 -11539491 7500959427 hp0431 protein phosphatase 2c homolog ptc1 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:similar to egad:31321 percent identity: 30.67;) (le:1820) (re:2506) (di:direct) HPAE000559 AE000559 g2313538 Helicobacter pylori 210 -11539491 7502853371 hp0431 protein phosphatase 2c homolog ptc1 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:similar to egad:31321 percent identity: 30.67;) (le:1820) (re:2506) (di:direct) HPAE000559 AE000559 g2313538 Helicobacter pylori 26695 85962 -11539491

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910398	18137	40293	423	140

Description

GTC ORF with score 177 to: (or:Rhizobium sp. NGR234) (db:genpept-bct1) (de:rhizobium sp. ngr234 plasmid pngr234a, section 26 of 46 of thecomplete plasmid sequence.) (nt:hypothetical 30.2 kd protein; similar to n-terminus) (le:6430) (re:7287) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910400	18138	40294	966	321

Description

6500735634 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0433 HP0433 Helicobacter pylori 210 -11539492 7000690150 hypothetical protein hp0433 (db:pir2.dat) A64574 A64574 Helicobacter pylori 210 -11539492 7500958934 hp0433 h. pylori predicted coding region hp0433 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3415) (re:3858) (di:direct) HPAE000559 AE000559 g2313544 Helicobacter pylori 210 -11539492 7502853372 hp0433 h. pylori predicted coding region hp0433 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3415) (re:3858) (di:direct) HPAE000559 AE000559 g2313544 Helicobacter pylori 26695 85962 -11539492

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910410	18139	40295	702	233

Description

GTC ORF with score 626 to: (or:Rhizobium sp. NGR234) (db:genpept-bct1) (de:rhizobium sp. ngr234 plasmid pngr234a, section 26 of 46 of thecomplete plasmid sequence.) (nt:hypothetical 30.2 kd protein; similar to n-terminus) (le:6430) (re:7287) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910412	18140	40296	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910424	18141	40297	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910430	18142	40298	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910439	18143	40299	525	174

Description

6500735635 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0434 HP0434 Helicobacter pylori 210 -11539493 7000690151 hypothetical protein hp0434 (db:pir2.dat) B64574 B64574 Helicobacter pylori 210 -11539493 7500958935 hp0434 h. pylori predicted coding region hp0434 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3852) (re:5021) (di:direct) HPAE000559 AE000559 g2313545 Helicobacter pylori 210 -11539493 7502853373 hp0434 h. pylori predicted coding region hp0434 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3852) (re:5021) (di:direct) HPAE000559 AE000559 g2313545 Helicobacter pylori 26695 85962 -11539493

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910440	18144	40300	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910442	18145	40301	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910449	18146	40302	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910477	18147	40303	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910485	18148	40304	270	89

Description

6500735636 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0435 HP0435 Helicobacter pylori 210 -11539494 7000690152 hypothetical protein hp0435 (db:pir2.dat) C64574 C64574 Helicobacter pylori 210 -11539494 7500958936 hp0435 h. pylori predicted coding region hp0435 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5092) (re:5667) (di:direct) HPAE000559 AE000559 g2313546 Helicobacter pylori 210 -11539494 7502853374 hp0435 h. pylori predicted coding region hp0435 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5092) (re:5667) (di:direct) HPAE000559 AE000559 g2313546 Helicobacter pylori 26695 85962 -11539494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910496	18149	40305	387	128

Description

6500735637 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0436 HP0436 Helicobacter pylori 210 -11539495 7000690153 hypothetical protein hp0436 (db:pir2.dat) D64574 D64574 Helicobacter pylori 210 -11539495 7500958937 hp0436 h. pylori predicted coding region hp0436 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5651) (re:6016) (di:direct) HPAE000559 AE000559 g2313547 Helicobacter pylori 210 -11539495 7502853375 hp0436 h. pylori predicted coding region hp0436 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5651) (re:6016) (di:direct) HPAE000559 AE000559 g2313547 Helicobacter pylori 26695 85962 -11539495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910497	18150	40306	369	122

Description

6500735638 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0439 HP0439 Helicobacter pylori 210 -11539496 7000690154 hypothetical protein hp0439 (db:pir2.dat) G64574 G64574 Helicobacter pylori 210 -11539496 7500958938 hp0439 h. pylori predicted coding region hp0439 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7773) (re:8873) (di:complement) HPAE000559 AE000559 g2313548 Helicobacter pylori 210 -11539496 7502853376 hp0439 h. pylori predicted coding region hp0439 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7773) (re:8873) (di:complement) HPAE000559 AE000559 g2313548 Helicobacter pylori 26695 85962 -11539496

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910502	18151	40307	282	93

Description

6500735639 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0442 HP0442 Helicobacter pylori 210 -11539497 7000690155 hypothetical protein hp0442 (db:pir2.dat) B64575 B64575 Helicobacter pylori 210 -11539497 7500958939 hp0442 h. pylori predicted coding region hp0442 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13442) (re:13708) (di:complement) HPAE000559 AE000559 g2313549 Helicobacter pylori 210 -11539497 7502853377 hp0442 h. pylori predicted coding region hp0442 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13442) (re:13708) (di:complement) HPAE000559 AE000559 g2313549 Helicobacter pylori 26695 85962 -11539497

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910504	18152	40308	1803	600

Description

6500735640 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0443 HP0443 Helicobacter pylori 210 -11539498 7000690156 hypothetical protein hp0443 (db:pir2.dat) C64575 C64575 Helicobacter pylori 210 -11539498 7500958940 hp0443 h. pylori predicted coding region hp0443 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13709) (re:14011) (di:complement) HPAE000559 AE000559 g2313550 Helicobacter pylori 210 -11539498 7502853378 hp0443 h. pylori predicted coding region hp0443 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13709) (re:14011) (di:complement) HPAE000559 AE000559 g2313550 Helicobacter pylori 26695 85962 -11539498

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910529	18153	40309	4290	1429

Description

GTC ORF with score 764 to: (fn:antibiotic-biosynthesis) (db:genpept) (de:bacillus licheniformis lichenysin biosynthesis operon: lichenysinsynthetase a (lica), lichenysin synthetase b (licb), lichenysinsynthetase c (licc), and thioesterase (licte) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910531	18154	40310	1068	355

Description

6500735641 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0444 HP0444 Helicobacter pylori 210 -11539499 7000690157 hypothetical protein hp0444 (db:pir2.dat) D64575 D64575 Helicobacter pylori 210 -11539499 7500958941 hp0444 h. pylori predicted coding region hp0444 (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14008) (re:15531) (di:complement) HPAE000559 AE000559 g2313551 Helicobacter pylori 210 -11539499 7502853379 hp0444 h. pylori predicted coding region hp0444 (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14008) (re:15531) (di:complement) HPAE000559 AE000559 g2313551 Helicobacter pylori 26695 85962 -11539499

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910587	18155	40311	285	94

Description

6500735642 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0445 HP0445 Helicobacter pylori 210 -11539500 7000690158 hypothetical protein hp0445 (db:pir2.dat) E64575 E64575 Helicobacter pylori 210 -11539500 7500958942 hp0445 h. pylori predicted coding region hp0445 (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:88) (re:273) (di:complement) HPAE000560 AE000560 g2313562 Helicobacter pylori 210 -11539500 7502853380 hp0445 h. pylori predicted coding region hp0445 (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:88) (re:273) (di:complement) HPAE000560 AE000560 g2313562 Helicobacter pylori 26695 85962 -11539500

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910600	18156	40312	1551	516

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910601	18157	40313	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910607	18158	40314	342	113

Description

GTC ORF with score 120 to: (sr:alcaligenes eutrophus (strain h16 sk4040) dna) (db:genpept-bct2) (de:alcaligenes eutrophus 4-hydroxybutyrate dehydrogenase (gbd), orf 2and 4-10 genes, complete cds, and orf3 and 11, 3' end.) (nt:orf8) (le:3762) (re:4856) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910608	18159	40315	264	88

Description

6500735643 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0446 HP0446 Helicobacter pylori 210 -11539501 7000690159 hypothetical protein hp0446 (db:pir2.dat) F64575 F64575 Helicobacter pylori 210 -11539501 7500958943 hp0446 h. pylori predicted coding region hp0446 (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:292) (re:1071) (di:complement) HPAE000560 AE000560 g2313557 Helicobacter pylori 210 -11539501 7502853381 hp0446 h. pylori predicted coding region hp0446 (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:292) (re:1071) (di:complement) HPAE000560 AE000560 g2313557 Helicobacter pylori 26695 85962 -11539501

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910615	18160	40316	576	192

Description

6500735644 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0448 HP0448 Helicobacter pylori 210 -11539502 7000690160 hypothetical protein hp0448 (db:pir2.dat) H64575 H64575 Helicobacter pylori 210 -11539502 7500958944 hp0448 h. pylori predicted coding region hp0448 (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2258) (re:2644) (di:direct) HPAE000560 AE000560 g2313558 Helicobacter pylori 210 -11539502 7502853382 hp0448 h. pylori predicted coding region hp0448 (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2258) (re:2644) (di:direct) HPAE000560 AE000560 g2313558 Helicobacter pylori 26695 85962 -11539502

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910622	18161	40317	279	92

Description

6500735645 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0449 HP0449 Helicobacter pylori 210 -11539503 7000690161 hypothetical protein hp0449 (db:pir2.dat) A64576 A64576 Helicobacter pylori 210 -11539503 7500958945 hp0449 h. pylori predicted coding region hp0449 (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2891) (re:4309) (di:direct) HPAE000560 AE000560 g2313559 Helicobacter pylori 210 -11539503 7502853383 hp0449 h. pylori predicted coding region hp0449 (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2891) (re:4309) (di:direct) HPAE000560 AE000560 g2313559 Helicobacter pylori 26695 85962 -11539503

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910634	18162	40318	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910638	18163	40319	555	184

Description

6500735646 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0450 HP0450 Helicobacter pylori 210 -11539504 7000690162 hypothetical protein hp0450 (db:pir2.dat) B64576 B64576 Helicobacter pylori 210 -11539504 7500958946 hp0450 h. pylori predicted coding region hp0450 (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4306) (re:4440) (di:direct) HPAE000560 AE000560 g2313563 Helicobacter pylori 210 -11539504 7502853384 hp0450 h. pylori predicted coding region hp0450 (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4306) (re:4440) (di:direct) HPAE000560 AE000560 g2313563 Helicobacter pylori 26695 85962 -11539504

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910644	18164	40320	1656	551

Description

6500735647 hypothetical protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0452 HP0452 Helicobacter pylori 210 -11539505 7000690163 hypothetical protein hp0452 (db:pir2.dat) D64576 D64576 Helicobacter pylori 210 -11539505 7500958947 hp0452 hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:similar to egad:1606 percent identity: 34.36;) (le:4911) (re:6467) (di:direct) HPAE000560 AE000560 g2313556 Helicobacter pylori 210 -11539505 7502853385 hp0452 hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:similar to egad:1606 percent identity: 34.36;) (le:4911) (re:6467) (di:direct) HPAE000560 AE000560 g2313556 Helicobacter pylori 26695 85962 -11539505

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910678	18165	40321	186	61

Description

6500735648 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0453 HP0453 Helicobacter pylori 210 -11539506 7000690164 hypothetical protein hp0453 (db:pir2.dat) E64576 E64576 Helicobacter pylori 210 -11539506 7500958948 hp0453 h. pylori predicted coding region hp0453 (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6474) (re:9539) (di:direct) HPAE000560 AE000560 g2313560 Helicobacter pylori 210 -11539506 7502853386 hp0453 h. pylori predicted coding region hp0453 (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6474) (re:9539) (di:direct) HPAE000560 AE000560 g2313560 Helicobacter pylori 26695 85962 -11539506

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910684	18166	40322	246	82

Description

6500735649 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0454 HP0454 Helicobacter pylori 210 -11539507 7000690165 hypothetical protein hp0454 (db:pir2.dat) F64576 F64576 Helicobacter pylori 210 -11539507 7500958949 hp0454 h. pylori predicted coding region hp0454 (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9502) (re:10200) (di:direct) HPAE000560 AE000560 g2313561 Helicobacter pylori 210 -11539507 7502853387 hp0454 h. pylori predicted coding region hp0454 (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9502) (re:10200) (di:direct) HPAE000560 AE000560 g2313561 Helicobacter pylori 26695 85962 -11539507

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910688	18167	40323	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910694	18168	40324	2412	803

Description

6500735650 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0455 HP0455 Helicobacter pylori 210 -11539508 7000690166 hypothetical protein hp0455 (db:pir2.dat) G64576 G64576 Helicobacter pylori 210 -11539508 7500958950 hp0455 h. pylori predicted coding region hp0455 (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:154) (re:465) (di:direct) HPAE000561 AE000561 g2313575 Helicobacter pylori 210 -11539508 7502853388 hp0455 h. pylori predicted coding region hp0455 (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:154) (re:465) (di:direct) HPAE000561 AE000561 g2313575 Helicobacter pylori 26695 85962 -11539508

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910698	18169	40325	1011	336

Description

GTC ORF with score 642 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910699	18170	40326	306	101

Description

6500735651 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0456 HP0456 Helicobacter pylori 210 -11539509 7000690167 hypothetical protein hp0456 (db:pir2.dat) H64576 H64576 Helicobacter pylori 210 -11539509 7500958951 hp0456 h. pylori predicted coding region hp0456 (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:897) (re:1349) (di:direct) HPAE000561 AE000561 g2313576 Helicobacter pylori 210 -11539509 7502853389 hp0456 h. pylori predicted coding region hp0456 (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:897) (re:1349) (di:direct) HPAE000561 AE000561 g2313576 Helicobacter pylori 26695 85962 -11539509

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910703	18171	40327	957	318

Description

6500735652 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0457 HP0457 Helicobacter pylori 210 -11539510 7000690168 hypothetical protein hp0457 (db:pir2.dat) A64577 A64577 Helicobacter pylori 210 -11539510 7500958952 hp0457 h. pylori predicted coding region hp0457 (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1667) (re:1930) (di:direct) HPAE000561 AE000561 g2313577 Helicobacter pylori 210 -11539510 7502853390 hp0457 h. pylori predicted coding region hp0457 (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1667) (re:1930) (di:direct) HPAE000561 AE000561 g2313577 Helicobacter pylori 26695 85962 -11539510

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910708	18172	40328	396	131

Description

6500735653 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0458 HP0458 Helicobacter pylori 210 -11539511 7000690169 hypothetical protein hp0458 (db:pir2.dat) B64577 B64577 Helicobacter pylori 210 -11539511 7500958953 hp0458 h. pylori predicted coding region hp0458 (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1942) (re:2178) (di:direct) HPAE000561 AE000561 g2313578 Helicobacter pylori 210 -11539511 7502853391 hp0458 h. pylori predicted coding region hp0458 (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1942) (re:2178) (di:direct) HPAE000561 AE000561 g2313578 Helicobacter pylori 26695 85962 -11539511

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910709	18173	40329	558	185

Description

GTC ORF with score 203 to: (db:genpept-bct2) (de:streptomyces caelestis cytochrome p-450 hydroxylase homolog (nidi)gene, partial cds; polyketide synthase modules 1 through 7 (nida)genes, complete cds; and n-methyltransferase homolog gene, partialcds.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910714	18174	40330	552	183

Description

6500735654 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0460 HP0460 Helicobacter pylori 210 -11539512 7000690170 hypothetical protein hp0460 (db:pir2.dat) D64577 D64577 Helicobacter pylori 210 -11539512 7500958954 hp0460 h. pylori predicted coding region hp0460 (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4884) (re:5372) (di:direct) HPAE000561 AE000561 g2313579 Helicobacter pylori 210 -11539512 7502853392 hp0460 h. pylori predicted coding region hp0460 (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4884) (re:5372) (di:direct) HPAE000561 AE000561 g2313579 Helicobacter pylori 26695 85962 -11539512

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910715	18175	40331	1125	374

Description

GTC ORF with score 522 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910716	18176	40332	621	206

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910720	18177	40333	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910721	18178	40334	477	158

Description

GTC ORF with score 227 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910756	18179	40335	966	322

Description

6500735655 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0461 HP0461 Helicobacter pylori 210 -11539513 7000690171 hypothetical protein hp0461 (db:pir2.dat) E64577 E64577 Helicobacter pylori 210 -11539513 7500958955 hp0461 h. pylori predicted coding region hp0461 (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5398) (re:5490) (di:complement) HPAE000561 AE000561 g2313580 Helicobacter pylori 210 -11539513 7502853393 hp0461 h. pylori predicted coding region hp0461 (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5398) (re:5490) (di:complement) HPAE000561 AE000561 g2313580 Helicobacter pylori 26695 85962 -11539513

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910758	18180	40336	441	146

Description

6500735656 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0479 HP0479 Helicobacter pylori 210 -11539514 7000690172 hypothetical protein hp0479 (db:pir2.dat) G64579 G64579 Helicobacter pylori 210 -11539514 7500958956 hp0479 h. pylori predicted coding region hp0479 (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9004) (re:9852) (di:direct) HPAE000562 AE000562 g2313592 Helicobacter pylori 210 -11539514 7502853394 hp0479 h. pylori predicted coding region hp0479 (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9004) (re:9852) (di:direct) HPAE000562 AE000562 g2313592 Helicobacter pylori 26695 85962 -11539514

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910761	18181	40337	2481	826

Description

6500735657 yihk:hp0480 gtp-binding protein:fusa-homolog (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0480 HP0480 Helicobacter pylori 210 -11539515 7500893598 typa:hp0480 (sr:,campylobacter pylori) (de:gtp-binding protein typa/bipa homolog) (db:swissprot) TYPA_HELPY O25225 HELICOBACTER PYLORI 210 -11539515 7000689979 gtp-binding protein:fusa-homolog (cl:translation elongation factor tu homology) (db:pir2.dat) H64579 H64579 Helicobacter pylori 210 -11539515 7500893600 hp0480 gtp-binding protein:fusa-homolog yihk (db:genpept-bct1) (de:helicobacter pylori section 40 of 134 of the complete genome.) (nt:similar to egad:24044 percent identity: 54.08;) (le:9898) (re:11697) (di:direct) HPAE000562 AE000562 g2313589 Helicobacter pylori 210 -11539515 7502853395 hp0480 gtp-binding protein:fusa-homolog yihk (db:genpept) (de:helicobacter pylori 26695 section 40 of 134 of the complete genome.) (nt:similar to egad:24044 percent identity: 54.08;) (le:9898) (re:11697) (di:direct) HPAE000562 AE000562 g2313589 Helicobacter pylori 26695 85962 -11539515

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910765	18182	40338	366	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910766	18183	40339	456	151

Description

6500735658 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0482 HP0482 Helicobacter pylori 210 -11539516 7000690173 hypothetical protein hp0482 (db:pir2.dat) B64580 B64580 Helicobacter pylori 210 -11539516 7500958957 hp0482 h. pylori predicted coding region hp0482 (db:genpept-bct1) (de:helicobacter pylori section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:178) (re:690) (di:direct) HPAE000563 AE000563 g2313596 Helicobacter pylori 210 -11539516 7502853396 hp0482 h. pylori predicted coding region hp0482 (db:genpept) (de:helicobacter pylori 26695 section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:178) (re:690) (di:direct) HPAE000563 AE000563 g2313596 Helicobacter pylori 26695 85962 -11539516

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910771	18184	40340	240	79

Description

GTC ORF with score 105 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid r04e5.) (nt:proline rich; coded for by c. elegans cdna) (le:8839:9150:9494) (re:8875:9435:10157) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910773	18185	40341	747	248

Description

6500735659 hp0483:hpy_478 cytosine specific dna methyltransferase:hphimc (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HPY_478 HPY_478 Helicobacter pylori 210 -11539517 7500975635 hp0483 cytosine specific dna methyltransferase (db:genpept-bct1) (de:helicobacter pylori section 41 of 134 of the complete genome.) (nt:similar to egad:33274 percent identity: 38.67;) (le:949) (re:1938) (di:direct) HPAE000563 AE000563 g2313594 Helicobacter pylori 210 -11539517 7502853397 hp0483 cytosine specific dna methyltransferase (db:genpept) (de:helicobacter pylori 26695 section 41 of 134 of the complete genome.) (nt:similar to egad:33274 percent identity: 38.67;) (le:949) (re:1938) (di:direct) HPAE000563 AE000563 g2313594 Helicobacter pylori 26695 85962 -11539517

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910777	18186	40342	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910782	18187	40343	429	143

Description

GTC ORF with score 124 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f25b5.) (nt:similar to myoblast cell surface antigen) (le:17524:17682:18907) (re:17618:18206:19103) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910783	18188	40344	852	283

Description

GTC ORF with score 497 to: (fn:cleavage of oligopeptides) (sr:schizophyllum commune (strain uvm 4-40) homokaryon haploid dna) (db:genpept-pln1) (de:schizophyllum commune (strain uvm 4-40) metalloendopeptidase (mep)gene, 3'end; a-alphaz4 protein ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910785	18189	40345	798	265

Description

6500735660 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0484 HP0484 Helicobacter pylori 210 -11539518 7000690174 hypothetical protein hp0484 (db:pir2.dat) D64580 D64580 Helicobacter pylori 210 -11539518 7500958958 hp0484 h. pylori predicted coding region hp0484 (db:genpept-bct1) (de:helicobacter pylori section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1940) (re:2692) (di:direct) HPAE000563 AE000563 g2313597 Helicobacter pylori 210 -11539518 7502853398 hp0484 h. pylori predicted coding region hp0484 (db:genpept) (de:helicobacter pylori 26695 section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1940) (re:2692) (di:direct) HPAE000563 AE000563 g2313597 Helicobacter pylori 26695 85962 -11539518

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910787	18190	40346	570	189

Description

6500735661 catalase-like protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0485 HP0485 Helicobacter pylori 210 -11539519 7000689695 catalase-like protein (db:pir2.dat) E64580 E64580 Helicobacter pylori 210 -11539519 7500958506 hp0485 catalase-like protein (db:genpept-bct1) (de:helicobacter pylori section 41 of 134 of the complete genome.) (nt:similar to egad:42507 percent identity: 30.80;) (le:2926) (re:3870) (di:complement) HPAE000563 AE000563 g2313595 Helicobacter pylori 210 -11539519 7502853399 hp0485 catalase-like protein (db:genpept) (de:helicobacter pylori 26695 section 41 of 134 of the complete genome.) (nt:similar to egad:42507 percent identity: 30.80;) (le:2926) (re:3870) (di:complement) HPAE000563 AE000563 g2313595 Helicobacter pylori 26695 85962 -11539519

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910788	18191	40347	462	153

Description

6500735662 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0486 HP0486 Helicobacter pylori 210 -11539520 7000690175 hypothetical protein hp0486 (db:pir2.dat) F64580 F64580 Helicobacter pylori 210 -11539520 7500958959 hp0486 h. pylori predicted coding region hp0486 (db:genpept-bct1) (de:helicobacter pylori section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4156) (re:5742) (di:direct) HPAE000563 AE000563 g2313598 Helicobacter pylori 210 -11539520 7502853400 hp0486 h. pylori predicted coding region hp0486 (db:genpept) (de:helicobacter pylori 26695 section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4156) (re:5742) (di:direct) HPAE000563 AE000563 g2313598 Helicobacter pylori 26695 85962 -11539520

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910789	18192	40348	438	145

Description

6500735663 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0487 HP0487 Helicobacter pylori 210 -11539521 7000690176 hypothetical protein hp0487 (db:pir2.dat) G64580 G64580 Helicobacter pylori 210 -11539521 7500958960 hp0487 h. pylori predicted coding region hp0487 (db:genpept-bct1) (de:helicobacter pylori section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5769) (re:7211) (di:direct) HPAE000563 AE000563 g2313599 Helicobacter pylori 210 -11539521 7502853401 hp0487 h. pylori predicted coding region hp0487 (db:genpept) (de:helicobacter pylori 26695 section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5769) (re:7211) (di:direct) HPAE000563 AE000563 g2313599 Helicobacter pylori 26695 85962 -11539521

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910790	18193	40349	561	187

Description

6500735664 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0488 HP0488 Helicobacter pylori 210 -11539522 7000690177 hypothetical protein hp0488/hp1116 (db:pir2.dat) D64659 D64659 Helicobacter pylori 210 -11539522 7500958961 hp0488 h. pylori predicted coding region hp0488 (db:genpept-bct1) (de:helicobacter pylori section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7610) (re:10483) (di:direct) HPAE000563 AE000563 g2313600 Helicobacter pylori 210 -11539522 7500958962 hp1116 h. pylori predicted coding region hp1116 (db:genpept-bct1) (de:helicobacter pylori section 96 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:765) (re:3638) (di:complement) HPAE000618 AE000618 g2314275 Helicobacter pylori 210 -11539522 7502853402 hp0488 h. pylori predicted coding region hp0488 (db:genpept) (de:helicobacter pylori 26695 section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7610) (re:10483) (di:direct) HPAE000563 AE000563 g2313600 Helicobacter pylori 26695 85962 -11539522 7502853403 hp1116 h. pylori predicted coding region hp1116 (db:genpept) (de:helicobacter pylori 26695 section 96 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:765) (re:3638) (di:complement) HPAE000618 AE000618 g2314275 Helicobacter pylori 26695 85962 -11539522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910796	18194	40350	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910799	18195	40351	240	79

Description

6500735665 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0489 HP0489 Helicobacter pylori 210 -11539523 7000690721 surface-located membrane protein 3 (db:pir2.dat) A64581 A64581 Helicobacter pylori 210 -11539523 7500959487 hp0489 h. pylori predicted coding region hp0489 (db:genpept-bct1) (de:helicobacter pylori section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10497) (re:11384) (di:direct) HPAE000563 AE000563 g2313601 Helicobacter pylori 210 -11539523 7502853404 hp0489 h. pylori predicted coding region hp0489 (db:genpept) (de:helicobacter pylori 26695 section 41 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10497) (re:11384) (di:direct) HPAE000563 AE000563 g2313601 Helicobacter pylori 26695 85962 -11539523

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910802	18196	40352	438	145

Description

6500735666 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0492 HP0492 Helicobacter pylori 210 -11539524 7000690178 hypothetical protein hp0492 (db:pir2.dat) D64581 D64581 Helicobacter pylori 210 -11539524 7500958963 hp0492 h. pylori predicted coding region hp0492 (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1813) (re:2649) (di:complement) HPAE000564 AE000564 g2313613 Helicobacter pylori 210 -11539524 7502853405 hp0492 h. pylori predicted coding region hp0492 (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1813) (re:2649) (di:complement) HPAE000564 AE000564 g2313613 Helicobacter pylori 26695 85962 -11539524

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910803	18197	40353	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910810	18198	40354	519	172

Description

6500735667 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0495 HP0495 Helicobacter pylori 210 -11539525 7000690179 hypothetical protein hp0495 (db:pir2.dat) G64581 G64581 Helicobacter pylori 210 -11539525 7500958964 hp0495 h. pylori predicted coding region hp0495 (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5102) (re:5362) (di:complement) HPAE000564 AE000564 g2313614 Helicobacter pylori 210 -11539525 7502853406 hp0495 h. pylori predicted coding region hp0495 (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5102) (re:5362) (di:complement) HPAE000564 AE000564 g2313614 Helicobacter pylori 26695 85962 -11539525

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910815	18199	40355	2307	768

Description

6500735668 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0502 HP0502 Helicobacter pylori 210 -11539526 7000690180 hypothetical protein hp0502 (db:pir2.dat) F64582 F64582 Helicobacter pylori 210 -11539526 7500958965 hp0502 h. pylori predicted coding region hp0502 (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13293) (re:13457) (di:direct) HPAE000564 AE000564 g2313615 Helicobacter pylori 210 -11539526 7502853407 hp0502 h. pylori predicted coding region hp0502 (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13293) (re:13457) (di:direct) HPAE000564 AE000564 g2313615 Helicobacter pylori 26695 85962 -11539526

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910817	18200	40356	291	96

Description

6500735669 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0503 HP0503 Helicobacter pylori 210 -11539527 7000690181 hypothetical protein hp0503 (db:pir2.dat) G64582 G64582 Helicobacter pylori 210 -11539527 7500958966 hp0503 h. pylori predicted coding region hp0503 (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:75) (re:815) (di:direct) HPAE000565 AE000565 g2313622 Helicobacter pylori 210 -11539527 7502853408 hp0503 h. pylori predicted coding region hp0503 (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:75) (re:815) (di:direct) HPAE000565 AE000565 g2313622 Helicobacter pylori 26695 85962 -11539527

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910819	18201	40357	396	131

Description

6500735670 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0504 HP0504 Helicobacter pylori 210 -11539528 7000690182 hypothetical protein hp0504 (db:pir2.dat) H64582 H64582 Helicobacter pylori 210 -11539528 7500958967 hp0504 h. pylori predicted coding region hp0504 (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:802) (re:951) (di:direct) HPAE000565 AE000565 g2313626 Helicobacter pylori 210 -11539528 7502853409 hp0504 h. pylori predicted coding region hp0504 (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:802) (re:951) (di:direct) HPAE000565 AE000565 g2313626 Helicobacter pylori 26695 85962 -11539528

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910820	18202	40358	420	139

Description

6500735671 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0505 HP0505 Helicobacter pylori 210 -11539529 7000690183 hypothetical protein hp0505 (db:pir2.dat) A64583 A64583 Helicobacter pylori 210 -11539529 7500958968 hp0505 h. pylori predicted coding region hp0505 (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1092) (re:1556) (di:direct) HPAE000565 AE000565 g2313623 Helicobacter pylori 210 -11539529 7502853410 hp0505 h. pylori predicted coding region hp0505 (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1092) (re:1556) (di:direct) HPAE000565 AE000565 g2313623 Helicobacter pylori 26695 85962 -11539529

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910846	18203	40359	456	151

Description

6500735672 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0508 HP0508 Helicobacter pylori 210 -11539530 7000690184 hypothetical protein hp0508 (db:pir2.dat) D64583 D64583 Helicobacter pylori 210 -11539530 7500958969 hp0508 h. pylori predicted coding region hp0508 (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3620) (re:4978) (di:direct) HPAE000565 AE000565 g2313624 Helicobacter pylori 210 -11539530 7502853411 hp0508 h. pylori predicted coding region hp0508 (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3620) (re:4978) (di:direct) HPAE000565 AE000565 g2313624 Helicobacter pylori 26695 85962 -11539530

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910850	18204	40360	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910867	18205	40361	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910875	18206	40362	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910877	18207	40363	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910879	18208	40364	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910894	18209	40365	408	135

Description

6500735673 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0511 HP0511 Helicobacter pylori 210 -11539531 7000690185 hypothetical protein hp0511 (db:pir2.dat) G64583 G64583 Helicobacter pylori 210 -11539531 7500958970 hp0511 h. pylori predicted coding region hp0511 (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7571) (re:7687) (di:direct) HPAE000565 AE000565 g2313627 Helicobacter pylori 210 -11539531 7502853412 hp0511 h. pylori predicted coding region hp0511 (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7571) (re:7687) (di:direct) HPAE000565 AE000565 g2313627 Helicobacter pylori 26695 85962 -11539531

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910916	18210	40366	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910921	18211	40367	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910944	18212	40368	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910950	18213	40369	1002	333

Description

6500735674 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0513 HP0513 Helicobacter pylori 210 -11539532 7000690186 hypothetical protein hp0513 (db:pir2.dat) A64584 A64584 Helicobacter pylori 210 -11539532 7500958971 hp0513 h. pylori predicted coding region hp0513 (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9742) (re:11718) (di:direct) HPAE000565 AE000565 g2313625 Helicobacter pylori 210 -11539532 7502853413 hp0513 h. pylori predicted coding region hp0513 (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9742) (re:11718) (di:direct) HPAE000565 AE000565 g2313625 Helicobacter pylori 26695 85962 -11539532

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910959	18214	40370	231	76

Description

6500735675 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0533 HP0533 Helicobacter pylori 210 -11539533 7000690187 hypothetical protein hp0533 (db:pir2.dat) E64586 E64586 Helicobacter pylori 210 -11539533 7500958972 hp0533 h. pylori predicted coding region hp0533 (db:genpept-bct1) (de:helicobacter pylori section 46 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1877) (re:1966) (di:complement) HPAE000568 AE000568 g2313662 Helicobacter pylori 210 -11539533 7502853414 hp0533 h. pylori predicted coding region hp0533 (db:genpept) (de:helicobacter pylori 26695 section 46 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1877) (re:1966) (di:complement) HPAE000568 AE000568 g2313662 Helicobacter pylori 26695 85962 -11539533

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910967	18215	40371	486	161

Description

6500735676 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0554 HP0554 Helicobacter pylori 210 -11539534 7000690188 hypothetical protein hp0554 (db:pir2.dat) B64589 B64589 Helicobacter pylori 210 -11539534 7500958973 hp0554 h. pylori predicted coding region hp0554 (db:genpept-bct1) (de:helicobacter pylori section 47 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9294) (re:10259) (di:direct) HPAE000569 AE000569 g2313670 Helicobacter pylori 210 -11539534 7502853415 hp0554 h. pylori predicted coding region hp0554 (db:genpept) (de:helicobacter pylori 26695 section 47 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9294) (re:10259) (di:direct) HPAE000569 AE000569 g2313670 Helicobacter pylori 26695 85962 -11539534

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910970	18216	40372	387	128

Description

6500735677 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0555 HP0555 Helicobacter pylori 210 -11539535 7000690189 hypothetical protein hp0555 (db:pir2.dat) C64589 C64589 Helicobacter pylori 210 -11539535 7500958974 hp0555 h. pylori predicted coding region hp0555 (db:genpept-bct1) (de:helicobacter pylori section 47 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10256) (re:11077) (di:direct) HPAE000569 AE000569 g2313671 Helicobacter pylori 210 -11539535 7502853416 hp0555 h. pylori predicted coding region hp0555 (db:genpept) (de:helicobacter pylori 26695 section 47 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10256) (re:11077) (di:direct) HPAE000569 AE000569 g2313671 Helicobacter pylori 26695 85962 -11539535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501910989	18217	40373	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911006	18218	40374	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911009	18219	40375	729	242

Description

6500735678 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0556 HP0556 Helicobacter pylori 210 -11539536 7000690190 hypothetical protein hp0556 (db:pir2.dat) D64589 D64589 Helicobacter pylori 210 -11539536 7500958975 hp0556 h. pylori predicted coding region hp0556 (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:67) (re:504) (di:complement) HPAE000570 AE000570 g2313682 Helicobacter pylori 210 -11539536 7502853417 hp0556 h. pylori predicted coding region hp0556 (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:67) (re:504) (di:complement) HPAE000570 AE000570 g2313682 Helicobacter pylori 26695 85962 -11539536

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911014	18220	40376	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911032	18221	40377	651	216

Description

7500958977 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0560 HP0560 Helicobacter pylori 210 -11539537 7000690191 hypothetical protein hp0560 (db:pir2.dat) H64589 H64589 Helicobacter pylori 210 -11539537 7500958976 hp0560 h. pylori predicted coding region hp0560 (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3769) (re:3849) (di:complement) HPAE000570 AE000570 g2313684 Helicobacter pylori 210 -11539537 7502853418 jhp0507 putative (db:genpept) (de:helicobacter pylori, strain j99 section 45 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0560) (le:3575) (re:3655) (di:complement) AE001484 AE001484 g4155046 Helicobacter pylori J99 85963 -11539537 6500735679 hp0560 h. pylori predicted coding region hp0560 (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3769) (re:3849) (di:complement) HPAE000570 AE000570 g2313684 Helicobacter pylori 26695 85962 -11539537

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911039	18222	40378	528	175

Description

6500735680 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0563 HP0563 Helicobacter pylori 210 -11539538 7000690192 hypothetical protein hp0563 (db:pir2.dat) C64590 C64590 Helicobacter pylori 210 -11539538 7500958978 hp0563 h. pylori predicted coding region hp0563 (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5045) (re:6295) (di:complement) HPAE000570 AE000570 g2313683 Helicobacter pylori 210 -11539538 7502853419 hp0563 h. pylori predicted coding region hp0563 (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5045) (re:6295) (di:complement) HPAE000570 AE000570 g2313683 Helicobacter pylori 26695 85962 -11539538

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911046	18223	40379	279	92

Description

6500735681 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0564 HP0564 Helicobacter pylori 210 -11539539 7500975636 hp0564 h. pylori predicted coding region hp0564 (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6543) (re:6713) (di:direct) HPAE000570 AE000570 g2313685 Helicobacter pylori 210 -11539539 7502853420 hp0564 h. pylori predicted coding region hp0564 (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6543) (re:6713) (di:direct) HPAE000570 AE000570 g2313685 Helicobacter pylori 26695 85962 -11539539

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911050	18224	40380	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911073	18225	40381	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911084	18226	40382	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911097	18227	40383	2454	817

Description

GTC ORF with score 151 to: (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.).) (nt:orf_id:o263#22; similar to (swissprot accession) (le:14961) (re:18323) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911114	18228	40384	504	167

Description

GTC ORF with score 125 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t29e15 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:47291:47473:47779:47946) (re:47374:47666:47863:48011) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911121	18229	40385	1434	477

Description

6500735682 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0565 HP0565 Helicobacter pylori 210 -11539540 7000690194 hypothetical protein hp0565 (cl:conserved hypothetical protein hi0219) (db:pir2.dat) E64590 E64590 Helicobacter pylori 210 -11539540 7500958979 hp0565 h. pylori predicted coding region hp0565 (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6736) (re:7383) (di:complement) HPAE000570 AE000570 g2313680 Helicobacter pylori 210 -11539540 7502853421 hp0565 h. pylori predicted coding region hp0565 (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6736) (re:7383) (di:complement) HPAE000570 AE000570 g2313680 Helicobacter pylori 26695 85962 -11539540

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911129	18230	40386	252	83

Description

6500735683 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0568 HP0568 Helicobacter pylori 210 -11539541 7000690195 hypothetical protein hp0568 (db:pir2.dat) H64590 H64590 Helicobacter pylori 210 -11539541 7500958980 hp0568 h. pylori predicted coding region hp0568 (db:genpept-bct1) (de:helicobacter pylori section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9620) (re:10387) (di:complement) HPAE000570 AE000570 g2313681 Helicobacter pylori 210 -11539541 7502853422 hp0568 h. pylori predicted coding region hp0568 (db:genpept) (de:helicobacter pylori 26695 section 48 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9620) (re:10387) (di:complement) HPAE000570 AE000570 g2313681 Helicobacter pylori 26695 85962 -11539541

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911136	18231	40387	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911137	18232	40388	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911138	18233	40389	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911144	18234	40390	414	137

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911163	18235	40391	201	66

Description

GTC ORF with score 99 to: (fn:cytoplasmic aldehyde dehydrogenase;) (sr:short-eared elephant shrew) (db:genpept-mam) (ec:1.2.1.3) (de:macroscelides proboscideus cytoplasmic aldehyde dehydrogenasealdh1-nl mrna, partial cds.) (le:<1) (re:724) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911177	18236	40392	1164	388

Description

6500735684 gtp-binding protein:gtp1 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0569 HP0569 Helicobacter pylori 210 -11539542 7000689976 gtp1 probable gtp-binding protein gtp1 (cl:yeast probable purine nucleotide-binding protein ybr025c) (db:pir2.dat) A64591 A64591 Helicobacter pylori 210 -11539542 7500959420 hp0569 gtp-binding protein gtp1 (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:31237 percent identity: 48.10;) (le:98) (re:1198) (di:complement) HPAE000571 AE000571 g2313689 Helicobacter pylori 210 -11539542 7502853423 hp0569 gtp-binding protein gtp1 (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:31237 percent identity: 48.10;) (le:98) (re:1198) (di:complement) HPAE000571 AE000571 g2313689 Helicobacter pylori 26695 85962 -11539542

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911193	18237	40393	1425	474

Description

6500735685 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0573 HP0573 Helicobacter pylori 210 -11539543 7000690196 hypothetical protein hp0573 (db:pir2.dat) E64591 E64591 Helicobacter pylori 210 -11539543 7500958981 hp0573 h. pylori predicted coding region hp0573 (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3928) (re:4260) (di:complement) HPAE000571 AE000571 g2313701 Helicobacter pylori 210 -11539543 7502853424 hp0573 h. pylori predicted coding region hp0573 (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3928) (re:4260) (di:complement) HPAE000571 AE000571 g2313701 Helicobacter pylori 26695 85962 -11539543

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911210	18238	40394	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911225	18239	40395	321	106

Description

6500735686 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0578 HP0578 Helicobacter pylori 210 -11539544 7000690197 hypothetical protein hp0578 (db:pir2.dat) B64592 B64592 Helicobacter pylori 210 -11539544 7500958982 hp0578 h. pylori predicted coding region hp0578 (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7319) (re:9355) (di:complement) HPAE000571 AE000571 g2313702 Helicobacter pylori 210 -11539544 7502853425 hp0578 h. pylori predicted coding region hp0578 (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7319) (re:9355) (di:complement) HPAE000571 AE000571 g2313702 Helicobacter pylori 26695 85962 -11539544

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911230	18240	40396	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911247	18241	40397	564	187

Description

6500735687 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0579 HP0579 Helicobacter pylori 210 -11539545 7000690198 hypothetical protein hp0579 (db:pir2.dat) C64592 C64592 Helicobacter pylori 210 -11539545 7500958983 hp0579 h. pylori predicted coding region hp0579 (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9361) (re:9915) (di:complement) HPAE000571 AE000571 g2313697 Helicobacter pylori 210 -11539545 7502853426 hp0579 h. pylori predicted coding region hp0579 (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9361) (re:9915) (di:complement) HPAE000571 AE000571 g2313697 Helicobacter pylori 26695 85962 -11539545

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911254	18242	40398	963	320

Description

6500735688 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0580 HP0580 Helicobacter pylori 210 -11539546 7000690199 hypothetical protein hp0580 (db:pir2.dat) D64592 D64592 Helicobacter pylori 210 -11539546 7500958984 hp0580 h. pylori predicted coding region hp0580 (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9922) (re:11040) (di:complement) HPAE000571 AE000571 g2313698 Helicobacter pylori 210 -11539546 7502853427 hp0580 h. pylori predicted coding region hp0580 (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9922) (re:11040) (di:complement) HPAE000571 AE000571 g2313698 Helicobacter pylori 26695 85962 -11539546

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911266	18243	40399	1167	388

Description

6500735689 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0582 HP0582 Helicobacter pylori 210 -11539547 7000690200 hypothetical protein hp0582 (db:pir2.dat) F64592 F64592 Helicobacter pylori 210 -11539547 7500958985 hp0582 h. pylori predicted coding region hp0582 (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12039) (re:13013) (di:complement) HPAE000571 AE000571 g2313699 Helicobacter pylori 210 -11539547 7502853428 hp0582 h. pylori predicted coding region hp0582 (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12039) (re:13013) (di:complement) HPAE000571 AE000571 g2313699 Helicobacter pylori 26695 85962 -11539547

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911269	18244	40400	627	208

Description

6500735690 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0583 HP0583 Helicobacter pylori 210 -11539548 7000690201 hypothetical protein hp0583 (db:pir2.dat) G64592 G64592 Helicobacter pylori 210 -11539548 7500958986 hp0583 h. pylori predicted coding region hp0583 (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12997) (re:13878) (di:complement) HPAE000571 AE000571 g2313700 Helicobacter pylori 210 -11539548 7502853429 hp0583 h. pylori predicted coding region hp0583 (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12997) (re:13878) (di:complement) HPAE000571 AE000571 g2313700 Helicobacter pylori 26695 85962 -11539548

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911299	18245	40401	231	76

Description

6500735691 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0586 HP0586 Helicobacter pylori 210 -11539549 7000690202 hypothetical protein hp0586 (db:pir2.dat) B64593 B64593 Helicobacter pylori 210 -11539549 7500958987 hp0586 h. pylori predicted coding region hp0586 (db:genpept-bct1) (de:helicobacter pylori section 50 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:956) (re:3889) (di:complement) HPAE000572 AE000572 g2313711 Helicobacter pylori 210 -11539549 7502853430 hp0586 h. pylori predicted coding region hp0586 (db:genpept) (de:helicobacter pylori 26695 section 50 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:956) (re:3889) (di:complement) HPAE000572 AE000572 g2313711 Helicobacter pylori 26695 85962 -11539549

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911304	18246	40402	528	175

Description

6500735692 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0594 HP0594 Helicobacter pylori 210 -11539550 7000690203 hypothetical protein hp0594 (db:pir2.dat) B64594 B64594 Helicobacter pylori 210 -11539550 7500958988 hp0594 h. pylori predicted coding region hp0594 (db:genpept-bct1) (de:helicobacter pylori section 51 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1960) (re:2124) (di:direct) HPAE000573 AE000573 g2313720 Helicobacter pylori 210 -11539550 7502853431 hp0594 h. pylori predicted coding region hp0594 (db:genpept) (de:helicobacter pylori 26695 section 51 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1960) (re:2124) (di:direct) HPAE000573 AE000573 g2313720 Helicobacter pylori 26695 85962 -11539550

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911308	18247	40403	1926	641

Description

6500735693 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0595 HP0595 Helicobacter pylori 210 -11539551 7000690204 hypothetical protein hp0595 (db:pir2.dat) C64594 C64594 Helicobacter pylori 210 -11539551 7500958989 hp0595 h. pylori predicted coding region hp0595 (db:genpept-bct1) (de:helicobacter pylori section 51 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2134) (re:3606) (di:direct) HPAE000573 AE000573 g2313718 Helicobacter pylori 210 -11539551 7502853432 hp0595 h. pylori predicted coding region hp0595 (db:genpept) (de:helicobacter pylori 26695 section 51 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2134) (re:3606) (di:direct) HPAE000573 AE000573 g2313718 Helicobacter pylori 26695 85962 -11539551

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911310	18248	40404	642	213

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911322	18249	40405	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911325	18250	40406	402	133

Description

6500735694 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0596 HP0596 Helicobacter pylori 210 -11539552 7000690205 hypothetical protein hp0596 (db:pir2.dat) D64594 D64594 Helicobacter pylori 210 -11539552 7500958990 hp0596 h. pylori predicted coding region hp0596 (db:genpept-bct1) (de:helicobacter pylori section 51 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4080) (re:4658) (di:direct) HPAE000573 AE000573 g2313719 Helicobacter pylori 210 -11539552 7502853433 hp0596 h. pylori predicted coding region hp0596 (db:genpept) (de:helicobacter pylori 26695 section 51 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4080) (re:4658) (di:direct) HPAE000573 AE000573 g2313719 Helicobacter pylori 26695 85962 -11539552

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911326	18251	40407	924	307

Description

6500735695 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0603 HP0603 Helicobacter pylori 210 -11539553 7000690206 hypothetical protein hp0603 (db:pir2.dat) C64595 C64595 Helicobacter pylori 210 -11539553 7500958991 hp0603 h. pylori predicted coding region hp0603 (db:genpept-bct1) (de:helicobacter pylori section 52 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2463) (re:3032) (di:direct) HPAE000574 AE000574 g2313727 Helicobacter pylori 210 -11539553 7502853434 hp0603 h. pylori predicted coding region hp0603 (db:genpept) (de:helicobacter pylori 26695 section 52 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2463) (re:3032) (di:direct) HPAE000574 AE000574 g2313727 Helicobacter pylori 26695 85962 -11539553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911331	18252	40408	261	86

Description

6500735696 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0605 HP0605 Helicobacter pylori 210 -11539554 7000690207 hypothetical protein hp0605 (db:pir2.dat) E64595 E64595 Helicobacter pylori 210 -11539554 7500958992 hp0605 h. pylori predicted coding region hp0605 (db:genpept-bct1) (de:helicobacter pylori section 52 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4129) (re:5562) (di:direct) HPAE000574 AE000574 g2313728 Helicobacter pylori 210 -11539554 7502853435 hp0605 h. pylori predicted coding region hp0605 (db:genpept) (de:helicobacter pylori 26695 section 52 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4129) (re:5562) (di:direct) HPAE000574 AE000574 g2313728 Helicobacter pylori 26695 85962 -11539554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911338	18253	40409	624	208

Description

6500735697 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0608 HP0608 Helicobacter pylori 210 -11539555 7000690208 hypothetical protein hp0608 (db:pir2.dat) H64595 H64595 Helicobacter pylori 210 -11539555 7500958993 hp0608 h. pylori predicted coding region hp0608 (db:genpept-bct1) (de:helicobacter pylori section 52 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9460) (re:9942) (di:direct) HPAE000574 AE000574 g2313729 Helicobacter pylori 210 -11539555 7502853436 hp0608 h. pylori predicted coding region hp0608 (db:genpept) (de:helicobacter pylori 26695 section 52 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9460) (re:9942) (di:direct) HPAE000574 AE000574 g2313729 Helicobacter pylori 26695 85962 -11539555

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911345	18254	40410	420	139

Description

6500735698 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0609 HP0609 Helicobacter pylori 210 -11539556 7000690209 hypothetical protein hp0609 (db:pir2.dat) A64596 A64596 Helicobacter pylori 210 -11539556 7500958994 hp0609 h. pylori predicted coding region hp0609 (db:genpept-bct1) (de:helicobacter pylori section 53 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:103) (re:3819) (di:direct) HPAE000575 AE000575 g2313733 Helicobacter pylori 210 -11539556 7502853437 hp0609 h. pylori predicted coding region hp0609 (db:genpept) (de:helicobacter pylori 26695 section 53 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:103) (re:3819) (di:direct) HPAE000575 AE000575 g2313733 Helicobacter pylori 26695 85962 -11539556

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911360	18255	40411	642	213

Description

6500735699 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0611 HP0611 Helicobacter pylori 210 -11539557 7000690210 hypothetical protein hp0611 (db:pir2.dat) C64596 C64596 Helicobacter pylori 210 -11539557 7500958995 hp0611 h. pylori predicted coding region hp0611 (db:genpept-bct1) (de:helicobacter pylori section 53 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9724) (re:10224) (di:complement) HPAE000575 AE000575 g2313734 Helicobacter pylori 210 -11539557 7502853438 hp0611 h. pylori predicted coding region hp0611 (db:genpept) (de:helicobacter pylori 26695 section 53 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9724) (re:10224) (di:complement) HPAE000575 AE000575 g2313734 Helicobacter pylori 26695 85962 -11539557

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911376	18256	40412	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911377	18257	40413	576	191

Description

6500735700 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0612 HP0612 Helicobacter pylori 210 -11539558 7000690211 hypothetical protein hp0612 (db:pir2.dat) D64596 D64596 Helicobacter pylori 210 -11539558 7500958996 hp0612 h. pylori predicted coding region hp0612 (db:genpept-bct1) (de:helicobacter pylori section 53 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10241) (re:10480) (di:complement) HPAE000575 AE000575 g2313735 Helicobacter pylori 210 -11539558 7502853439 hp0612 h. pylori predicted coding region hp0612 (db:genpept) (de:helicobacter pylori 26695 section 53 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10241) (re:10480) (di:complement) HPAE000575 AE000575 g2313735 Helicobacter pylori 26695 85962 -11539558

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911379	18258	40414	216	71

Description

6500735701 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0614 HP0614 Helicobacter pylori 210 -11539559 7000690212 hypothetical protein hp0614 (db:pir2.dat) F64596 F64596 Helicobacter pylori 210 -11539559 7500958997 hp0614 h. pylori predicted coding region hp0614 (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:178) (re:513) (di:complement) HPAE000576 AE000576 g2313745 Helicobacter pylori 210 -11539559 7502853440 hp0614 h. pylori predicted coding region hp0614 (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:178) (re:513) (di:complement) HPAE000576 AE000576 g2313745 Helicobacter pylori 26695 85962 -11539559

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911387	18259	40415	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911390	18260	40416	246	81

Description

6500735702 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0622 HP0622 Helicobacter pylori 210 -11539560 7000690213 hypothetical protein hp0622 (db:pir2.dat) F64597 F64597 Helicobacter pylori 210 -11539560 7500958998 hp0622 h. pylori predicted coding region hp0622 (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10207) (re:10569) (di:complement) HPAE000576 AE000576 g2313746 Helicobacter pylori 210 -11539560 7502853441 hp0622 h. pylori predicted coding region hp0622 (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10207) (re:10569) (di:complement) HPAE000576 AE000576 g2313746 Helicobacter pylori 26695 85962 -11539560

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911391	18261	40417	366	121

Description

6500735703 aspb:hp0624 solute-binding signature and mitochondrialsignature protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0624 HP0624 Helicobacter pylori 210 -11539561 7500958999 hypothetical protein hp0624 (db:pir2.dat) H64597 H64597 Helicobacter pylori 210 -11539561 7500959000 hp0624 solute-binding signature and mitochondrial (db:genpept-bct1) (de:helicobacter pylori section 54 of 134 of the complete genome.) (nt:similar to egad:37753 percent identity: 26.39;) (le:11911) (re:13038) (di:complement) HPAE000576 AE000576 g2313744 Helicobacter pylori 210 -11539561 7502853442 hp0624 solute-binding signature and mitochondrial (db:genpept) (de:helicobacter pylori 26695 section 54 of 134 of the complete genome.) (nt:similar to egad:37753 percent identity: 26.39;) (le:11911) (re:13038) (di:complement) HPAE000576 AE000576 g2313744 Helicobacter pylori 26695 85962 -11539561

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911396	18262	40418	963	320

Description

6500735704 gcpe:hp0625 protein e (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0625 HP0625 Helicobacter pylori 210 -11539562 7000689475 protein e (cl:gcpe protein) (db:pir2.dat) A64598 A64598 Helicobacter pylori 210 -11539562 7500955773 hp0625 protein e gcpe (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:similar to egad:29004 percent identity: 47.71;) (le:90) (re:1169) (di:direct) HPAE000577 AE000577 g2313753 Helicobacter pylori 210 -11539562 7502853443 hp0625 protein e gcpe (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:similar to egad:29004 percent identity: 47.71;) (le:90) (re:1169) (di:direct) HPAE000577 AE000577 g2313753 Helicobacter pylori 26695 85962 -11539562

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911401	18263	40419	579	192

Description

6500735705 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0627 HP0627 Helicobacter pylori 210 -11539563 7000690214 hypothetical protein hp0627 (db:pir2.dat) C64598 C64598 Helicobacter pylori 210 -11539563 7500959001 hp0627 h. pylori predicted coding region hp0627 (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2389) (re:2721) (di:direct) HPAE000577 AE000577 g2313756 Helicobacter pylori 210 -11539563 7502853444 hp0627 h. pylori predicted coding region hp0627 (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2389) (re:2721) (di:direct) HPAE000577 AE000577 g2313756 Helicobacter pylori 26695 85962 -11539563

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911402	18264	40420	480	159

Description

6500735706 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0628 HP0628 Helicobacter pylori 210 -11539564 7000690215 hypothetical protein hp0628 (db:pir2.dat) D64598 D64598 Helicobacter pylori 210 -11539564 7500959002 hp0628 h. pylori predicted coding region hp0628 (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2770) (re:3447) (di:direct) HPAE000577 AE000577 g2313757 Helicobacter pylori 210 -11539564 7502853445 hp0628 h. pylori predicted coding region hp0628 (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2770) (re:3447) (di:direct) HPAE000577 AE000577 g2313757 Helicobacter pylori 26695 85962 -11539564

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911403	18265	40421	579	192

Description

6500735707 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0629 HP0629 Helicobacter pylori 210 -11539565 7000690216 hypothetical protein hp0629 (db:pir2.dat) E64598 E64598 Helicobacter pylori 210 -11539565 7500959003 hp0629 h. pylori predicted coding region hp0629 (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3604) (re:5649) (di:direct) HPAE000577 AE000577 g2313758 Helicobacter pylori 210 -11539565 7502853446 hp0629 h. pylori predicted coding region hp0629 (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3604) (re:5649) (di:direct) HPAE000577 AE000577 g2313758 Helicobacter pylori 26695 85962 -11539565

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911421	18266	40422	738	245

Description

6500735708 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0635 HP0635 Helicobacter pylori 210 -11539566 7000690217 hypothetical protein hp0635 (db:pir2.dat) C64599 C64599 Helicobacter pylori 210 -11539566 7500959004 hp0635 h. pylori predicted coding region hp0635 (db:genpept-bct1) (de:helicobacter pylori section 55 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10560) (re:12098) (di:direct) HPAE000577 AE000577 g2313755 Helicobacter pylori 210 -11539566 7502853447 hp0635 h. pylori predicted coding region hp0635 (db:genpept) (de:helicobacter pylori 26695 section 55 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10560) (re:12098) (di:direct) HPAE000577 AE000577 g2313755 Helicobacter pylori 26695 85962 -11539566

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911435	18267	40423	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911438	18268	40424	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911439	18269	40425	834	277

Description

6500735709 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0636 HP0636 Helicobacter pylori 210 -11539567 7000690218 hypothetical protein hp0636 (db:pir2.dat) D64599 D64599 Helicobacter pylori 210 -11539567 7500959005 hp0636 h. pylori predicted coding region hp0636 (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:91) (re:369) (di:complement) HPAE000578 AE000578 g2313772 Helicobacter pylori 210 -11539567 7502853448 hp0636 h. pylori predicted coding region hp0636 (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:91) (re:369) (di:complement) HPAE000578 AE000578 g2313772 Helicobacter pylori 26695 85962 -11539567

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911440	18270	40426	651	216

Description

6500735710 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0637 HP0637 Helicobacter pylori 210 -11539568 7000690219 hypothetical protein hp0637 (db:pir2.dat) E64599 E64599 Helicobacter pylori 210 -11539568 7500959006 hp0637 h. pylori predicted coding region hp0637 (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:498) (re:950) (di:complement) HPAE000578 AE000578 g2313773 Helicobacter pylori 210 -11539568 7502853449 hp0637 h. pylori predicted coding region hp0637 (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:498) (re:950) (di:complement) HPAE000578 AE000578 g2313773 Helicobacter pylori 26695 85962 -11539568

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911473	18271	40427	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911482	18272	40428	300	99

Description

6500735711 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0641 HP0641 Helicobacter pylori 210 -11539569 7000690220 hypothetical protein hp0641 (db:pir2.dat) A64600 A64600 Helicobacter pylori 210 -11539569 7500959007 hp0641 h. pylori predicted coding region hp0641 (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4051) (re:4278) (di:direct) HPAE000578 AE000578 g2313775 Helicobacter pylori 210 -11539569 7502853450 hp0641 h. pylori predicted coding region hp0641 (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4051) (re:4278) (di:direct) HPAE000578 AE000578 g2313775 Helicobacter pylori 26695 85962 -11539569

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911489	18273	40429	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911496	18274	40430	597	198

Description

6500735712 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0647 HP0647 Helicobacter pylori 210 -11539570 7000690221 hypothetical protein hp0647 (db:pir2.dat) G64600 G64600 Helicobacter pylori 210 -11539570 7500959008 hp0647 h. pylori predicted coding region hp0647 (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9228) (re:9635) (di:direct) HPAE000578 AE000578 g2313776 Helicobacter pylori 210 -11539570 7502853451 hp0647 h. pylori predicted coding region hp0647 (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9228) (re:9635) (di:direct) HPAE000578 AE000578 g2313776 Helicobacter pylori 26695 85962 -11539570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911500	18275	40431	582	193

Description

6500735713 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0650 HP0650 Helicobacter pylori 210 -11539571 7000690222 hypothetical protein hp0650 (db:pir2.dat) B64601 B64601 Helicobacter pylori 210 -11539571 7500959009 hp0650 h. pylori predicted coding region hp0650 (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12415) (re:13005) (di:direct) HPAE000578 AE000578 g2313777 Helicobacter pylori 210 -11539571 7502853452 hp0650 h. pylori predicted coding region hp0650 (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12415) (re:13005) (di:direct) HPAE000578 AE000578 g2313777 Helicobacter pylori 26695 85962 -11539571

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911505	18276	40432	267	88

Description

6500735714 pet112-like protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0658 HP0658 Helicobacter pylori 210 -11539572 7000689481 pet112-like protein (cl:pet112 protein) (db:pir2.dat) B64602 B64602 Helicobacter pylori 210 -11539572 7500955779 hp0658 pet112-like protein (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to gp:1354211 percent identity: 45.36;) (le:6458) (re:7885) (di:direct) HPAE000579 AE000579 g2313783 Helicobacter pylori 210 -11539572 7502853453 hp0658 pet112-like protein (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to gp:1354211 percent identity: 45.36;) (le:6458) (re:7885) (di:direct) HPAE000579 AE000579 g2313783 Helicobacter pylori 26695 85962 -11539572

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911509	18277	40433	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911523	18278	40434	981	326

Description

6500735715 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0659 HP0659 Helicobacter pylori 210 -11539573 7000690223 hypothetical protein hp0659 (db:pir2.dat) C64602 C64602 Helicobacter pylori 210 -11539573 7500959010 hp0659 h. pylori predicted coding region hp0659 (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7885) (re:9129) (di:direct) HPAE000579 AE000579 g2313789 Helicobacter pylori 210 -11539573 7502853454 hp0659 h. pylori predicted coding region hp0659 (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7885) (re:9129) (di:direct) HPAE000579 AE000579 g2313789 Helicobacter pylori 26695 85962 -11539573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911542	18279	40435	1170	389

Description

6500735716 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0660 HP0660 Helicobacter pylori 210 -11539574 7000690224 hypothetical protein hp0660 (db:pir2.dat) D64602 D64602 Helicobacter pylori 210 -11539574 7500959011 hp0660 h. pylori predicted coding region hp0660 (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9139) (re:10155) (di:direct) HPAE000579 AE000579 g2313790 Helicobacter pylori 210 -11539574 7502853455 hp0660 h. pylori predicted coding region hp0660 (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9139) (re:10155) (di:direct) HPAE000579 AE000579 g2313790 Helicobacter pylori 26695 85962 -11539574

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911543	18280	40436	567	188

Description

7500959013 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0664 HP0664 Helicobacter pylori 210 -11539575 7000690225 hypothetical protein hp0664 (db:pir2.dat) H64602 H64602 Helicobacter pylori 210 -11539575 7500959012 hp0664 h. pylori predicted coding region hp0664 (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12436) (re:12951) (di:direct) HPAE000579 AE000579 g2313791 Helicobacter pylori 210 -11539575 7502853456 jhp0609 putative (db:genpept) (de:helicobacter pylori, strain j99 section 53 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0664) (le:12418) (re:12933) (di:direct) AE001492 AE001492 g4155148 Helicobacter pylori J99 85963 -11539575 6500735717 hp0664 h. pylori predicted coding region hp0664 (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12436) (re:12951) (di:direct) HPAE000579 AE000579 g2313791 Helicobacter pylori 26695 85962 -11539575

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911544	18281	40437	462	153

Description

6500735718 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0667 HP0667 Helicobacter pylori 210 -11539576 7000690226 hypothetical protein hp0667 (db:pir2.dat) C64603 C64603 Helicobacter pylori 210 -11539576 7500959014 hp0667 h. pylori predicted coding region hp0667 (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:68) (re:325) (di:direct) HPAE000580 AE000580 g2313796 Helicobacter pylori 210 -11539576 7502853457 hp0667 h. pylori predicted coding region hp0667 (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:68) (re:325) (di:direct) HPAE000580 AE000580 g2313796 Helicobacter pylori 26695 85962 -11539576

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911552	18282	40438	225	74

Description

GTC ORF with score 118 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 9931.) (nt:similar to rna helicases (swissprot accession) (le:21627) (re:25934) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911579	18283	40439	564	187

Description

6500735719 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0668 HP0668 Helicobacter pylori 210 -11539577 7000690227 hypothetical protein hp0668 (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) D64603 D64603 Helicobacter pylori 210 -11539577 7500954374 hp0668 h. pylori predicted coding region hp0668 (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:300) (re:2123) (di:direct) HPAE000580 AE000580 g2313797 Helicobacter pylori 210 -11539577 7502853458 hp0668 h. pylori predicted coding region hp0668 (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:300) (re:2123) (di:direct) HPAE000580 AE000580 g2313797 Helicobacter pylori 26695 85962 -11539577

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911603	18284	40440	318	105

Description

GTC ORF with score 170 to: (or:Magnaporthe grisea) (db:genpept-pln2) (de:magnaporthe grisea map kinase mps1 (mps1) gene, complete cds.) (nt:similar to s. cerevisiae protein kinase slt2) (le:332:592:827:1012:1426) (re:444:724:893:1326:2045) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911604	18285	40441	372	123

Description

GTC ORF with score 563 to: (or:Magnaporthe grisea) (db:genpept-pln2) (de:magnaporthe grisea map kinase mps1 (mps1) gene, complete cds.) (nt:similar to s. cerevisiae protein kinase slt2) (le:332:592:827:1012:1426) (re:444:724:893:1326:2045) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911607	18286	40442	1452	483

Description

6500735720 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0669 HP0669 Helicobacter pylori 210 -11539578 7000690228 hypothetical protein hp0669 (db:pir2.dat) E64603 E64603 Helicobacter pylori 210 -11539578 7500959015 hp0669 h. pylori predicted coding region hp0669 (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2038) (re:4839) (di:direct) HPAE000580 AE000580 g2313798 Helicobacter pylori 210 -11539578 7502853459 hp0669 h. pylori predicted coding region hp0669 (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2038) (re:4839) (di:direct) HPAE000580 AE000580 g2313798 Helicobacter pylori 26695 85962 -11539578

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911619	18287	40443	672	223

Description

GTC ORF with score 786 to: (or:Magnaporthe grisea) (db:genpept-pln2) (de:magnaporthe grisea map kinase mps1 (mps1) gene, complete cds.) (nt:similar to s. cerevisiae protein kinase slt2) (le:332:592:827:1012:1426) (re:444:724:893:1326:2045) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911625	18288	40444	231	76

Description

GTC ORF with score 101 to: (or:Caenorhabditis elegans) (db:genpept-inv) (de:caenorhabditis elegans cosmid c41g7, complete sequence.) (nt:cdna est embl:c13282 comes from this gene; cdna est) (le:17670:17756:18346) (re:17699:18296:18434) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911633	18289	40445	324	107

Description

GTC ORF with score 172 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t11j7 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:43486:43733:43982) (re:43635:43861:44454) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911634	18290	40446	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911643	18291	40447	603	200

Description

GTC ORF with score 191 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t11j7 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:43486:43733:43982) (re:43635:43861:44454) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911654	18292	40448	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911663	18293	40449	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911675	18294	40450	864	288

Description

6500735721 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0670 HP0670 Helicobacter pylori 210 -11539579 7000690229 hypothetical protein hp0670 (db:pir2.dat) F64603 F64603 Helicobacter pylori 210 -11539579 7500959016 hp0670 h. pylori predicted coding region hp0670 (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4836) (re:6185) (di:direct) HPAE000580 AE000580 g2313799 Helicobacter pylori 210 -11539579 7502853460 hp0670 h. pylori predicted coding region hp0670 (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4836) (re:6185) (di:direct) HPAE000580 AE000580 g2313799 Helicobacter pylori 26695 85962 -11539579

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911691	18295	40451	345	114

Description

6500735722 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0673 HP0673 Helicobacter pylori 210 -11539580 7000690230 hypothetical protein hp0673 (db:pir2.dat) A64604 A64604 Helicobacter pylori 210 -11539580 7500959019 hp0673 h. pylori predicted coding region hp0673 (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8532) (re:9812) (di:direct) HPAE000580 AE000580 g2313800 Helicobacter pylori 210 -11539580 7502853461 hp0673 h. pylori predicted coding region hp0673 (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8532) (re:9812) (di:direct) HPAE000580 AE000580 g2313800 Helicobacter pylori 26695 85962 -11539580

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911695	18296	40452	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911696	18297	40453	318	105

Description

6500735723 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0674 HP0674 Helicobacter pylori 210 -11539581 7000690231 hypothetical protein hp0674 (db:pir2.dat) B64604 B64604 Helicobacter pylori 210 -11539581 7500959020 hp0674 h. pylori predicted coding region hp0674 (db:genpept-bct1) (de:helicobacter pylori section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9784) (re:10470) (di:direct) HPAE000580 AE000580 g2313801 Helicobacter pylori 210 -11539581 7502853462 hp0674 h. pylori predicted coding region hp0674 (db:genpept) (de:helicobacter pylori 26695 section 58 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9784) (re:10470) (di:direct) HPAE000580 AE000580 g2313801 Helicobacter pylori 26695 85962 -11539581

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911697	18298	40454	396	131

Description

6500735724 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0678 HP0678 Helicobacter pylori 210 -11539582 7000690232 hypothetical protein hp0678 (db:pir2.dat) F64604 F64604 Helicobacter pylori 210 -11539582 7500959021 hp0678 h. pylori predicted coding region hp0678 (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1452) (re:1562) (di:complement) HPAE000581 AE000581 g2313811 Helicobacter pylori 210 -11539582 7502853463 hp0678 h. pylori predicted coding region hp0678 (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1452) (re:1562) (di:complement) HPAE000581 AE000581 g2313811 Helicobacter pylori 26695 85962 -11539582

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911706	18299	40455	687	228

Description

6500735725 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0681 HP0681 Helicobacter pylori 210 -11539583 7000690233 hypothetical protein hp0681 (db:pir2.dat) A64605 A64605 Helicobacter pylori 210 -11539583 7500959022 hp0681 h. pylori predicted coding region hp0681 (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5000) (re:5506) (di:complement) HPAE000581 AE000581 g2313809 Helicobacter pylori 210 -11539583 7502853464 hp0681 h. pylori predicted coding region hp0681 (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5000) (re:5506) (di:complement) HPAE000581 AE000581 g2313809 Helicobacter pylori 26695 85962 -11539583

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911713	18300	40456	744	247

Description

6500735726 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0682 HP0682 Helicobacter pylori 210 -11539584 7000690234 hypothetical protein hp0682 (db:pir2.dat) B64605 B64605 Helicobacter pylori 210 -11539584 7500959023 hp0682 h. pylori predicted coding region hp0682 (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5546) (re:5926) (di:complement) HPAE000581 AE000581 g2313810 Helicobacter pylori 210 -11539584 7502853465 hp0682 h. pylori predicted coding region hp0682 (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5546) (re:5926) (di:complement) HPAE000581 AE000581 g2313810 Helicobacter pylori 26695 85962 -11539584

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911715	18301	40457	477	158

Description

6500735727 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0688 HP0688 Helicobacter pylori 210 -11539585 7000690235 hypothetical protein hp0688 (db:pir2.dat) H64605 H64605 Helicobacter pylori 210 -11539585 7500959024 hp0688 h. pylori predicted coding region hp0688 (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2226) (re:2726) (di:direct) HPAE000582 AE000582 g2313822 Helicobacter pylori 210 -11539585 7502853466 hp0688 h. pylori predicted coding region hp0688 (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2226) (re:2726) (di:direct) HPAE000582 AE000582 g2313822 Helicobacter pylori 26695 85962 -11539585

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911716	18302	40458	669	222

Description

6500735728 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0689 HP0689 Helicobacter pylori 210 -11539586 7000690236 hypothetical protein hp0689 (db:pir2.dat) A64606 A64606 Helicobacter pylori 210 -11539586 7500959025 hp0689 h. pylori predicted coding region hp0689 (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2747) (re:3037) (di:direct) HPAE000582 AE000582 g2313823 Helicobacter pylori 210 -11539586 7502853467 hp0689 h. pylori predicted coding region hp0689 (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2747) (re:3037) (di:direct) HPAE000582 AE000582 g2313823 Helicobacter pylori 26695 85962 -11539586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911726	18303	40459	879	292

Description

6500735729 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0694 HP0694 Helicobacter pylori 210 -11539587 7000690237 hypothetical protein hp0694 (db:pir2.dat) F64606 F64606 Helicobacter pylori 210 -11539587 7500959026 hp0694 h. pylori predicted coding region hp0694 (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7332) (re:8105) (di:direct) HPAE000582 AE000582 g2313820 Helicobacter pylori 210 -11539587 7502853468 hp0694 h. pylori predicted coding region hp0694 (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7332) (re:8105) (di:direct) HPAE000582 AE000582 g2313820 Helicobacter pylori 26695 85962 -11539587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911729	18304	40460	489	162

Description

6500735730 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0697 HP0697 Helicobacter pylori 210 -11539588 7000690238 hypothetical protein hp0697 (db:pir2.dat) A64607 A64607 Helicobacter pylori 210 -11539588 7500959027 hp0697 h. pylori predicted coding region hp0697 (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13022) (re:13528) (di:direct) HPAE000582 AE000582 g2313821 Helicobacter pylori 210 -11539588 7502853469 hp0697 h. pylori predicted coding region hp0697 (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13022) (re:13528) (di:direct) HPAE000582 AE000582 g2313821 Helicobacter pylori 26695 85962 -11539588

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911730	18305	40461	339	112

Description

6500735731 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0698 HP0698 Helicobacter pylori 210 -11539589 7000690239 hypothetical protein hp0698 (db:pir2.dat) B64607 B64607 Helicobacter pylori 210 -11539589 7500959028 hp0698 h. pylori predicted coding region hp0698 (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:124) (re:213) (di:direct) HPAE000583 AE000583 g2313832 Helicobacter pylori 210 -11539589 7502853470 hp0698 h. pylori predicted coding region hp0698 (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:124) (re:213) (di:direct) HPAE000583 AE000583 g2313832 Helicobacter pylori 26695 85962 -11539589

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911739	18306	40462	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911771	18307	40463	453	150

Description

6500735732 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0699 HP0699 Helicobacter pylori 210 -11539590 7000690240 hypothetical protein hp0699 (db:pir2.dat) C64607 C64607 Helicobacter pylori 210 -11539590 7500959029 hp0699 h. pylori predicted coding region hp0699 (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:253) (re:1281) (di:direct) HPAE000583 AE000583 g2313830 Helicobacter pylori 210 -11539590 7502853471 hp0699 h. pylori predicted coding region hp0699 (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:253) (re:1281) (di:direct) HPAE000583 AE000583 g2313830 Helicobacter pylori 26695 85962 -11539590

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911772	18308	40464	549	182

Description

6500735733 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0702 HP0702 Helicobacter pylori 210 -11539591 7000690241 hypothetical protein hp0702 (db:pir2.dat) F64607 F64607 Helicobacter pylori 210 -11539591 7500959030 hp0702 h. pylori predicted coding region hp0702 (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4160) (re:4636) (di:direct) HPAE000583 AE000583 g2313831 Helicobacter pylori 210 -11539591 7502853472 hp0702 h. pylori predicted coding region hp0702 (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4160) (re:4636) (di:direct) HPAE000583 AE000583 g2313831 Helicobacter pylori 26695 85962 -11539591

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911793	18309	40465	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911804	18310	40466	813	270

Description

GTC ORF with score 600 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911812	18311	40467	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911817	18312	40468	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911820	18313	40469	750	249

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911837	18314	40470	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911842	18315	40471	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911848	18316	40472	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911849	18317	40473	219	72

Description

6500735734 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0704 HP0704 Helicobacter pylori 210 -11539592 7000690242 hypothetical protein hp0704 (db:pir2.dat) H64607 H64607 Helicobacter pylori 210 -11539592 7500959031 hp0704 h. pylori predicted coding region hp0704 (db:genpept-bct1) (de:helicobacter pylori section 61 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6239) (re:6349) (di:direct) HPAE000583 AE000583 g2313833 Helicobacter pylori 210 -11539592 7502853473 hp0704 h. pylori predicted coding region hp0704 (db:genpept) (de:helicobacter pylori 26695 section 61 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6239) (re:6349) (di:direct) HPAE000583 AE000583 g2313833 Helicobacter pylori 26695 85962 -11539592

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911850	18318	40474	228	75

Description

6500735735 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0708 HP0708 Helicobacter pylori 210 -11539593 7000690243 hypothetical protein hp0708 (db:pir2.dat) D64608 D64608 Helicobacter pylori 210 -11539593 7500959032 hp0708 h. pylori predicted coding region hp0708 (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1067) (re:1411) (di:direct) HPAE000584 AE000584 g2313842 Helicobacter pylori 210 -11539593 7502853474 hp0708 h. pylori predicted coding region hp0708 (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1067) (re:1411) (di:direct) HPAE000584 AE000584 g2313842 Helicobacter pylori 26695 85962 -11539593

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911870	18319	40475	420	139

Description

6500735736 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0711 HP0711 Helicobacter pylori 210 -11539594 7000690244 hypothetical protein hp0711 (db:pir2.dat) G64608 G64608 Helicobacter pylori 210 -11539594 7500959033 hp0711 h. pylori predicted coding region hp0711 (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5002) (re:6222) (di:direct) HPAE000584 AE000584 g2313843 Helicobacter pylori 210 -11539594 7502853475 hp0711 h. pylori predicted coding region hp0711 (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5002) (re:6222) (di:direct) HPAE000584 AE000584 g2313843 Helicobacter pylori 26695 85962 -11539594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911871	18320	40476	561	186

Description

6500735737 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0712 HP0712 Helicobacter pylori 210 -11539595 7000690245 hypothetical protein hp0712 (db:pir2.dat) H64608 H64608 Helicobacter pylori 210 -11539595 7500959034 hp0712 h. pylori predicted coding region hp0712 (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6222) (re:6596) (di:direct) HPAE000584 AE000584 g2313844 Helicobacter pylori 210 -11539595 7502853476 hp0712 h. pylori predicted coding region hp0712 (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6222) (re:6596) (di:direct) HPAE000584 AE000584 g2313844 Helicobacter pylori 26695 85962 -11539595

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911875	18321	40477	420	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911892	18322	40478	306	101

Description

6500735738 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0719 HP0719 Helicobacter pylori 210 -11539596 7000690246 hypothetical protein hp0719 (db:pir2.dat) G64609 G64609 Helicobacter pylori 210 -11539596 7500959035 hp0719 h. pylori predicted coding region hp0719 (db:genpept-bct1) (de:helicobacter pylori section 63 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:905) (re:1234) (di:direct) HPAE000585 AE000585 g2313850 Helicobacter pylori 210 -11539596 7502853477 hp0719 h. pylori predicted coding region hp0719 (db:genpept) (de:helicobacter pylori 26695 section 63 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:905) (re:1234) (di:direct) HPAE000585 AE000585 g2313850 Helicobacter pylori 26695 85962 -11539596

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911899	18323	40479	1440	479

Description

6500735739 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0720 HP0720 Helicobacter pylori 210 -11539597 7000690247 hypothetical protein hp0720 (db:pir2.dat) H64609 H64609 Helicobacter pylori 210 -11539597 7500959036 hp0720 h. pylori predicted coding region hp0720 (db:genpept-bct1) (de:helicobacter pylori section 63 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1227) (re:1388) (di:direct) HPAE000585 AE000585 g2313853 Helicobacter pylori 210 -11539597 7502853478 hp0720 h. pylori predicted coding region hp0720 (db:genpept) (de:helicobacter pylori 26695 section 63 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1227) (re:1388) (di:direct) HPAE000585 AE000585 g2313853 Helicobacter pylori 26695 85962 -11539597

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911917	18324	40480	396	131

Description

6500735740 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0721 HP0721 Helicobacter pylori 210 -11539598 7000690248 hypothetical protein hp0721 (db:pir2.dat) A64610 A64610 Helicobacter pylori 210 -11539598 7500959037 hp0721 h. pylori predicted coding region hp0721 (db:genpept-bct1) (de:helicobacter pylori section 63 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1416) (re:1874) (di:direct) HPAE000585 AE000585 g2313852 Helicobacter pylori 210 -11539598 7502853479 hp0721 h. pylori predicted coding region hp0721 (db:genpept) (de:helicobacter pylori 26695 section 63 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1416) (re:1874) (di:direct) HPAE000585 AE000585 g2313852 Helicobacter pylori 26695 85962 -11539598

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911924	18325	40481	390	129

Description

GTC ORF with score 169 to: (sr:human) (db:genpept-pri2) (de:homo sapiens dna sequence from pac 422h11 on chromosome6p21.1-22.2. contains the gene coding for two isoforms of a knownserine kinase. contains ests, stss and a gss, complete sequence.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911932	18326	40482	312	103

Description

6500735741 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0726 HP0726 Helicobacter pylori 210 -11539599 7000690249 hypothetical protein hp0726 (db:pir2.dat) F64610 F64610 Helicobacter pylori 210 -11539599 7500959038 hp0726 h. pylori predicted coding region hp0726 (db:genpept-bct1) (de:helicobacter pylori section 63 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8975) (re:9892) (di:complement) HPAE000585 AE000585 g2313851 Helicobacter pylori 210 -11539599 7502853480 hp0726 h. pylori predicted coding region hp0726 (db:genpept) (de:helicobacter pylori 26695 section 63 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8975) (re:9892) (di:complement) HPAE000585 AE000585 g2313851 Helicobacter pylori 26695 85962 -11539599

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911937	18327	40483	909	302

Description

6500735742 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0729 HP0729 Helicobacter pylori 210 -11539600 7000690250 hypothetical protein hp0729 (db:pir2.dat) A64611 A64611 Helicobacter pylori 210 -11539600 7500959039 hp0729 h. pylori predicted coding region hp0729 (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1129) (re:2196) (di:complement) HPAE000586 AE000586 g2313864 Helicobacter pylori 210 -11539600 7502853481 hp0729 h. pylori predicted coding region hp0729 (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1129) (re:2196) (di:complement) HPAE000586 AE000586 g2313864 Helicobacter pylori 26695 85962 -11539600

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911943	18328	40484	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911949	18329	40485	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911956	18330	40486	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911958	18331	40487	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911964	18332	40488	696	231

Description

6500735743 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0730 HP0730 Helicobacter pylori 210 -11539601 7000690251 hypothetical protein hp0730 (db:pir2.dat) B64611 B64611 Helicobacter pylori 210 -11539601 7500959040 hp0730 h. pylori predicted coding region hp0730 (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2205) (re:2510) (di:complement) HPAE000586 AE000586 g2313865 Helicobacter pylori 210 -11539601 7502853482 hp0730 h. pylori predicted coding region hp0730 (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2205) (re:2510) (di:complement) HPAE000586 AE000586 g2313865 Helicobacter pylori 26695 85962 -11539601

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911973	18333	40489	732	243

Description

6500735744 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0731 HP0731 Helicobacter pylori 210 -11539602 7000690252 hypothetical protein hp0731 (db:pir2.dat) C64611 C64611 Helicobacter pylori 210 -11539602 7500959041 hp0731 h. pylori predicted coding region hp0731 (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2602) (re:4323) (di:complement) HPAE000586 AE000586 g2313866 Helicobacter pylori 210 -11539602 7502853483 hp0731 h. pylori predicted coding region hp0731 (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2602) (re:4323) (di:complement) HPAE000586 AE000586 g2313866 Helicobacter pylori 26695 85962 -11539602

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911978	18334	40490	1800	599

Description

6500735745 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0732 HP0732 Helicobacter pylori 210 -11539603 7500975638 hp0732 h. pylori predicted coding region hp0732 (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4313) (re:4669) (di:complement) HPAE000586 AE000586 g2313867 Helicobacter pylori 210 -11539603 7502853484 hp0732 h. pylori predicted coding region hp0732 (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4313) (re:4669) (di:complement) HPAE000586 AE000586 g2313867 Helicobacter pylori 26695 85962 -11539603

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501911979	18335	40491	411	136

Description

6500735746 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0733 HP0733 Helicobacter pylori 210 -11539604 7000690254 hypothetical protein hp0733 (db:pir2.dat) E64611 E64611 Helicobacter pylori 210 -11539604 7500959042 hp0733 h. pylori predicted coding region hp0733 (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4618) (re:6183) (di:complement) HPAE000586 AE000586 g2313868 Helicobacter pylori 210 -11539604 7502853485 hp0733 h. pylori predicted coding region hp0733 (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4618) (re:6183) (di:complement) HPAE000586 AE000586 g2313868 Helicobacter pylori 26695 85962 -11539604

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912003	18336	40492	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912011	18337	40493	504	168

Description

6500735747 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0746 HP0746 Helicobacter pylori 210 -11539605 7000690255 hypothetical protein hp0746 (db:pir2.dat) B64613 B64613 Helicobacter pylori 210 -11539605 7500959044 hp0746 h. pylori predicted coding region hp0746 (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4553) (re:5812) (di:direct) HPAE000587 AE000587 g2313878 Helicobacter pylori 210 -11539605 7502853486 hp0746 h. pylori predicted coding region hp0746 (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4553) (re:5812) (di:direct) HPAE000587 AE000587 g2313878 Helicobacter pylori 26695 85962 -11539605

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912016	18338	40494	252	83

Description

6500735748 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0750 HP0750 Helicobacter pylori 210 -11539606 7000690256 hypothetical protein hp0750 (db:pir2.dat) F64613 F64613 Helicobacter pylori 210 -11539606 7500959045 hp0750 h. pylori predicted coding region hp0750 (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8458) (re:9660) (di:direct) HPAE000587 AE000587 g2313879 Helicobacter pylori 210 -11539606 7502853487 hp0750 h. pylori predicted coding region hp0750 (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8458) (re:9660) (di:direct) HPAE000587 AE000587 g2313879 Helicobacter pylori 26695 85962 -11539606

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912025	18339	40495	456	151

Description

6500735749 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0754 HP0754 Helicobacter pylori 210 -11539607 7000690257 hypothetical protein hp0754 (db:pir2.dat) B64614 B64614 Helicobacter pylori 210 -11539607 7500959046 hp0754 h. pylori predicted coding region hp0754 (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:433) (re:672) (di:direct) HPAE000588 AE000588 g2313888 Helicobacter pylori 210 -11539607 7502853488 hp0754 h. pylori predicted coding region hp0754 (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:433) (re:672) (di:direct) HPAE000588 AE000588 g2313888 Helicobacter pylori 26695 85962 -11539607

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912026	18340	40496	600	199

Description

6500735750 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0756 HP0756 Helicobacter pylori 210 -11539608 7000690258 hypothetical protein hp0756 (db:pir2.dat) D64614 D64614 Helicobacter pylori 210 -11539608 7500959047 hp0756 h. pylori predicted coding region hp0756 (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1399) (re:1545) (di:direct) HPAE000588 AE000588 g2313894 Helicobacter pylori 210 -11539608 7502853489 hp0756 h. pylori predicted coding region hp0756 (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1399) (re:1545) (di:direct) HPAE000588 AE000588 g2313894 Helicobacter pylori 26695 85962 -11539608

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912037	18341	40497	462	153

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912040	18342	40498	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912046	18343	40499	1749	582

Description

6500735751 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0761 HP0761 Helicobacter pylori 210 -11539609 7000690259 hypothetical protein hp0761 (db:pir2.dat) A64615 A64615 Helicobacter pylori 210 -11539609 7500959048 hp0761 h. pylori predicted coding region hp0761 (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6675) (re:7277) (di:complement) HPAE000588 AE000588 g2313889 Helicobacter pylori 210 -11539609 7502853490 hp0761 h. pylori predicted coding region hp0761 (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6675) (re:7277) (di:complement) HPAE000588 AE000588 g2313889 Helicobacter pylori 26695 85962 -11539609

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912048	18344	40500	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912057	18345	40501	858	285

Description

6500735752 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0762 HP0762 Helicobacter pylori 210 -11539610 7000690260 hypothetical protein hp0762 (db:pir2.dat) B64615 B64615 Helicobacter pylori 210 -11539610 7500959049 hp0762 h. pylori predicted coding region hp0762 (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7447) (re:8004) (di:direct) HPAE000588 AE000588 g2313890 Helicobacter pylori 210 -11539610 7502853491 hp0762 h. pylori predicted coding region hp0762 (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7447) (re:8004) (di:direct) HPAE000588 AE000588 g2313890 Helicobacter pylori 26695 85962 -11539610

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912071	18346	40502	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912073	18347	40503	954	317

Description

6500735753 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0764 HP0764 Helicobacter pylori 210 -11539611 7000690261 hypothetical protein hp0764 (db:pir2.dat) D64615 D64615 Helicobacter pylori 210 -11539611 7500959050 hp0764 h. pylori predicted coding region hp0764 (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8903) (re:10189) (di:complement) HPAE000588 AE000588 g2313891 Helicobacter pylori 210 -11539611 7502853492 hp0764 h. pylori predicted coding region hp0764 (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8903) (re:10189) (di:complement) HPAE000588 AE000588 g2313891 Helicobacter pylori 26695 85962 -11539611

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912097	18348	40504	243	80

Description

6500735754 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0765 HP0765 Helicobacter pylori 210 -11539612 7000690262 hypothetical protein hp0765 (db:pir2.dat) E64615 E64615 Helicobacter pylori 210 -11539612 7500959051 hp0765 h. pylori predicted coding region hp0765 (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10200) (re:10508) (di:complement) HPAE000588 AE000588 g2313892 Helicobacter pylori 210 -11539612 7502853493 hp0765 h. pylori predicted coding region hp0765 (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10200) (re:10508) (di:complement) HPAE000588 AE000588 g2313892 Helicobacter pylori 26695 85962 -11539612

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912109	18349	40505	1356	451

Description

6500735755 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0766 HP0766 Helicobacter pylori 210 -11539613 7000690263 hypothetical protein hp0766 (db:pir2.dat) F64615 F64615 Helicobacter pylori 210 -11539613 7500959052 hp0766 h. pylori predicted coding region hp0766 (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10519) (re:11343) (di:complement) HPAE000588 AE000588 g2313893 Helicobacter pylori 210 -11539613 7502853494 hp0766 h. pylori predicted coding region hp0766 (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10519) (re:11343) (di:complement) HPAE000588 AE000588 g2313893 Helicobacter pylori 26695 85962 -11539613

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912116	18350	40506	4470	1489

Description

6500735756 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0767 HP0767 Helicobacter pylori 210 -11539614 7000690264 hypothetical protein hp0767 (db:pir2.dat) G64615 G64615 Helicobacter pylori 210 -11539614 7500959053 hp0767 h. pylori predicted coding region hp0767 (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:73) (re:147) (di:complement) HPAE000589 AE000589 g2313906 Helicobacter pylori 210 -11539614 7502853495 hp0767 h. pylori predicted coding region hp0767 (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:73) (re:147) (di:complement) HPAE000589 AE000589 g2313906 Helicobacter pylori 26695 85962 -11539614

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912124	18351	40507	2130	709

Description

6500735757 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0771 HP0771 Helicobacter pylori 210 -11539615 7000690265 hypothetical protein hp0771 (db:pir2.dat) C64616 C64616 Helicobacter pylori 210 -11539615 7500959054 hp0771 h. pylori predicted coding region hp0771 (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3051) (re:3788) (di:complement) HPAE000589 AE000589 g2313903 Helicobacter pylori 210 -11539615 7502853496 hp0771 h. pylori predicted coding region hp0771 (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3051) (re:3788) (di:complement) HPAE000589 AE000589 g2313903 Helicobacter pylori 26695 85962 -11539615

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912126	18352	40508	498	165

Description

6500735758 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0773 HP0773 Helicobacter pylori 210 -11539616 7000690266 hypothetical protein hp0773 (db:pir2.dat) E64616 E64616 Helicobacter pylori 210 -11539616 7500959055 hp0773 h. pylori predicted coding region hp0773 (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5136) (re:6227) (di:complement) HPAE000589 AE000589 g2313904 Helicobacter pylori 210 -11539616 7502853497 hp0773 h. pylori predicted coding region hp0773 (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5136) (re:6227) (di:complement) HPAE000589 AE000589 g2313904 Helicobacter pylori 26695 85962 -11539616

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912129	18353	40509	351	116

Description

6500735759 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0776 HP0776 Helicobacter pylori 210 -11539617 7000690267 hypothetical protein hp0776 (db:pir2.dat) H64616 H64616 Helicobacter pylori 210 -11539617 7500959056 hp0776 h. pylori predicted coding region hp0776 (db:genpept-bct1) (de:helicobacter pylori section 67 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9790) (re:10044) (di:complement) HPAE000589 AE000589 g2313905 Helicobacter pylori 210 -11539617 7502853498 hp0776 h. pylori predicted coding region hp0776 (db:genpept) (de:helicobacter pylori 26695 section 67 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9790) (re:10044) (di:complement) HPAE000589 AE000589 g2313905 Helicobacter pylori 26695 85962 -11539617

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912131	18354	40510	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912138	18355	40511	528	175

Description

6500735760 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0778 HP0778 Helicobacter pylori 210 -11539618 7000690268 hypothetical protein hp0778 (db:pir2.dat) B64617 B64617 Helicobacter pylori 210 -11539618 7500959057 hp0778 h. pylori predicted coding region hp0778 (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:84) (re:767) (di:complement) HPAE000590 AE000590 g2313912 Helicobacter pylori 210 -11539618 7502853499 hp0778 h. pylori predicted coding region hp0778 (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:84) (re:767) (di:complement) HPAE000590 AE000590 g2313912 Helicobacter pylori 26695 85962 -11539618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912142	18356	40512	246	81

Description

GTC ORF with score 122 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0661.) (nt:unnamed protein product) (le:<1) (re:1087) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912143	18357	40513	402	133

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912147	18358	40514	918	305

Description

6500735761 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0780 HP0780 Helicobacter pylori 210 -11539619 7000690269 hypothetical protein hp0780 (db:pir2.dat) D64617 D64617 Helicobacter pylori 210 -11539619 7500959058 hp0780 h. pylori predicted coding region hp0780 (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3531) (re:3803) (di:direct) HPAE000590 AE000590 g2313913 Helicobacter pylori 210 -11539619 7502853500 hp0780 h. pylori predicted coding region hp0780 (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3531) (re:3803) (di:direct) HPAE000590 AE000590 g2313913 Helicobacter pylori 26695 85962 -11539619

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912171	18359	40515	504	167

Description

6500735762 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0781 HP0781 Helicobacter pylori 210 -11539620 7000690270 hypothetical protein hp0781 (db:pir2.dat) E64617 E64617 Helicobacter pylori 210 -11539620 7500959059 hp0781 h. pylori predicted coding region hp0781 (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4074) (re:5363) (di:direct) HPAE000590 AE000590 g2313914 Helicobacter pylori 210 -11539620 7502853501 hp0781 h. pylori predicted coding region hp0781 (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4074) (re:5363) (di:direct) HPAE000590 AE000590 g2313914 Helicobacter pylori 26695 85962 -11539620

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912172	18360	40516	402	133

Description

6500735763 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0782 HP0782 Helicobacter pylori 210 -11539621 7000690271 hypothetical protein hp0782 (db:pir2.dat) F64617 F64617 Helicobacter pylori 210 -11539621 7500959060 hp0782 h. pylori predicted coding region hp0782 (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5457) (re:6824) (di:direct) HPAE000590 AE000590 g2313915 Helicobacter pylori 210 -11539621 7502853502 hp0782 h. pylori predicted coding region hp0782 (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5457) (re:6824) (di:direct) HPAE000590 AE000590 g2313915 Helicobacter pylori 26695 85962 -11539621

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912190	18361	40517	498	165

Description

6500735764 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0783 HP0783 Helicobacter pylori 210 -11539622 7000690272 hypothetical protein hp0783 (db:pir2.dat) G64617 G64617 Helicobacter pylori 210 -11539622 7500959061 hp0783 h. pylori predicted coding region hp0783 (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6831) (re:7328) (di:complement) HPAE000590 AE000590 g2313916 Helicobacter pylori 210 -11539622 7502853503 hp0783 h. pylori predicted coding region hp0783 (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6831) (re:7328) (di:complement) HPAE000590 AE000590 g2313916 Helicobacter pylori 26695 85962 -11539622

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912195	18362	40518	930	309

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912208	18363	40519	759	252

Description

6500735765 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0784 HP0784 Helicobacter pylori 210 -11539623 7000690273 hypothetical protein hp0784 (db:pir2.dat) H64617 H64617 Helicobacter pylori 210 -11539623 7500959062 hp0784 h. pylori predicted coding region hp0784 (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7691) (re:7825) (di:direct) HPAE000590 AE000590 g2313917 Helicobacter pylori 210 -11539623 7502853504 hp0784 h. pylori predicted coding region hp0784 (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7691) (re:7825) (di:direct) HPAE000590 AE000590 g2313917 Helicobacter pylori 26695 85962 -11539623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912228	18364	40520	618	205

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912239	18365	40521	918	305

Description

6500735766 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0788 HP0788 Helicobacter pylori 210 -11539624 7000690274 hypothetical protein hp0788 (db:pir2.dat) D64618 D64618 Helicobacter pylori 210 -11539624 7500959063 hp0788 h. pylori predicted coding region hp0788 (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:170) (re:1669) (di:direct) HPAE000591 AE000591 g2313926 Helicobacter pylori 210 -11539624 7502853505 hp0788 h. pylori predicted coding region hp0788 (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:170) (re:1669) (di:direct) HPAE000591 AE000591 g2313926 Helicobacter pylori 26695 85962 -11539624

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912250	18366	40522	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912273	18367	40523	711	237

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912286	18368	40524	1416	471

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912289	18369	40525	312	103

Description

6500735767 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0789 HP0789 Helicobacter pylori 210 -11539625 7000690275 hypothetical protein hp0789 (db:pir2.dat) E64618 E64618 Helicobacter pylori 210 -11539625 7500959064 hp0789 h. pylori predicted coding region hp0789 (db:genpept-bct1) (de:helicobacter pylori section 69 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1748) (re:1894) (di:complement) HPAE000591 AE000591 g2313928 Helicobacter pylori 210 -11539625 7502853506 hp0789 h. pylori predicted coding region hp0789 (db:genpept) (de:helicobacter pylori 26695 section 69 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1748) (re:1894) (di:complement) HPAE000591 AE000591 g2313928 Helicobacter pylori 26695 85962 -11539625

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912298	18370	40526	657	218

Description

6500735768 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0803 HP0803 Helicobacter pylori 210 -11539626 7000690276 hypothetical protein hp0803 (db:pir2.dat) C64620 C64620 Helicobacter pylori 210 -11539626 7500959065 hp0803 h. pylori predicted coding region hp0803 (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2520) (re:3359) (di:complement) HPAE000592 AE000592 g2313940 Helicobacter pylori 210 -11539626 7502853507 hp0803 h. pylori predicted coding region hp0803 (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2520) (re:3359) (di:complement) HPAE000592 AE000592 g2313940 Helicobacter pylori 26695 85962 -11539626

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912299	18371	40527	321	106

Description

6500735769 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0806 HP0806 Helicobacter pylori 210 -11539627 7000690277 hypothetical protein hp0806 (db:pir2.dat) F64620 F64620 Helicobacter pylori 210 -11539627 7500959066 hp0806 h. pylori predicted coding region hp0806 (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5589) (re:6209) (di:direct) HPAE000592 AE000592 g2313941 Helicobacter pylori 210 -11539627 7502853508 hp0806 h. pylori predicted coding region hp0806 (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5589) (re:6209) (di:direct) HPAE000592 AE000592 g2313941 Helicobacter pylori 26695 85962 -11539627

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912326	18372	40528	879	292

Description

6500735770 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0809 HP0809 Helicobacter pylori 210 -11539628 7000690278 hypothetical protein hp0809 (cl:flagellar formation protein flil) (db:pir2.dat) A64621 A64621 Helicobacter pylori 210 -11539628 7500959067 hp0809 h. pylori predicted coding region hp0809 (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9149) (re:9700) (di:complement) HPAE000592 AE000592 g2313942 Helicobacter pylori 210 -11539628 7502853509 hp0809 h. pylori predicted coding region hp0809 (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9149) (re:9700) (di:complement) HPAE000592 AE000592 g2313942 Helicobacter pylori 26695 85962 -11539628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912327	18373	40529	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912332	18374	40530	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912347	18375	40531	1368	455

Description

6500735771 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0811 HP0811 Helicobacter pylori 210 -11539629 7000690279 hypothetical protein hp0811 (db:pir2.dat) C64621 C64621 Helicobacter pylori 210 -11539629 7500959068 hp0811 h. pylori predicted coding region hp0811 (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10290) (re:10616) (di:complement) HPAE000592 AE000592 g2313943 Helicobacter pylori 210 -11539629 7502853510 hp0811 h. pylori predicted coding region hp0811 (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10290) (re:10616) (di:complement) HPAE000592 AE000592 g2313943 Helicobacter pylori 26695 85962 -11539629

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912348	18376	40532	423	140

Description

GTC ORF with score 93 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome 1 bac f15k9 sequence, completesequence.) (nt:ests gb|h36966, gb|r65511, gb|t42324 and gb|t20569) (le:25716:26162:26306) (re:26016:26208:26485) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912349	18377	40533	1029	342

Description

6500735772 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0812 HP0812 Helicobacter pylori 210 -11539630 7000690280 hypothetical protein hp0812 (db:pir2.dat) D64621 D64621 Helicobacter pylori 210 -11539630 7500959069 hp0812 h. pylori predicted coding region hp0812 (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:257) (re:1267) (di:complement) HPAE000593 AE000593 g2313954 Helicobacter pylori 210 -11539630 7502853511 hp0812 h. pylori predicted coding region hp0812 (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:257) (re:1267) (di:complement) HPAE000593 AE000593 g2313954 Helicobacter pylori 26695 85962 -11539630

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912354	18378	40534	954	317

Description

6500735773 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0817 HP0817 Helicobacter pylori 210 -11539631 7000690281 hypothetical protein hp0817 (db:pir2.dat) A64622 A64622 Helicobacter pylori 210 -11539631 7500959070 hp0817 h. pylori predicted coding region hp0817 (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4347) (re:4793) (di:direct) HPAE000593 AE000593 g2313955 Helicobacter pylori 210 -11539631 7502853512 hp0817 h. pylori predicted coding region hp0817 (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4347) (re:4793) (di:direct) HPAE000593 AE000593 g2313955 Helicobacter pylori 26695 85962 -11539631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912355	18379	40535	432	143

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912358	18380	40536	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912389	18381	40537	1155	384

Description

6500735774 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0820 HP0820 Helicobacter pylori 210 -11539632 7000690282 hypothetical protein hp0820 (db:pir2.dat) D64622 D64622 Helicobacter pylori 210 -11539632 7500959071 hp0820 h. pylori predicted coding region hp0820 (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7351) (re:7812) (di:direct) HPAE000593 AE000593 g2313956 Helicobacter pylori 210 -11539632 7502853513 hp0820 h. pylori predicted coding region hp0820 (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7351) (re:7812) (di:direct) HPAE000593 AE000593 g2313956 Helicobacter pylori 26695 85962 -11539632

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912391	18382	40538	387	128

Description

GTC ORF with score 98 to: (fn:cellular receptor for hepatitis a virus in cv-1) (sr:african green monkey) (db:genpept-pri3) (de:cercopithecus aethiops hepatitis a virus cellular receptor 1 shortform (havcr-1) mrna, complete cds.) (nt:mucin-like class i ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912394	18383	40539	489	162

Description

6500735775 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0833 HP0833 Helicobacter pylori 210 -11539633 7000690283 hypothetical protein hp0833 (db:pir2.dat) A64624 A64624 Helicobacter pylori 210 -11539633 7500959072 hp0833 h. pylori predicted coding region hp0833 (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8300) (re:9178) (di:complement) HPAE000594 AE000594 g2313968 Helicobacter pylori 210 -11539633 7502853514 hp0833 h. pylori predicted coding region hp0833 (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8300) (re:9178) (di:complement) HPAE000594 AE000594 g2313968 Helicobacter pylori 26695 85962 -11539633

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912400	18384	40540	549	182

Description

6500735776 yphc:hp0834 gtp-binding protein homologue (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0834 HP0834 Helicobacter pylori 210 -11539634 7502853515 hp0834 (sr:,campylobacter pylori) (de:hypothetical gtp-binding protein hp0834) (db:swissprot) Y834_HELPY O25505 HELICOBACTER PYLORI 210 -11539634 7000689978 gtp-binding protein homolog (cl:mycobacterium leprae probable gtp-binding protein:translation elongation factor tu homology) (db:pir2.dat) B64624 B64624 Helicobacter pylori 210 -11539634 7500958760 hp0834 gtp-binding protein homologue yphc (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:37738 percent identity: 36.66;) (le:9255) (re:10631) (di:direct) HPAE000594 AE000594 g2313967 Helicobacter pylori 210 -11539634 7502853516 hp0834 gtp-binding protein homologue yphc (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:37738 percent identity: 36.66;) (le:9255) (re:10631) (di:direct) HPAE000594 AE000594 g2313967 Helicobacter pylori 26695 85962 -11539634

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912419	18385	40541	972	323

Description

6500735777 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0836 HP0836 Helicobacter pylori 210 -11539635 7000690284 hypothetical protein hp0836 (db:pir2.dat) D64624 D64624 Helicobacter pylori 210 -11539635 7500959073 hp0836 h. pylori predicted coding region hp0836 (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:987) (re:1346) (di:direct) HPAE000595 AE000595 g2313978 Helicobacter pylori 210 -11539635 7502853517 hp0836 h. pylori predicted coding region hp0836 (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:987) (re:1346) (di:direct) HPAE000595 AE000595 g2313978 Helicobacter pylori 26695 85962 -11539635

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912444	18386	40542	1038	345

Description

6500735778 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0837 HP0837 Helicobacter pylori 210 -11539636 7000690285 hypothetical protein hp0837 (db:pir2.dat) E64624 E64624 Helicobacter pylori 210 -11539636 7500959074 hp0837 h. pylori predicted coding region hp0837 (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1289) (re:1597) (di:direct) HPAE000595 AE000595 g2313979 Helicobacter pylori 210 -11539636 7502853518 hp0837 h. pylori predicted coding region hp0837 (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1289) (re:1597) (di:direct) HPAE000595 AE000595 g2313979 Helicobacter pylori 26695 85962 -11539636

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912454	18387	40543	2271	756

Description

6500735779 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0838 HP0838 Helicobacter pylori 210 -11539637 7000690286 hypothetical protein hp0838 (db:pir2.dat) F64624 F64624 Helicobacter pylori 210 -11539637 7500959075 hp0838 h. pylori predicted coding region hp0838 (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1617) (re:2234) (di:direct) HPAE000595 AE000595 g2313980 Helicobacter pylori 210 -11539637 7502853519 hp0838 h. pylori predicted coding region hp0838 (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1617) (re:2234) (di:direct) HPAE000595 AE000595 g2313980 Helicobacter pylori 26695 85962 -11539637

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912468	18388	40544	1062	354

Description

6500735780 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0842 HP0842 Helicobacter pylori 210 -11539638 7000690287 hypothetical protein hp0842 (db:pir2.dat) B64625 B64625 Helicobacter pylori 210 -11539638 7500959076 hp0842 h. pylori predicted coding region hp0842 (db:genpept-bct1) (de:helicobacter pylori section 73 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6273) (re:7010) (di:direct) HPAE000595 AE000595 g2313981 Helicobacter pylori 210 -11539638 7502853520 hp0842 h. pylori predicted coding region hp0842 (db:genpept) (de:helicobacter pylori 26695 section 73 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6273) (re:7010) (di:direct) HPAE000595 AE000595 g2313981 Helicobacter pylori 26695 85962 -11539638

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912473	18389	40545	1149	382

Description

6500735781 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0847 HP0847 Helicobacter pylori 210 -11539639 7000690288 hypothetical protein hp0847 (db:pir2.dat) G64625 G64625 Helicobacter pylori 210 -11539639 7500959077 hp0847 h. pylori predicted coding region hp0847 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:176) (re:277) (di:complement) HPAE000596 AE000596 g2314006 Helicobacter pylori 210 -11539639 7502853521 hp0847 h. pylori predicted coding region hp0847 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:176) (re:277) (di:complement) HPAE000596 AE000596 g2314006 Helicobacter pylori 26695 85962 -11539639

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912477	18390	40546	3828	1275

Description

6500735782 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0849 HP0849 Helicobacter pylori 210 -11539640 7000690289 hypothetical protein hp0849 (db:pir2.dat) A64626 A64626 Helicobacter pylori 210 -11539640 7500959078 hp0849 h. pylori predicted coding region hp0849 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1277) (re:1567) (di:complement) HPAE000596 AE000596 g2313998 Helicobacter pylori 210 -11539640 7502853522 hp0849 h. pylori predicted coding region hp0849 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1277) (re:1567) (di:complement) HPAE000596 AE000596 g2313998 Helicobacter pylori 26695 85962 -11539640

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912508	18391	40547	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912523	18392	40548	1671	556

Description

6500735783 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0852 HP0852 Helicobacter pylori 210 -11539641 7000690290 hypothetical protein hp0852 (db:pir2.dat) D64626 D64626 Helicobacter pylori 210 -11539641 7500959079 hp0852 h. pylori predicted coding region hp0852 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4230) (re:5171) (di:complement) HPAE000596 AE000596 g2313999 Helicobacter pylori 210 -11539641 7502853523 hp0852 h. pylori predicted coding region hp0852 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4230) (re:5171) (di:complement) HPAE000596 AE000596 g2313999 Helicobacter pylori 26695 85962 -11539641

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912526	18393	40549	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912534	18394	40550	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912553	18395	40551	732	243

Description

6500735784 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0856 HP0856 Helicobacter pylori 210 -11539642 7000690291 hypothetical protein hp0856 (db:pir2.dat) H64626 H64626 Helicobacter pylori 210 -11539642 7500959080 hp0856 h. pylori predicted coding region hp0856 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9683) (re:10777) (di:direct) HPAE000596 AE000596 g2314000 Helicobacter pylori 210 -11539642 7502853524 hp0856 h. pylori predicted coding region hp0856 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9683) (re:10777) (di:direct) HPAE000596 AE000596 g2314000 Helicobacter pylori 26695 85962 -11539642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912562	18396	40552	1464	487

Description

6500735785 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0861 HP0861 Helicobacter pylori 210 -11539643 7000690292 hypothetical protein hp0861 (db:pir2.dat) E64627 E64627 Helicobacter pylori 210 -11539643 7500959081 hp0861 h. pylori predicted coding region hp0861 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14245) (re:14985) (di:complement) HPAE000596 AE000596 g2314001 Helicobacter pylori 210 -11539643 7502853525 hp0861 h. pylori predicted coding region hp0861 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14245) (re:14985) (di:complement) HPAE000596 AE000596 g2314001 Helicobacter pylori 26695 85962 -11539643

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912573	18397	40553	663	220

Description

6500735786 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0862 HP0862 Helicobacter pylori 210 -11539644 7000690293 hypothetical protein hp0862 (db:pir2.dat) F64627 F64627 Helicobacter pylori 210 -11539644 7500959082 hp0862 h. pylori predicted coding region hp0862 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14976) (re:15647) (di:complement) HPAE000596 AE000596 g2314002 Helicobacter pylori 210 -11539644 7502853526 hp0862 h. pylori predicted coding region hp0862 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14976) (re:15647) (di:complement) HPAE000596 AE000596 g2314002 Helicobacter pylori 26695 85962 -11539644

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912574	18398	40554	864	287

Description

6500735787 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0863 HP0863 Helicobacter pylori 210 -11539645 7000690294 hypothetical protein hp0863 (db:pir2.dat) G64627 G64627 Helicobacter pylori 210 -11539645 7500959083 hp0863 h. pylori predicted coding region hp0863 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:15652) (re:17280) (di:complement) HPAE000596 AE000596 g2314003 Helicobacter pylori 210 -11539645 7502853527 hp0863 h. pylori predicted coding region hp0863 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:15652) (re:17280) (di:complement) HPAE000596 AE000596 g2314003 Helicobacter pylori 26695 85962 -11539645

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912578	18399	40555	486	161

Description

6500735788 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0864 HP0864 Helicobacter pylori 210 -11539646 7000690295 hypothetical protein hp0864 (db:pir2.dat) H64627 H64627 Helicobacter pylori 210 -11539646 7500959084 hp0864 h. pylori predicted coding region hp0864 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:17285) (re:17941) (di:complement) HPAE000596 AE000596 g2314004 Helicobacter pylori 210 -11539646 7502853528 hp0864 h. pylori predicted coding region hp0864 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:17285) (re:17941) (di:complement) HPAE000596 AE000596 g2314004 Helicobacter pylori 26695 85962 -11539646

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912612	18400	40556	300	99

Description

6500735789 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0868 HP0868 Helicobacter pylori 210 -11539647 7000690296 hypothetical protein hp0868 (db:pir2.dat) D64628 D64628 Helicobacter pylori 210 -11539647 7500959085 hp0868 h. pylori predicted coding region hp0868 (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:19982) (re:20443) (di:complement) HPAE000596 AE000596 g2314005 Helicobacter pylori 210 -11539647 7502853529 hp0868 h. pylori predicted coding region hp0868 (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:19982) (re:20443) (di:complement) HPAE000596 AE000596 g2314005 Helicobacter pylori 26695 85962 -11539647

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912629	18401	40557	789	262

Description

GTC ORF with score 244 to: (sr:thale cress) (db:genpept-pln1) (de:sequence of bac t1g11 from arabidopsis thaliana chromosome 1,complete sequence.) (nt:contains similarity to human dimethylaniline) (le:51751:52311:52845) (re:51978:52682:53558) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912631	18402	40558	813	270

Description

6500735790 phna:hp0872 alkylphosphonate uptake protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0872 HP0872 Helicobacter pylori 210 -11539648 7000689629 alkylphosphonate uptake protein (db:pir2.dat) H64628 H64628 Helicobacter pylori 210 -11539648 7500958447 hp0872 alkylphosphonate uptake protein phna (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:similar to egad:9876 percent identity: 61.11;) (le:1220) (re:1549) (di:direct) HPAE000597 AE000597 g2314009 Helicobacter pylori 210 -11539648 7502853530 hp0872 alkylphosphonate uptake protein phna (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:similar to egad:9876 percent identity: 61.11;) (le:1220) (re:1549) (di:direct) HPAE000597 AE000597 g2314009 Helicobacter pylori 26695 85962 -11539648

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912639	18403	40559	609	202

Description

6500735791 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0873 HP0873 Helicobacter pylori 210 -11539649 7000690297 hypothetical protein hp0873 (db:pir2.dat) A64629 A64629 Helicobacter pylori 210 -11539649 7500959086 hp0873 h. pylori predicted coding region hp0873 (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1604) (re:1819) (di:complement) HPAE000597 AE000597 g2314016 Helicobacter pylori 210 -11539649 7502853531 hp0873 h. pylori predicted coding region hp0873 (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1604) (re:1819) (di:complement) HPAE000597 AE000597 g2314016 Helicobacter pylori 26695 85962 -11539649

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912646	18404	40560	249	82

Description

6500735792 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0874 HP0874 Helicobacter pylori 210 -11539650 7000690298 hypothetical protein hp0874 (db:pir2.dat) B64629 B64629 Helicobacter pylori 210 -11539650 7500959087 hp0874 h. pylori predicted coding region hp0874 (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1904) (re:2779) (di:complement) HPAE000597 AE000597 g2314013 Helicobacter pylori 210 -11539650 7502853532 hp0874 h. pylori predicted coding region hp0874 (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1904) (re:2779) (di:complement) HPAE000597 AE000597 g2314013 Helicobacter pylori 26695 85962 -11539650

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912656	18405	40561	405	134

Description

6500735793 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0878 HP0878 Helicobacter pylori 210 -11539651 7000690299 hypothetical protein hp0878 (db:pir2.dat) F64629 F64629 Helicobacter pylori 210 -11539651 7500959088 hp0878 h. pylori predicted coding region hp0878 (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7744) (re:7917) (di:direct) HPAE000597 AE000597 g2314018 Helicobacter pylori 210 -11539651 7502853533 hp0878 h. pylori predicted coding region hp0878 (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7744) (re:7917) (di:direct) HPAE000597 AE000597 g2314018 Helicobacter pylori 26695 85962 -11539651

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912659	18406	40562	741	246

Description

6500735794 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0879 HP0879 Helicobacter pylori 210 -11539652 7000690300 hypothetical protein hp0879 (db:pir2.dat) G64629 G64629 Helicobacter pylori 210 -11539652 7500959089 hp0879 h. pylori predicted coding region hp0879 (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7868) (re:8476) (di:direct) HPAE000597 AE000597 g2314014 Helicobacter pylori 210 -11539652 7502853534 hp0879 h. pylori predicted coding region hp0879 (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7868) (re:8476) (di:direct) HPAE000597 AE000597 g2314014 Helicobacter pylori 26695 85962 -11539652

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912660	18407	40563	300	99

Description

6500735795 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0880 HP0880 Helicobacter pylori 210 -11539653 7000690301 hypothetical protein hp0880 (db:pir2.dat) H64629 H64629 Helicobacter pylori 210 -11539653 7500959090 hp0880 h. pylori predicted coding region hp0880 (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8956) (re:9378) (di:complement) HPAE000597 AE000597 g2314015 Helicobacter pylori 210 -11539653 7502853535 hp0880 h. pylori predicted coding region hp0880 (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8956) (re:9378) (di:complement) HPAE000597 AE000597 g2314015 Helicobacter pylori 26695 85962 -11539653

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912661	18408	40564	711	236

Description

6500735796 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0881 HP0881 Helicobacter pylori 210 -11539654 7000690302 hypothetical protein hp0881 (db:pir2.dat) A64630 A64630 Helicobacter pylori 210 -11539654 7500959091 hp0881 h. pylori predicted coding region hp0881 (db:genpept-bct1) (de:helicobacter pylori section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9386) (re:9481) (di:complement) HPAE000597 AE000597 g2314017 Helicobacter pylori 210 -11539654 7502853536 hp0881 h. pylori predicted coding region hp0881 (db:genpept) (de:helicobacter pylori 26695 section 75 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9386) (re:9481) (di:complement) HPAE000597 AE000597 g2314017 Helicobacter pylori 26695 85962 -11539654

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912679	18409	40565	261	86

Description

6500735797 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0884 HP0884 Helicobacter pylori 210 -11539655 7000690304 hypothetical protein hp0884 (db:pir2.dat) D64630 D64630 Helicobacter pylori 210 -11539655 7500959092 hp0884 h. pylori predicted coding region hp0884 (db:genpept-bct1) (de:helicobacter pylori section 76 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:952) (re:2796) (di:complement) HPAE000598 AE000598 g2314027 Helicobacter pylori 210 -11539655 7502853537 hp0884 h. pylori predicted coding region hp0884 (db:genpept) (de:helicobacter pylori 26695 section 76 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:952) (re:2796) (di:complement) HPAE000598 AE000598 g2314027 Helicobacter pylori 26695 85962 -11539655

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912689	18410	40566	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912695	18411	40567	183	60

Description

6500735798 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0893 HP0893 Helicobacter pylori 210 -11539656 7000690305 hypothetical protein hp0893 (db:pir2.dat) E64631 E64631 Helicobacter pylori 210 -11539656 7500959093 hp0893 h. pylori predicted coding region hp0893 (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1041) (re:1328) (di:complement) HPAE000599 AE000599 g2314037 Helicobacter pylori 210 -11539656 7502853538 hp0893 h. pylori predicted coding region hp0893 (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1041) (re:1328) (di:complement) HPAE000599 AE000599 g2314037 Helicobacter pylori 26695 85962 -11539656

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912696	18412	40568	219	72

Description

6500735799 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0895 HP0895 Helicobacter pylori 210 -11539657 7000690306 hypothetical protein hp0895 (db:pir2.dat) G64631 G64631 Helicobacter pylori 210 -11539657 7500959094 hp0895 h. pylori predicted coding region hp0895 (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1656) (re:2033) (di:complement) HPAE000599 AE000599 g2314038 Helicobacter pylori 210 -11539657 7502853539 hp0895 h. pylori predicted coding region hp0895 (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1656) (re:2033) (di:complement) HPAE000599 AE000599 g2314038 Helicobacter pylori 26695 85962 -11539657

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912700	18413	40569	369	122

Description

6500735800 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0897 HP0897 Helicobacter pylori 210 -11539658 7000690307 hypothetical protein hp0897 (db:pir2.dat) A64632 A64632 Helicobacter pylori 210 -11539658 7500959095 hp0897 h. pylori predicted coding region hp0897 (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5086) (re:5712) (di:direct) HPAE000599 AE000599 g2314039 Helicobacter pylori 210 -11539658 7502853540 hp0897 h. pylori predicted coding region hp0897 (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5086) (re:5712) (di:direct) HPAE000599 AE000599 g2314039 Helicobacter pylori 26695 85962 -11539658

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912702	18414	40570	1080	359

Description

GTC ORF with score 192 to: (sr:house mouse) (db:genpept) (de:mus musculus major histocompatibility complex region ng27, ng28,rps28, nadh oxidoreductase, ng29, kifc1, fas-binding protein,bing1, tapasin, ralgds-like, ke2, bing4, beta ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912705	18415	40571	1002	334

Description

GTC ORF with score 213 to: (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #443(59.8-60.2 min.).) (nt:similar to (swissprot accession number p37339)) (le:10153) (re:11421) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912710	18416	40572	405	134

Description

6500735801 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0901 HP0901 Helicobacter pylori 210 -11539659 7000690308 hypothetical protein hp0901 (db:pir2.dat) E64632 E64632 Helicobacter pylori 210 -11539659 7500959096 hp0901 h. pylori predicted coding region hp0901 (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7992) (re:8117) (di:complement) HPAE000599 AE000599 g2314041 Helicobacter pylori 210 -11539659 7502853541 hp0901 h. pylori predicted coding region hp0901 (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7992) (re:8117) (di:complement) HPAE000599 AE000599 g2314041 Helicobacter pylori 26695 85962 -11539659

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912720	18417	40573	1179	392

Description

6500735802 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0902 HP0902 Helicobacter pylori 210 -11539660 7000690309 hypothetical protein hp0902 (db:pir2.dat) F64632 F64632 Helicobacter pylori 210 -11539660 7500959097 hp0902 h. pylori predicted coding region hp0902 (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8128) (re:8427) (di:complement) HPAE000599 AE000599 g2314040 Helicobacter pylori 210 -11539660 7502853542 hp0902 h. pylori predicted coding region hp0902 (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8128) (re:8427) (di:complement) HPAE000599 AE000599 g2314040 Helicobacter pylori 26695 85962 -11539660

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912732	18418	40574	522	173

Description

6500735803 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0906 HP0906 Helicobacter pylori 210 -11539661 7000690310 hypothetical protein hp0906 (db:pir2.dat) B64633 B64633 Helicobacter pylori 210 -11539661 7500959098 hp0906 h. pylori predicted coding region hp0906 (db:genpept-bct1) (de:helicobacter pylori section 78 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:160) (re:1743) (di:direct) HPAE000600 AE000600 g2314048 Helicobacter pylori 210 -11539661 7502853543 hp0906 h. pylori predicted coding region hp0906 (db:genpept) (de:helicobacter pylori 26695 section 78 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:160) (re:1743) (di:direct) HPAE000600 AE000600 g2314048 Helicobacter pylori 26695 85962 -11539661

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912734	18419	40575	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912740	18420	40576	498	165

Description

6500735804 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0909 HP0909 Helicobacter pylori 210 -11539662 7000690311 hypothetical protein hp0909 (db:pir2.dat) E64633 E64633 Helicobacter pylori 210 -11539662 7500959099 hp0909 h. pylori predicted coding region hp0909 (db:genpept-bct1) (de:helicobacter pylori section 78 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4565) (re:5170) (di:direct) HPAE000600 AE000600 g2314049 Helicobacter pylori 210 -11539662 7502853544 hp0909 h. pylori predicted coding region hp0909 (db:genpept) (de:helicobacter pylori 26695 section 78 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4565) (re:5170) (di:direct) HPAE000600 AE000600 g2314049 Helicobacter pylori 26695 85962 -11539662

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912762	18421	40577	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912764	18422	40578	705	234

Description

6500735805 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0914 HP0914 Helicobacter pylori 210 -11539663 7000690312 hypothetical protein hp0914 (db:pir2.dat) B64634 B64634 Helicobacter pylori 210 -11539663 7500959100 hp0914 h. pylori predicted coding region hp0914 (db:genpept-bct1) (de:helicobacter pylori section 79 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:482) (re:2026) (di:complement) HPAE000601 AE000601 g2314057 Helicobacter pylori 210 -11539663 7502853545 hp0914 h. pylori predicted coding region hp0914 (db:genpept) (de:helicobacter pylori 26695 section 79 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:482) (re:2026) (di:complement) HPAE000601 AE000601 g2314057 Helicobacter pylori 26695 85962 -11539663

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912771	18423	40579	1632	543

Description

6500735806 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0917 HP0917 Helicobacter pylori 210 -11539664 7000690313 hypothetical protein hp0917 (db:pir2.dat) E64634 E64634 Helicobacter pylori 210 -11539664 7500959101 hp0917 h. pylori predicted coding region hp0917 (db:genpept-bct1) (de:helicobacter pylori section 79 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4868) (re:4939) (di:direct) HPAE000601 AE000601 g2314059 Helicobacter pylori 210 -11539664 7502853546 hp0917 h. pylori predicted coding region hp0917 (db:genpept) (de:helicobacter pylori 26695 section 79 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4868) (re:4939) (di:direct) HPAE000601 AE000601 g2314059 Helicobacter pylori 26695 85962 -11539664

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912774	18424	40580	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912799	18425	40581	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912810	18426	40582	447	148

Description

6500735807 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0918 HP0918 Helicobacter pylori 210 -11539665 7000690314 hypothetical protein hp0918 (db:pir2.dat) F64634 F64634 Helicobacter pylori 210 -11539665 7500959102 hp0918 h. pylori predicted coding region hp0918 (db:genpept-bct1) (de:helicobacter pylori section 79 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4969) (re:5400) (di:complement) HPAE000601 AE000601 g2314058 Helicobacter pylori 210 -11539665 7502853547 hp0918 h. pylori predicted coding region hp0918 (db:genpept) (de:helicobacter pylori 26695 section 79 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4969) (re:5400) (di:complement) HPAE000601 AE000601 g2314058 Helicobacter pylori 26695 85962 -11539665

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912811	18427	40583	582	193

Description

6500735808 hp0923:hpy_907 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HPY_907 HPY_907 Helicobacter pylori 210 -11539666 7000690576 outer membrane protein (db:pir2.dat) C64635 C64635 Helicobacter pylori 210 -11539666 7500959358 hp0923 h. pylori predicted coding region hp0923 (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:outer membrane protein (omp22); identified by) (le:7712) (re:8821) (di:direct) HPAE000602 AE000602 g2314070 Helicobacter pylori 210 -11539666 7502853548 hp0923 h. pylori predicted coding region hp0923 (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:outer membrane protein (omp22); identified by) (le:7712) (re:8821) (di:direct) HPAE000602 AE000602 g2314070 Helicobacter pylori 26695 85962 -11539666

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912826	18428	40584	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912832	18429	40585	1503	500

Description

6500735809 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0931 HP0931 Helicobacter pylori 210 -11539667 7000690315 hypothetical protein hp0931 (db:pir2.dat) C64636 C64636 Helicobacter pylori 210 -11539667 7500959103 hp0931 h. pylori predicted coding region hp0931 (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14152) (re:14592) (di:direct) HPAE000602 AE000602 g2314071 Helicobacter pylori 210 -11539667 7502853549 hp0931 h. pylori predicted coding region hp0931 (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14152) (re:14592) (di:direct) HPAE000602 AE000602 g2314071 Helicobacter pylori 26695 85962 -11539667

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912833	18430	40586	1428	475

Description

6500735810 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0932 HP0932 Helicobacter pylori 210 -11539668 7000690316 hypothetical protein hp0932 (db:pir2.dat) D64636 D64636 Helicobacter pylori 210 -11539668 7500959104 hp0932 h. pylori predicted coding region hp0932 (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14508) (re:14810) (di:direct) HPAE000602 AE000602 g2314072 Helicobacter pylori 210 -11539668 7502853550 hp0932 h. pylori predicted coding region hp0932 (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14508) (re:14810) (di:direct) HPAE000602 AE000602 g2314072 Helicobacter pylori 26695 85962 -11539668

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912844	18431	40587	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912860	18432	40588	627	208

Description

6500735811 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0933 HP0933 Helicobacter pylori 210 -11539669 7000690317 hypothetical protein hp0933 (db:pir2.dat) E64636 E64636 Helicobacter pylori 210 -11539669 7500959105 hp0933 h. pylori predicted coding region hp0933 (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14812) (re:15414) (di:direct) HPAE000602 AE000602 g2314073 Helicobacter pylori 210 -11539669 7502853551 hp0933 h. pylori predicted coding region hp0933 (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14812) (re:15414) (di:direct) HPAE000602 AE000602 g2314073 Helicobacter pylori 26695 85962 -11539669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912867	18433	40589	210	69

Description

6500735812 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0935 HP0935 Helicobacter pylori 210 -11539670 7000690318 hypothetical protein hp0935 (db:pir2.dat) G64636 G64636 Helicobacter pylori 210 -11539670 7500959106 hp0935 h. pylori predicted coding region hp0935 (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:16183) (re:16668) (di:direct) HPAE000602 AE000602 g2314074 Helicobacter pylori 210 -11539670 7502853552 hp0935 h. pylori predicted coding region hp0935 (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:16183) (re:16668) (di:direct) HPAE000602 AE000602 g2314074 Helicobacter pylori 26695 85962 -11539670

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912868	18434	40590	192	63

Description

6500735813 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0937 HP0937 Helicobacter pylori 210 -11539671 7000690319 hypothetical protein hp0937 (db:pir2.dat) A64637 A64637 Helicobacter pylori 210 -11539671 7500959107 hp0937 h. pylori predicted coding region hp0937 (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2073) (re:2867) (di:complement) HPAE000603 AE000603 g2314083 Helicobacter pylori 210 -11539671 7502853553 hp0937 h. pylori predicted coding region hp0937 (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2073) (re:2867) (di:complement) HPAE000603 AE000603 g2314083 Helicobacter pylori 26695 85962 -11539671

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912869	18435	40591	465	154

Description

6500735814 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0938 HP0938 Helicobacter pylori 210 -11539672 7000690320 hypothetical protein hp0938 (db:pir2.dat) B64637 B64637 Helicobacter pylori 210 -11539672 7500959108 hp0938 h. pylori predicted coding region hp0938 (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2947) (re:3294) (di:complement) HPAE000603 AE000603 g2314084 Helicobacter pylori 210 -11539672 7502853554 hp0938 h. pylori predicted coding region hp0938 (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2947) (re:3294) (di:complement) HPAE000603 AE000603 g2314084 Helicobacter pylori 26695 85962 -11539672

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912870	18436	40592	417	138

Description

6500735815 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0945 HP0945 Helicobacter pylori 210 -11539673 7000690321 hypothetical protein hp0945 (db:pir2.dat) A64638 A64638 Helicobacter pylori 210 -11539673 7500959109 hp0945 h. pylori predicted coding region hp0945 (db:genpept-bct1) (de:helicobacter pylori section 81 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9536) (re:9832) (di:complement) HPAE000603 AE000603 g2314085 Helicobacter pylori 210 -11539673 7502853555 hp0945 h. pylori predicted coding region hp0945 (db:genpept) (de:helicobacter pylori 26695 section 81 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9536) (re:9832) (di:complement) HPAE000603 AE000603 g2314085 Helicobacter pylori 26695 85962 -11539673

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912880	18437	40593	513	170

Description

GTC ORF with score 168 to: (db:genpept-bct1) (de:methanobacterium thermoautotrophicum from bases 1655364 to 1666496(section 141 of 148) of the complete genome.) (nt:function code:5.03 - l-amino acid metabolism,) (le:6264) (re:7223) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912889	18438	40594	888	295

Description

6500735816 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0947 HP0947 Helicobacter pylori 210 -11539674 7000690322 hypothetical protein hp0947 (db:pir2.dat) C64638 C64638 Helicobacter pylori 210 -11539674 7500959110 hp0947 h. pylori predicted coding region hp0947 (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2213) (re:2575) (di:direct) HPAE000604 AE000604 g2314098 Helicobacter pylori 210 -11539674 7502853556 hp0947 h. pylori predicted coding region hp0947 (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2213) (re:2575) (di:direct) HPAE000604 AE000604 g2314098 Helicobacter pylori 26695 85962 -11539674

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912896	18439	40595	849	282

Description

6500735817 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0948 HP0948 Helicobacter pylori 210 -11539675 7000690323 hypothetical protein hp0948 (db:pir2.dat) D64638 D64638 Helicobacter pylori 210 -11539675 7500959111 hp0948 h. pylori predicted coding region hp0948 (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2942) (re:3955) (di:complement) HPAE000604 AE000604 g2314099 Helicobacter pylori 210 -11539675 7502853557 hp0948 h. pylori predicted coding region hp0948 (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2942) (re:3955) (di:complement) HPAE000604 AE000604 g2314099 Helicobacter pylori 26695 85962 -11539675

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912897	18440	40596	516	171

Description

6500735818 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0951 HP0951 Helicobacter pylori 210 -11539676 7000690324 hypothetical protein hp0951 (db:pir2.dat) G64638 G64638 Helicobacter pylori 210 -11539676 7500959112 hp0951 h. pylori predicted coding region hp0951 (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5378) (re:5995) (di:direct) HPAE000604 AE000604 g2314100 Helicobacter pylori 210 -11539676 7502853558 hp0951 h. pylori predicted coding region hp0951 (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5378) (re:5995) (di:direct) HPAE000604 AE000604 g2314100 Helicobacter pylori 26695 85962 -11539676

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912910	18441	40597	273	90

Description

6500735819 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0953 HP0953 Helicobacter pylori 210 -11539677 7000690325 hypothetical protein hp0953 (db:pir2.dat) A64639 A64639 Helicobacter pylori 210 -11539677 7500959113 hp0953 h. pylori predicted coding region hp0953 (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6665) (re:7231) (di:complement) HPAE000604 AE000604 g2314101 Helicobacter pylori 210 -11539677 7502853559 hp0953 h. pylori predicted coding region hp0953 (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6665) (re:7231) (di:complement) HPAE000604 AE000604 g2314101 Helicobacter pylori 26695 85962 -11539677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912916	18442	40598	555	184

Description

6500735820 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0958 HP0958 Helicobacter pylori 210 -11539678 7000690326 hypothetical protein hp0958 (db:pir2.dat) F64639 F64639 Helicobacter pylori 210 -11539678 7500959114 hp0958 h. pylori predicted coding region hp0958 (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10711) (re:11475) (di:complement) HPAE000604 AE000604 g2314102 Helicobacter pylori 210 -11539678 7502853560 hp0958 h. pylori predicted coding region hp0958 (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10711) (re:11475) (di:complement) HPAE000604 AE000604 g2314102 Helicobacter pylori 26695 85962 -11539678

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912919	18443	40599	519	172

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912925	18444	40600	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912931	18445	40601	417	138

Description

6500735821 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0963 HP0963 Helicobacter pylori 210 -11539679 7000690327 hypothetical protein hp0963 (db:pir2.dat) C64640 C64640 Helicobacter pylori 210 -11539679 7500959115 hp0963 h. pylori predicted coding region hp0963 (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:550) (re:1893) (di:complement) HPAE000605 AE000605 g2314110 Helicobacter pylori 210 -11539679 7502853561 hp0963 h. pylori predicted coding region hp0963 (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:550) (re:1893) (di:complement) HPAE000605 AE000605 g2314110 Helicobacter pylori 26695 85962 -11539679

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912933	18446	40602	459	152

Description

6500735822 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0964 HP0964 Helicobacter pylori 210 -11539680 7000690328 hypothetical protein hp0964 (db:pir2.dat) D64640 D64640 Helicobacter pylori 210 -11539680 7500959116 hp0964 h. pylori predicted coding region hp0964 (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1890) (re:2981) (di:complement) HPAE000605 AE000605 g2314111 Helicobacter pylori 210 -11539680 7502853562 hp0964 h. pylori predicted coding region hp0964 (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1890) (re:2981) (di:complement) HPAE000605 AE000605 g2314111 Helicobacter pylori 26695 85962 -11539680

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912934	18447	40603	696	231

Description

6500735823 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0965 HP0965 Helicobacter pylori 210 -11539681 7000690329 hypothetical protein hp0965 (db:pir2.dat) E64640 E64640 Helicobacter pylori 210 -11539681 7500959117 hp0965 h. pylori predicted coding region hp0965 (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2891) (re:4222) (di:complement) HPAE000605 AE000605 g2314112 Helicobacter pylori 210 -11539681 7502853563 hp0965 h. pylori predicted coding region hp0965 (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2891) (re:4222) (di:complement) HPAE000605 AE000605 g2314112 Helicobacter pylori 26695 85962 -11539681

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912942	18448	40604	1320	439

Description

GTC ORF with score 467 to: (sr:acinetobacter sp. (strain ncib 9871) dna, clone puc2d3) (db:genpept-bct1) (de:acinetobacter sp. cyclohexanone monooxygenase gene, complete cds.) (nt:cyclohexanone monoxygenase) (le:391) (re:2022) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912950	18449	40605	831	276

Description

6500735824 hp0968:hpy_952 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HPY_952 HPY_952 Helicobacter pylori 210 -11539682 7000690330 hypothetical protein hp0968 (db:pir2.dat) H64640 H64640 Helicobacter pylori 210 -11539682 7500959118 hp0968 h. pylori predicted coding region hp0968 (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6662) (re:6727) (di:complement) HPAE000605 AE000605 g2314114 Helicobacter pylori 210 -11539682 7502853564 hp0968 h. pylori predicted coding region hp0968 (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6662) (re:6727) (di:complement) HPAE000605 AE000605 g2314114 Helicobacter pylori 26695 85962 -11539682

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912954	18450	40606	210	69

Description

6500735825 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0971 HP0971 Helicobacter pylori 210 -11539683 7000690554 nickel and cobalt resistance protein (db:pir2.dat) C64641 C64641 Helicobacter pylori 210 -11539683 7500959341 hp0971 h. pylori predicted coding region hp0971 (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10878) (re:12119) (di:complement) HPAE000605 AE000605 g2314113 Helicobacter pylori 210 -11539683 7502853565 hp0971 h. pylori predicted coding region hp0971 (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10878) (re:12119) (di:complement) HPAE000605 AE000605 g2314113 Helicobacter pylori 26695 85962 -11539683

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912955	18451	40607	318	106

Description

6500735826 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0973 HP0973 Helicobacter pylori 210 -11539684 7000690331 hypothetical protein hp0973 (db:pir2.dat) E64641 E64641 Helicobacter pylori 210 -11539684 7500959119 hp0973 h. pylori predicted coding region hp0973 (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:86) (re:1147) (di:direct) HPAE000606 AE000606 g2314124 Helicobacter pylori 210 -11539684 7502853566 hp0973 h. pylori predicted coding region hp0973 (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:86) (re:1147) (di:direct) HPAE000606 AE000606 g2314124 Helicobacter pylori 26695 85962 -11539684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912962	18452	40608	732	243

Description

6500735827 xsea:hp0981 exonuclease vii-like protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0981 HP0981 Helicobacter pylori 210 -11539685 7000689915 exonuclease vii-like protein (db:pir2.dat) E64642 E64642 Helicobacter pylori 210 -11539685 7500958710 hp0981 exonuclease vii-like protein xsea (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:similar to egad:29033 percent identity: 42.50;) (le:10113) (re:10478) (di:direct) HPAE000606 AE000606 g2314123 Helicobacter pylori 210 -11539685 7502853567 hp0981 exonuclease vii-like protein xsea (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:similar to egad:29033 percent identity: 42.50;) (le:10113) (re:10478) (di:direct) HPAE000606 AE000606 g2314123 Helicobacter pylori 26695 85962 -11539685

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912969	18453	40609	228	75

Description

6500735828 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0982 HP0982 Helicobacter pylori 210 -11539686 7000690332 hypothetical protein hp0982 (db:pir2.dat) F64642 F64642 Helicobacter pylori 210 -11539686 7500959120 hp0982 h. pylori predicted coding region hp0982 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:189) (re:884) (di:direct) HPAE000607 AE000607 g2314129 Helicobacter pylori 210 -11539686 7502853568 hp0982 h. pylori predicted coding region hp0982 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:189) (re:884) (di:direct) HPAE000607 AE000607 g2314129 Helicobacter pylori 26695 85962 -11539686

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501912974	18454	40610	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913007	18455	40611	2091	696

Description

6500735829 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0984 HP0984 Helicobacter pylori 210 -11539687 7000690333 hypothetical protein hp0984 (db:pir2.dat) H64642 H64642 Helicobacter pylori 210 -11539687 7500959121 hp0984 h. pylori predicted coding region hp0984 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2638) (re:2745) (di:direct) HPAE000607 AE000607 g2314138 Helicobacter pylori 210 -11539687 7502853569 hp0984 h. pylori predicted coding region hp0984 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2638) (re:2745) (di:direct) HPAE000607 AE000607 g2314138 Helicobacter pylori 26695 85962 -11539687

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913008	18456	40612	543	181

Description

GTC ORF with score 170 to: (sr:baker's yeast) (db:genpept-pln1) (de:s.cerevisiae genes for histone h2a and h2b, trehalase, andhexaprenyl pyrophosphate synthetase.) (nt:overlap with accession j05547) (le:11534) (re:12388) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913020	18457	40613	2184	727

Description

6500735830 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0985 HP0985 Helicobacter pylori 210 -11539688 7000690334 hypothetical protein hp0985 (db:pir2.dat) A64643 A64643 Helicobacter pylori 210 -11539688 7500959122 hp0985 h. pylori predicted coding region hp0985 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2768) (re:3091) (di:complement) HPAE000607 AE000607 g2314130 Helicobacter pylori 210 -11539688 7502853570 hp0985 h. pylori predicted coding region hp0985 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2768) (re:3091) (di:complement) HPAE000607 AE000607 g2314130 Helicobacter pylori 26695 85962 -11539688

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913031	18458	40614	1812	603

Description

6500735831 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0986 HP0986 Helicobacter pylori 210 -11539689 7000690335 hypothetical protein hp0986 (db:pir2.dat) B64643 B64643 Helicobacter pylori 210 -11539689 7500959123 hp0986 h. pylori predicted coding region hp0986 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3394) (re:4107) (di:complement) HPAE000607 AE000607 g2314131 Helicobacter pylori 210 -11539689 7502853571 hp0986 h. pylori predicted coding region hp0986 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3394) (re:4107) (di:complement) HPAE000607 AE000607 g2314131 Helicobacter pylori 26695 85962 -11539689

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913039	18459	40615	408	135

Description

6500735832 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0987 HP0987 Helicobacter pylori 210 -11539690 7000690336 hypothetical protein hp0987 (db:pir2.dat) C64643 C64643 Helicobacter pylori 210 -11539690 7500959124 hp0987 h. pylori predicted coding region hp0987 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5492) (re:5725) (di:direct) HPAE000607 AE000607 g2314137 Helicobacter pylori 210 -11539690 7502853572 hp0987 h. pylori predicted coding region hp0987 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5492) (re:5725) (di:direct) HPAE000607 AE000607 g2314137 Helicobacter pylori 26695 85962 -11539690

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913046	18460	40616	600	199

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913056	18461	40617	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913058	18462	40618	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913074	18463	40619	696	231

Description

6500735833 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0990 HP0990 Helicobacter pylori 210 -11539691 7000690337 hypothetical protein hp0990 (db:pir2.dat) F64643 F64643 Helicobacter pylori 210 -11539691 7500959125 hp0990 h. pylori predicted coding region hp0990 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7607) (re:8275) (di:direct) HPAE000607 AE000607 g2314132 Helicobacter pylori 210 -11539691 7502853573 hp0990 h. pylori predicted coding region hp0990 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7607) (re:8275) (di:direct) HPAE000607 AE000607 g2314132 Helicobacter pylori 26695 85962 -11539691

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913083	18464	40620	2634	877

Description

6500735834 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0991 HP0991 Helicobacter pylori 210 -11539692 7000690338 hypothetical protein hp0991 (db:pir2.dat) G64643 G64643 Helicobacter pylori 210 -11539692 7500959126 hp0991 h. pylori predicted coding region hp0991 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8280) (re:8909) (di:complement) HPAE000607 AE000607 g2314133 Helicobacter pylori 210 -11539692 7502853574 hp0991 h. pylori predicted coding region hp0991 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8280) (re:8909) (di:complement) HPAE000607 AE000607 g2314133 Helicobacter pylori 26695 85962 -11539692

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913111	18465	40621	795	264

Description

6500735835 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0992 HP0992 Helicobacter pylori 210 -11539693 7000690339 hypothetical protein hp0992 (db:pir2.dat) H64643 H64643 Helicobacter pylori 210 -11539693 7500959127 hp0992 h. pylori predicted coding region hp0992 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9056) (re:9295) (di:complement) HPAE000607 AE000607 g2314134 Helicobacter pylori 210 -11539693 7502853575 hp0992 h. pylori predicted coding region hp0992 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9056) (re:9295) (di:complement) HPAE000607 AE000607 g2314134 Helicobacter pylori 26695 85962 -11539693

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913121	18466	40622	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913130	18467	40623	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913166	18468	40624	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913170	18469	40625	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913171	18470	40626	1080	359

Description

GTC ORF with score 567 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913175	18471	40627	402	133

Description

GTC ORF with score 158 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913176	18472	40628	861	286

Description

GTC ORF with score 309 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913178	18473	40629	450	149

Description

6500735836 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0993 HP0993 Helicobacter pylori 210 -11539694 7000690340 hypothetical protein hp0993 (db:pir2.dat) A64644 A64644 Helicobacter pylori 210 -11539694 7500959128 hp0993 h. pylori predicted coding region hp0993 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9495) (re:9746) (di:direct) HPAE000607 AE000607 g2314135 Helicobacter pylori 210 -11539694 7502853576 hp0993 h. pylori predicted coding region hp0993 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9495) (re:9746) (di:direct) HPAE000607 AE000607 g2314135 Helicobacter pylori 26695 85962 -11539694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913179	18474	40630	1698	565

Description

GTC ORF with score 268 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913181	18475	40631	1572	523

Description

GTC ORF with score 495 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913185	18476	40632	210	69

Description

GTC ORF with score 169 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913188	18477	40633	372	123

Description

6500735837 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0994 HP0994 Helicobacter pylori 210 -11539695 7000690341 hypothetical protein hp0994 (db:pir2.dat) B64644 B64644 Helicobacter pylori 210 -11539695 7500959129 hp0994 h. pylori predicted coding region hp0994 (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9718) (re:10521) (di:direct) HPAE000607 AE000607 g2314136 Helicobacter pylori 210 -11539695 7502853577 hp0994 h. pylori predicted coding region hp0994 (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9718) (re:10521) (di:direct) HPAE000607 AE000607 g2314136 Helicobacter pylori 26695 85962 -11539695

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913191	18478	40634	432	143

Description

GTC ORF with score 223 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913195	18479	40635	540	179

Description

GTC ORF with score 93 to: (or:Homo sapiens) (sr:homo sapiens (tissue library: lambda syg11 pcsy11 pcsy32 pcsy71) (db:genpept-pri3) (de:human synapsin i (syn1) gene, exon 13.) (le:m58321:2089:m58341:21:m58351:21) (re:2465:78:112) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913212	18480	40636	1554	517

Description

6500735838 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0996 HP0996 Helicobacter pylori 210 -11539696 7000690342 hypothetical protein hp0996 (db:pir2.dat) D64644 D64644 Helicobacter pylori 210 -11539696 7500959130 hp0996 h. pylori predicted coding region hp0996 (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2404) (re:4206) (di:complement) HPAE000608 AE000608 g2314144 Helicobacter pylori 210 -11539696 7502853578 hp0996 h. pylori predicted coding region hp0996 (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2404) (re:4206) (di:complement) HPAE000608 AE000608 g2314144 Helicobacter pylori 26695 85962 -11539696

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913213	18481	40637	444	147

Description

6500735839 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP0999 HP0999 Helicobacter pylori 210 -11539697 7500975640 hp0999 h. pylori predicted coding region hp0999 (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6267) (re:6452) (di:direct) HPAE000608 AE000608 g2314145 Helicobacter pylori 210 -11539697 7502853579 hp0999 h. pylori predicted coding region hp0999 (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6267) (re:6452) (di:direct) HPAE000608 AE000608 g2314145 Helicobacter pylori 26695 85962 -11539697

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913230	18482	40638	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913233	18483	40639	1281	426

Description

6500735840 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1001 HP1001 Helicobacter pylori 210 -11539698 7000690344 hypothetical protein hp1001 (db:pir2.dat) A64645 A64645 Helicobacter pylori 210 -11539698 7500959131 hp1001 h. pylori predicted coding region hp1001 (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7459) (re:7743) (di:direct) HPAE000608 AE000608 g2314146 Helicobacter pylori 210 -11539698 7502853580 hp1001 h. pylori predicted coding region hp1001 (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7459) (re:7743) (di:direct) HPAE000608 AE000608 g2314146 Helicobacter pylori 26695 85962 -11539698

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913243	18484	40640	405	134

Description

6500735841 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1002 HP1002 Helicobacter pylori 210 -11539699 7000690345 hypothetical protein hp1002 (db:pir2.dat) B64645 B64645 Helicobacter pylori 210 -11539699 7500959132 hp1002 h. pylori predicted coding region hp1002 (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7787) (re:8971) (di:direct) HPAE000608 AE000608 g2314147 Helicobacter pylori 210 -11539699 7502853581 hp1002 h. pylori predicted coding region hp1002 (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7787) (re:8971) (di:direct) HPAE000608 AE000608 g2314147 Helicobacter pylori 26695 85962 -11539699

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913244	18485	40641	336	111

Description

6500735842 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1003 HP1003 Helicobacter pylori 210 -11539700 7000690346 hypothetical protein hp1003 (db:pir2.dat) C64645 C64645 Helicobacter pylori 210 -11539700 7500959133 hp1003 h. pylori predicted coding region hp1003 (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8996) (re:10108) (di:complement) HPAE000608 AE000608 g2314148 Helicobacter pylori 210 -11539700 7502853582 hp1003 h. pylori predicted coding region hp1003 (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8996) (re:10108) (di:complement) HPAE000608 AE000608 g2314148 Helicobacter pylori 26695 85962 -11539700

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913247	18486	40642	2211	736

Description

6500735843 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1004 HP1004 Helicobacter pylori 210 -11539701 7000690347 hypothetical protein hp1004 (db:pir2.dat) D64645 D64645 Helicobacter pylori 210 -11539701 7500959134 hp1004 h. pylori predicted coding region hp1004 (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10084) (re:10905) (di:complement) HPAE000608 AE000608 g2314149 Helicobacter pylori 210 -11539701 7502853583 hp1004 h. pylori predicted coding region hp1004 (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10084) (re:10905) (di:complement) HPAE000608 AE000608 g2314149 Helicobacter pylori 26695 85962 -11539701

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913260	18487	40643	336	111

Description

6500735844 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1005 HP1005 Helicobacter pylori 210 -11539702 7000690348 hypothetical protein hp1005 (db:pir2.dat) E64645 E64645 Helicobacter pylori 210 -11539702 7500959135 hp1005 h. pylori predicted coding region hp1005 (db:genpept-bct1) (de:helicobacter pylori section 87 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:171) (re:485) (di:direct) HPAE000609 AE000609 g2314159 Helicobacter pylori 210 -11539702 7502853584 hp1005 h. pylori predicted coding region hp1005 (db:genpept) (de:helicobacter pylori 26695 section 87 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:171) (re:485) (di:direct) HPAE000609 AE000609 g2314159 Helicobacter pylori 26695 85962 -11539702

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913300	18488	40644	642	213

Description

6500735845 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1015 HP1015 Helicobacter pylori 210 -11539703 7500975641 hp1015 h. pylori predicted coding region hp1015 (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:86) (re:592) (di:direct) HPAE000610 AE000610 g2314169 Helicobacter pylori 210 -11539703 7502853585 hp1015 h. pylori predicted coding region hp1015 (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:86) (re:592) (di:direct) HPAE000610 AE000610 g2314169 Helicobacter pylori 26695 85962 -11539703

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913309	18489	40645	321	106

Description

6500735846 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1018 HP1018 Helicobacter pylori 210 -11539704 7000690350 hypothetical protein hp1018 (db:pir2.dat) B64647 B64647 Helicobacter pylori 210 -11539704 7500959136 hp1018 h. pylori predicted coding region hp1018 (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2833) (re:2979) (di:direct) HPAE000610 AE000610 g2314172 Helicobacter pylori 210 -11539704 7502853586 hp1018 h. pylori predicted coding region hp1018 (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2833) (re:2979) (di:direct) HPAE000610 AE000610 g2314172 Helicobacter pylori 26695 85962 -11539704

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913317	18490	40646	234	77

Description

6500735847 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1022 HP1022 Helicobacter pylori 210 -11539705 7000690351 hypothetical protein hp1022 (db:pir2.dat) F64647 F64647 Helicobacter pylori 210 -11539705 7500959137 hp1022 h. pylori predicted coding region hp1022 (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6677) (re:7513) (di:direct) HPAE000610 AE000610 g2314170 Helicobacter pylori 210 -11539705 7502853587 hp1022 h. pylori predicted coding region hp1022 (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6677) (re:7513) (di:direct) HPAE000610 AE000610 g2314170 Helicobacter pylori 26695 85962 -11539705

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913327	18491	40647	582	193

Description

6500735848 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1023 HP1023 Helicobacter pylori 210 -11539706 7000690352 hypothetical protein hp1023 (db:pir2.dat) G64647 G64647 Helicobacter pylori 210 -11539706 7500959138 hp1023 h. pylori predicted coding region hp1023 (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7608) (re:8858) (di:complement) HPAE000610 AE000610 g2314171 Helicobacter pylori 210 -11539706 7502853588 hp1023 h. pylori predicted coding region hp1023 (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7608) (re:8858) (di:complement) HPAE000610 AE000610 g2314171 Helicobacter pylori 26695 85962 -11539706

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913328	18492	40648	1131	376

Description

6500735849 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1028 HP1028 Helicobacter pylori 210 -11539707 7000690353 hypothetical protein hp1028 (db:pir2.dat) D64648 D64648 Helicobacter pylori 210 -11539707 7500959139 hp1028 h. pylori predicted coding region hp1028 (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:582) (re:1079) (di:complement) HPAE000611 AE000611 g2314184 Helicobacter pylori 210 -11539707 7502853589 hp1028 h. pylori predicted coding region hp1028 (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:582) (re:1079) (di:complement) HPAE000611 AE000611 g2314184 Helicobacter pylori 26695 85962 -11539707

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913329	18493	40649	336	111

Description

6500735850 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1029 HP1029 Helicobacter pylori 210 -11539708 7000690354 hypothetical protein hp1029 (db:pir2.dat) E64648 E64648 Helicobacter pylori 210 -11539708 7500959140 hp1029 h. pylori predicted coding region hp1029 (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1076) (re:1612) (di:complement) HPAE000611 AE000611 g2314185 Helicobacter pylori 210 -11539708 7502853590 hp1029 h. pylori predicted coding region hp1029 (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1076) (re:1612) (di:complement) HPAE000611 AE000611 g2314185 Helicobacter pylori 26695 85962 -11539708

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913332	18494	40650	393	130

Description

6500735851 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1033 HP1033 Helicobacter pylori 210 -11539709 7000690355 hypothetical protein hp1033 (db:pir2.dat) A64649 A64649 Helicobacter pylori 210 -11539709 7500959141 hp1033 h. pylori predicted coding region hp1033 (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4341) (re:4736) (di:direct) HPAE000611 AE000611 g2314186 Helicobacter pylori 210 -11539709 7502853591 hp1033 h. pylori predicted coding region hp1033 (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4341) (re:4736) (di:direct) HPAE000611 AE000611 g2314186 Helicobacter pylori 26695 85962 -11539709

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913333	18495	40651	369	122

Description

6500735852 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1039 HP1039 Helicobacter pylori 210 -11539710 7000690356 hypothetical protein hp1039 (db:pir2.dat) G64649 G64649 Helicobacter pylori 210 -11539710 7500959142 hp1039 h. pylori predicted coding region hp1039 (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9092) (re:10381) (di:complement) HPAE000611 AE000611 g2314187 Helicobacter pylori 210 -11539710 7502853592 hp1039 h. pylori predicted coding region hp1039 (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9092) (re:10381) (di:complement) HPAE000611 AE000611 g2314187 Helicobacter pylori 26695 85962 -11539710

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913342	18496	40652	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913345	18497	40653	240	79

Description

6500735853 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1042 HP1042 Helicobacter pylori 210 -11539711 7000690357 hypothetical protein hp1042 (db:pir2.dat) B64650 B64650 Helicobacter pylori 210 -11539711 7500959143 hp1042 h. pylori predicted coding region hp1042 (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2330) (re:3376) (di:direct) HPAE000612 AE000612 g2314198 Helicobacter pylori 210 -11539711 7502853593 hp1042 h. pylori predicted coding region hp1042 (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2330) (re:3376) (di:direct) HPAE000612 AE000612 g2314198 Helicobacter pylori 26695 85962 -11539711

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913356	18498	40654	465	154

Description

6500735854 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1051 HP1051 Helicobacter pylori 210 -11539712 7000690358 hypothetical protein hp1051 (db:pir2.dat) C64651 C64651 Helicobacter pylori 210 -11539712 7500959144 hp1051 h. pylori predicted coding region hp1051 (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13128) (re:13550) (di:complement) HPAE000612 AE000612 g2314199 Helicobacter pylori 210 -11539712 7502853594 hp1051 h. pylori predicted coding region hp1051 (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13128) (re:13550) (di:complement) HPAE000612 AE000612 g2314199 Helicobacter pylori 26695 85962 -11539712

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913365	18499	40655	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913371	18500	40656	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913387	18501	40657	1029	342

Description

6500735855 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1053 HP1053 Helicobacter pylori 210 -11539713 7000690359 hypothetical protein hp1053 (db:pir2.dat) E64651 E64651 Helicobacter pylori 210 -11539713 7500959145 hp1053 h. pylori predicted coding region hp1053 (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:951) (re:1604) (di:complement) HPAE000613 AE000613 g2314208 Helicobacter pylori 210 -11539713 7502853595 hp1053 h. pylori predicted coding region hp1053 (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:951) (re:1604) (di:complement) HPAE000613 AE000613 g2314208 Helicobacter pylori 26695 85962 -11539713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913400	18502	40658	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913407	18503	40659	1785	594

Description

6500735856 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1054 HP1054 Helicobacter pylori 210 -11539714 7000690360 hypothetical protein hp1054 (db:pir2.dat) F64651 F64651 Helicobacter pylori 210 -11539714 7500959146 hp1054 h. pylori predicted coding region hp1054 (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1541) (re:2809) (di:complement) HPAE000613 AE000613 g2314209 Helicobacter pylori 210 -11539714 7502853596 hp1054 h. pylori predicted coding region hp1054 (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1541) (re:2809) (di:complement) HPAE000613 AE000613 g2314209 Helicobacter pylori 26695 85962 -11539714

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913408	18504	40660	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913411	18505	40661	1002	333

Description

6500735857 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1055 HP1055 Helicobacter pylori 210 -11539715 7000690361 hypothetical protein hp1055 (db:pir2.dat) G64651 G64651 Helicobacter pylori 210 -11539715 7500959147 hp1055 h. pylori predicted coding region hp1055 (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2873) (re:3817) (di:complement) HPAE000613 AE000613 g2314210 Helicobacter pylori 210 -11539715 7502853597 hp1055 h. pylori predicted coding region hp1055 (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2873) (re:3817) (di:complement) HPAE000613 AE000613 g2314210 Helicobacter pylori 26695 85962 -11539715

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913420	18506	40662	429	142

Description

6500735858 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1056 HP1056 Helicobacter pylori 210 -11539716 7000690362 hypothetical protein hp1056 (db:pir2.dat) H64651 H64651 Helicobacter pylori 210 -11539716 7500959148 hp1056 h. pylori predicted coding region hp1056 (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3826) (re:4680) (di:complement) HPAE000613 AE000613 g2314211 Helicobacter pylori 210 -11539716 7502853598 hp1056 h. pylori predicted coding region hp1056 (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3826) (re:4680) (di:complement) HPAE000613 AE000613 g2314211 Helicobacter pylori 26695 85962 -11539716

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913422	18507	40663	609	202

Description

6500735859 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1057 HP1057 Helicobacter pylori 210 -11539717 7000690363 hypothetical protein hp1057 (db:pir2.dat) A64652 A64652 Helicobacter pylori 210 -11539717 7500959149 hp1057 h. pylori predicted coding region hp1057 (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4658) (re:5380) (di:complement) HPAE000613 AE000613 g2314212 Helicobacter pylori 210 -11539717 7502853599 hp1057 h. pylori predicted coding region hp1057 (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4658) (re:5380) (di:complement) HPAE000613 AE000613 g2314212 Helicobacter pylori 26695 85962 -11539717

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913423	18508	40664	543	180

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913436	18509	40665	321	106

Description

6500735860 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1060 HP1060 Helicobacter pylori 210 -11539718 7000690640 probable abc transporter (db:pir2.dat) D64652 D64652 Helicobacter pylori 210 -11539718 7500959417 hp1060 h. pylori predicted coding region hp1060 (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7419) (re:7901) (di:direct) HPAE000613 AE000613 g2314213 Helicobacter pylori 210 -11539718 7502853600 hp1060 h. pylori predicted coding region hp1060 (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7419) (re:7901) (di:direct) HPAE000613 AE000613 g2314213 Helicobacter pylori 26695 85962 -11539718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913452	18510	40666	2409	802

Description

6500735861 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1064 HP1064 Helicobacter pylori 210 -11539719 7000690364 hypothetical protein hp1064 (db:pir2.dat) H64652 H64652 Helicobacter pylori 210 -11539719 7500959150 hp1064 h. pylori predicted coding region hp1064 (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10169) (re:10450) (di:direct) HPAE000613 AE000613 g2314214 Helicobacter pylori 210 -11539719 7502853601 hp1064 h. pylori predicted coding region hp1064 (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10169) (re:10450) (di:direct) HPAE000613 AE000613 g2314214 Helicobacter pylori 26695 85962 -11539719

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913466	18511	40667	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913482	18512	40668	567	188

Description

GTC ORF with score 193 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid h38k22, complete sequence.) (nt:cdna est embl:c08541 comes from this gene; cdna est) (le:12527:13033:13260:13401) (re:12598:13215:13351:13585) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913485	18513	40669	186	61

Description

6500735862 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1065 HP1065 Helicobacter pylori 210 -11539720 7000690365 hypothetical protein hp1065 (db:pir2.dat) A64653 A64653 Helicobacter pylori 210 -11539720 7500959151 hp1065 h. pylori predicted coding region hp1065 (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10453) (re:10860) (di:direct) HPAE000613 AE000613 g2314215 Helicobacter pylori 210 -11539720 7502853602 hp1065 h. pylori predicted coding region hp1065 (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10453) (re:10860) (di:direct) HPAE000613 AE000613 g2314215 Helicobacter pylori 26695 85962 -11539720

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913486	18514	40670	732	243

Description

6500735863 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1070 HP1070 Helicobacter pylori 210 -11539721 5500686463 hp1070 (sr:,campylobacter pylori) (de:hypothetical protein hp1070 (orfx)) (db:swissprot) YA70_HELPY O07680 HELICOBACTER PYLORI 210 -11539721 7000687101 hypothetical protein hp1070 (db:pir2.dat) F64653 F64653 Helicobacter pylori 210 -11539721 7500895911 hp1070 h. pylori predicted coding region hp1070 (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3462) (re:3716) (di:direct) HPAE000614 AE000614 g2314225 Helicobacter pylori 210 -11539721 7502853603 hp1070 h. pylori predicted coding region hp1070 (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3462) (re:3716) (di:direct) HPAE000614 AE000614 g2314225 Helicobacter pylori 26695 85962 -11539721

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913507	18515	40671	738	245

Description

GTC ORF with score 120 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone 1750.) (le:33913:35113) (re:35040:35475) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913517	18516	40672	273	90

Description

6500735864 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1074 HP1074 Helicobacter pylori 210 -11539722 7000690366 hypothetical protein hp1074 (db:pir2.dat) B64654 B64654 Helicobacter pylori 210 -11539722 7500959152 hp1074 h. pylori predicted coding region hp1074 (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6999) (re:7787) (di:direct) HPAE000614 AE000614 g2314226 Helicobacter pylori 210 -11539722 7502853604 hp1074 h. pylori predicted coding region hp1074 (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6999) (re:7787) (di:direct) HPAE000614 AE000614 g2314226 Helicobacter pylori 26695 85962 -11539722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913518	18517	40673	297	98

Description

6500735865 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1076 HP1076 Helicobacter pylori 210 -11539723 7000690367 hypothetical protein hp1076 (db:pir2.dat) D64654 D64654 Helicobacter pylori 210 -11539723 7500959153 hp1076 h. pylori predicted coding region hp1076 (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9294) (re:9809) (di:direct) HPAE000614 AE000614 g2314227 Helicobacter pylori 210 -11539723 7502853605 hp1076 h. pylori predicted coding region hp1076 (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9294) (re:9809) (di:direct) HPAE000614 AE000614 g2314227 Helicobacter pylori 26695 85962 -11539723

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913520	18518	40674	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913531	18519	40675	402	133

Description

6500735866 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1078 HP1078 Helicobacter pylori 210 -11539724 7000690368 hypothetical protein hp1078 (db:pir2.dat) F64654 F64654 Helicobacter pylori 210 -11539724 7500959154 hp1078 h. pylori predicted coding region hp1078 (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10866) (re:11552) (di:complement) HPAE000614 AE000614 g2314228 Helicobacter pylori 210 -11539724 7502853606 hp1078 h. pylori predicted coding region hp1078 (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10866) (re:11552) (di:complement) HPAE000614 AE000614 g2314228 Helicobacter pylori 26695 85962 -11539724

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913533	18520	40676	741	246

Description

6500735867 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1079 HP1079 Helicobacter pylori 210 -11539725 7000690369 hypothetical protein hp1079 (db:pir2.dat) G64654 G64654 Helicobacter pylori 210 -11539725 7500959155 hp1079 h. pylori predicted coding region hp1079 (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11581) (re:12693) (di:complement) HPAE000614 AE000614 g2314229 Helicobacter pylori 210 -11539725 7502853607 hp1079 h. pylori predicted coding region hp1079 (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:11581) (re:12693) (di:complement) HPAE000614 AE000614 g2314229 Helicobacter pylori 26695 85962 -11539725

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913539	18521	40677	681	226

Description

6500735868 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1081 HP1081 Helicobacter pylori 210 -11539726 7000690370 hypothetical protein hp1081 (db:pir2.dat) A64655 A64655 Helicobacter pylori 210 -11539726 7500959156 hp1081 h. pylori predicted coding region hp1081 (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:659) (re:1282) (di:complement) HPAE000615 AE000615 g2314238 Helicobacter pylori 210 -11539726 7502853608 hp1081 h. pylori predicted coding region hp1081 (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:659) (re:1282) (di:complement) HPAE000615 AE000615 g2314238 Helicobacter pylori 26695 85962 -11539726

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913551	18522	40678	306	101

Description

6500735869 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1083 HP1083 Helicobacter pylori 210 -11539727 7000690371 hypothetical protein hp1083 (db:pir2.dat) C64655 C64655 Helicobacter pylori 210 -11539727 7500959157 hp1083 h. pylori predicted coding region hp1083 (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3023) (re:4462) (di:complement) HPAE000615 AE000615 g2314239 Helicobacter pylori 210 -11539727 7502853609 hp1083 h. pylori predicted coding region hp1083 (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3023) (re:4462) (di:complement) HPAE000615 AE000615 g2314239 Helicobacter pylori 26695 85962 -11539727

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913552	18523	40679	726	241

Description

6500735870 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1085 HP1085 Helicobacter pylori 210 -11539728 7000690372 hypothetical protein hp1085 (db:pir2.dat) E64655 E64655 Helicobacter pylori 210 -11539728 7500959158 hp1085 h. pylori predicted coding region hp1085 (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5707) (re:6222) (di:direct) HPAE000615 AE000615 g2314240 Helicobacter pylori 210 -11539728 7502853610 hp1085 h. pylori predicted coding region hp1085 (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5707) (re:6222) (di:direct) HPAE000615 AE000615 g2314240 Helicobacter pylori 26695 85962 -11539728

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913559	18524	40680	249	82

Description

6500735871 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1089 HP1089 Helicobacter pylori 210 -11539729 7000690373 hypothetical protein hp1089 (db:pir2.dat) A64656 A64656 Helicobacter pylori 210 -11539729 7500959159 hp1089 h. pylori predicted coding region hp1089 (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9706) (re:12042) (di:direct) HPAE000615 AE000615 g2314241 Helicobacter pylori 210 -11539729 7502853611 hp1089 h. pylori predicted coding region hp1089 (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9706) (re:12042) (di:direct) HPAE000615 AE000615 g2314241 Helicobacter pylori 26695 85962 -11539729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913564	18525	40681	720	240

Description

GTC ORF with score 114 to: (sr:soybean) (db:genpept-pln1) (ec:2.7.7.6) (de:soybean rpb1-b1 gene for the largest subunit of rna polymerase ii(ec 2.7.7.6).) (nt:largest subunit of rna polymerase ii) (le:<1:2062:2196) (re:1736:2133:2265) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913566	18526	40682	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913577	18527	40683	279	92

Description

6500735872 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1093 HP1093 Helicobacter pylori 210 -11539730 7000690374 hypothetical protein hp1093 (db:pir2.dat) E64656 E64656 Helicobacter pylori 210 -11539730 7500959160 hp1093 h. pylori predicted coding region hp1093 (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2620) (re:2706) (di:complement) HPAE000616 AE000616 g2314255 Helicobacter pylori 210 -11539730 7502853612 hp1093 h. pylori predicted coding region hp1093 (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2620) (re:2706) (di:complement) HPAE000616 AE000616 g2314255 Helicobacter pylori 26695 85962 -11539730

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913582	18528	40684	342	113

Description

6500735873 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1094 HP1094 Helicobacter pylori 210 -11539731 7000690375 hypothetical protein hp1094 (db:pir2.dat) F64656 F64656 Helicobacter pylori 210 -11539731 7500959161 hp1094 h. pylori predicted coding region hp1094 (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2883) (re:3239) (di:direct) HPAE000616 AE000616 g2314253 Helicobacter pylori 210 -11539731 7502853613 hp1094 h. pylori predicted coding region hp1094 (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2883) (re:3239) (di:direct) HPAE000616 AE000616 g2314253 Helicobacter pylori 26695 85962 -11539731

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913597	18529	40685	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913599	18530	40686	624	207

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913606	18531	40687	582	193

Description

6500735874 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1097 HP1097 Helicobacter pylori 210 -11539732 7000690376 hypothetical protein hp1097 (db:pir2.dat) A64657 A64657 Helicobacter pylori 210 -11539732 7500959162 hp1097 h. pylori predicted coding region hp1097 (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5087) (re:5182) (di:complement) HPAE000616 AE000616 g2314254 Helicobacter pylori 210 -11539732 7502853614 hp1097 h. pylori predicted coding region hp1097 (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5087) (re:5182) (di:complement) HPAE000616 AE000616 g2314254 Helicobacter pylori 26695 85962 -11539732

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913612	18532	40688	717	238

Description

6500735875 cad:hp1104 cinnamyl-alcohol dehydrogenase eli3-2 (gtcfc:1.1) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1104 HP1104 Helicobacter pylori 210 -11539733 7000689714 probable cinnamyl-alcohol dehydrogenase (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.195) (db:pir2.dat) H64657 H64657 Helicobacter pylori 210 -11539733 7500953778 hp1104 cinnamyl-alcohol dehydrogenase eli3-2 cad (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:similar to egad:25465 percent identity: 43.97;) (le:111) (re:1157) (di:direct) HPAE000617 AE000617 g2314257 Helicobacter pylori 210 -11539733 7502853615 hp1104 cinnamyl-alcohol dehydrogenase eli3-2 cad (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:similar to egad:25465 percent identity: 43.97;) (le:111) (re:1157) (di:direct) HPAE000617 AE000617 g2314257 Helicobacter pylori 26695 85962 -11539733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913630	18533	40689	561	186

Description

6500735876 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1106 HP1106 Helicobacter pylori 210 -11539734 7000690377 hypothetical protein hp1106 (db:pir2.dat) B64658 B64658 Helicobacter pylori 210 -11539734 7500959163 hp1106 h. pylori predicted coding region hp1106 (db:genpept-bct1) (de:helicobacter pylori section 95 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2655) (re:3962) (di:direct) HPAE000617 AE000617 g2314266 Helicobacter pylori 210 -11539734 7502853616 hp1106 h. pylori predicted coding region hp1106 (db:genpept) (de:helicobacter pylori 26695 section 95 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2655) (re:3962) (di:direct) HPAE000617 AE000617 g2314266 Helicobacter pylori 26695 85962 -11539734

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913645	18534	40690	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913659	18535	40691	1245	414

Description

6500735877 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1115 HP1115 Helicobacter pylori 210 -11539735 7000690378 hypothetical protein hp1115 (db:pir2.dat) C64659 C64659 Helicobacter pylori 210 -11539735 7500959164 hp1115 h. pylori predicted coding region hp1115 (db:genpept-bct1) (de:helicobacter pylori section 96 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:65) (re:751) (di:complement) HPAE000618 AE000618 g2314273 Helicobacter pylori 210 -11539735 7502853617 hp1115 h. pylori predicted coding region hp1115 (db:genpept) (de:helicobacter pylori 26695 section 96 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:65) (re:751) (di:complement) HPAE000618 AE000618 g2314273 Helicobacter pylori 26695 85962 -11539735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913661	18536	40692	897	298

Description

6500735878 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1120 HP1120 Helicobacter pylori 210 -11539736 7000690379 hypothetical protein hp1120 (db:pir2.dat) H64659 H64659 Helicobacter pylori 210 -11539736 7500959165 hp1120 h. pylori predicted coding region hp1120 (db:genpept-bct1) (de:helicobacter pylori section 96 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8823) (re:9257) (di:complement) HPAE000618 AE000618 g2314274 Helicobacter pylori 210 -11539736 7502853618 hp1120 h. pylori predicted coding region hp1120 (db:genpept) (de:helicobacter pylori 26695 section 96 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8823) (re:9257) (di:complement) HPAE000618 AE000618 g2314274 Helicobacter pylori 26695 85962 -11539736

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913667	18537	40693	1155	384

Description

GTC ORF with score 111 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f16m14 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:49427:51857:52670) (re:50571:52603:52799) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913668	18538	40694	579	192

Description

GTC ORF with score 101 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c33h5.) (nt:similar to pre-mrna splicing factor srp20; coded) (le:16484:16625:17217) (re:16577:16777:17324) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913687	18539	40695	513	170

Description

6500735879 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1122 HP1122 Helicobacter pylori 210 -11539737 7000690380 hypothetical protein hp1122 (db:pir2.dat) B64660 B64660 Helicobacter pylori 210 -11539737 7500959166 hp1122 h. pylori predicted coding region hp1122 (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:111) (re:341) (di:complement) HPAE000619 AE000619 g2314289 Helicobacter pylori 210 -11539737 7502853619 hp1122 h. pylori predicted coding region hp1122 (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:111) (re:341) (di:complement) HPAE000619 AE000619 g2314289 Helicobacter pylori 26695 85962 -11539737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913692	18540	40696	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913693	18541	40697	666	221

Description

6500735880 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1124 HP1124 Helicobacter pylori 210 -11539738 7000690381 hypothetical protein hp1124 (db:pir2.dat) D64660 D64660 Helicobacter pylori 210 -11539738 7500959167 hp1124 h. pylori predicted coding region hp1124 (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1160) (re:2155) (di:complement) HPAE000619 AE000619 g2314290 Helicobacter pylori 210 -11539738 7502853620 hp1124 h. pylori predicted coding region hp1124 (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1160) (re:2155) (di:complement) HPAE000619 AE000619 g2314290 Helicobacter pylori 26695 85962 -11539738

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913709	18542	40698	1725	574

Description

GTC ORF with score 367 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone c1241.) (nt:similar to s.cerevisiae hypothetical 229.9kd) (le:11010:11253:11494) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913714	18543	40699	1335	445

Description

GTC ORF with score 232 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone c1241.) (nt:similar to s.cerevisiae hypothetical 229.9kd) (le:11010:11253:11494) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913715	18544	40700	1104	367

Description

6500735881 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1127 HP1127 Helicobacter pylori 210 -11539739 7000690382 hypothetical protein hp1127 (db:pir2.dat) G64660 G64660 Helicobacter pylori 210 -11539739 7500959168 hp1127 h. pylori predicted coding region hp1127 (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4019) (re:4600) (di:complement) HPAE000619 AE000619 g2314291 Helicobacter pylori 210 -11539739 7502853621 hp1127 h. pylori predicted coding region hp1127 (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4019) (re:4600) (di:complement) HPAE000619 AE000619 g2314291 Helicobacter pylori 26695 85962 -11539739

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913716	18545	40701	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913726	18546	40702	303	100

Description

6500735882 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1128 HP1128 Helicobacter pylori 210 -11539740 7000690383 hypothetical protein hp1128 (db:pir2.dat) H64660 H64660 Helicobacter pylori 210 -11539740 7500959169 hp1128 h. pylori predicted coding region hp1128 (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4590) (re:4844) (di:complement) HPAE000619 AE000619 g2314292 Helicobacter pylori 210 -11539740 7502853622 hp1128 h. pylori predicted coding region hp1128 (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4590) (re:4844) (di:complement) HPAE000619 AE000619 g2314292 Helicobacter pylori 26695 85962 -11539740

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913736	18547	40703	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913737	18548	40704	207	68

Description

6500735883 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1142 HP1142 Helicobacter pylori 210 -11539741 7000690739 trans-golgi membrane protein p230 (db:pir2.dat) F64662 F64662 Helicobacter pylori 210 -11539741 7500959504 hp1142 h. pylori predicted coding region hp1142 (db:genpept-bct1) (de:helicobacter pylori section 98 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3328) (re:5607) (di:complement) HPAE000620 AE000620 g2314298 Helicobacter pylori 210 -11539741 7502853623 hp1142 h. pylori predicted coding region hp1142 (db:genpept) (de:helicobacter pylori 26695 section 98 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3328) (re:5607) (di:complement) HPAE000620 AE000620 g2314298 Helicobacter pylori 26695 85962 -11539741

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913743	18549	40705	210	69

Description

6500735884 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1143 HP1143 Helicobacter pylori 210 -11539742 7000690384 hypothetical protein hp1143 (db:pir2.dat) G64662 G64662 Helicobacter pylori 210 -11539742 7500959170 hp1143 h. pylori predicted coding region hp1143 (db:genpept-bct1) (de:helicobacter pylori section 98 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5647) (re:6948) (di:complement) HPAE000620 AE000620 g2314299 Helicobacter pylori 210 -11539742 7502853624 hp1143 h. pylori predicted coding region hp1143 (db:genpept) (de:helicobacter pylori 26695 section 98 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5647) (re:6948) (di:complement) HPAE000620 AE000620 g2314299 Helicobacter pylori 26695 85962 -11539742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913748	18550	40706	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913750	18551	40707	1293	430

Description

GTC ORF with score 117 to: (sr:drosophila melanogaster (strain canton s) (library: lambda zap ii) (db:genpept-inv) (de:drosophila melanogaster calcium-binding protein mrna, complete cds.) (nt:leucine zipper encoded in base pairs 2615-2742) (le:167) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913753	18552	40708	1797	598

Description

6500735885 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1144 HP1144 Helicobacter pylori 210 -11539743 7000690385 hypothetical protein hp1144 (db:pir2.dat) H64662 H64662 Helicobacter pylori 210 -11539743 7500959171 hp1144 h. pylori predicted coding region hp1144 (db:genpept-bct1) (de:helicobacter pylori section 98 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7192) (re:7449) (di:direct) HPAE000620 AE000620 g2314300 Helicobacter pylori 210 -11539743 7502853625 hp1144 h. pylori predicted coding region hp1144 (db:genpept) (de:helicobacter pylori 26695 section 98 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7192) (re:7449) (di:direct) HPAE000620 AE000620 g2314300 Helicobacter pylori 26695 85962 -11539743

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913765	18553	40709	612	203

Description

6500735886 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1145 HP1145 Helicobacter pylori 210 -11539744 7000690386 hypothetical protein hp1145 (db:pir2.dat) A64663 A64663 Helicobacter pylori 210 -11539744 7500959172 hp1145 h. pylori predicted coding region hp1145 (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:405) (re:716) (di:complement) HPAE000621 AE000621 g2314311 Helicobacter pylori 210 -11539744 7502853626 hp1145 h. pylori predicted coding region hp1145 (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:405) (re:716) (di:complement) HPAE000621 AE000621 g2314311 Helicobacter pylori 26695 85962 -11539744

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913778	18554	40710	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913781	18555	40711	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913785	18556	40712	1113	370

Description

6500735887 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1146 HP1146 Helicobacter pylori 210 -11539745 7000690387 hypothetical protein hp1146 (db:pir2.dat) B64663 B64663 Helicobacter pylori 210 -11539745 7500959173 hp1146 h. pylori predicted coding region hp1146 (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:776) (re:1285) (di:complement) HPAE000621 AE000621 g2314312 Helicobacter pylori 210 -11539745 7502853627 hp1146 h. pylori predicted coding region hp1146 (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:776) (re:1285) (di:complement) HPAE000621 AE000621 g2314312 Helicobacter pylori 26695 85962 -11539745

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913801	18557	40713	1797	598

Description

GTC ORF with score 500 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone t5k18 (essaiiproject).) (nt:similarity to predicted protein mtcy20g9,) (le:46441:50174) (re:48222:50428) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913802	18558	40714	819	272

Description

GTC ORF with score 245 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone t5k18 (essaiiproject).) (nt:similarity to predicted protein mtcy20g9,) (le:46441:50174) (re:48222:50428) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913821	18559	40715	276	91

Description

GTC ORF with score 96 to: (db:genpept-bct2) (de:mycobacterium smegmatis exochelin gene cluster, exit (exit) andfxbb (fxbb) genes, complete cds; and fxbc (fxbc) gene, partial cds.) (nt:abc transporter; this abc transporter probably) (le:489) (re:3857) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913827	18560	40716	972	323

Description

6500735888 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1150 HP1150 Helicobacter pylori 210 -11539746 7000690388 hypothetical protein hp1150 (db:pir2.dat) F64663 F64663 Helicobacter pylori 210 -11539746 7500959174 hp1150 h. pylori predicted coding region hp1150 (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3428) (re:3775) (di:complement) HPAE000621 AE000621 g2314313 Helicobacter pylori 210 -11539746 7502853628 hp1150 h. pylori predicted coding region hp1150 (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3428) (re:3775) (di:complement) HPAE000621 AE000621 g2314313 Helicobacter pylori 26695 85962 -11539746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913839	18561	40717	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913841	18562	40718	3615	1204

Description

6500735889 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1154 HP1154 Helicobacter pylori 210 -11539747 7000689478 hypothetical protein hp1154 (cl:hypothetical protein hp1154) (db:pir2.dat) B64664 B64664 Helicobacter pylori 210 -11539747 7500955776 hp1154 h. pylori predicted coding region hp1154 (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8212) (re:8619) (di:direct) HPAE000621 AE000621 g2314314 Helicobacter pylori 210 -11539747 7502853629 hp1154 h. pylori predicted coding region hp1154 (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8212) (re:8619) (di:direct) HPAE000621 AE000621 g2314314 Helicobacter pylori 26695 85962 -11539747

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913872	18563	40719	804	267

Description

7500959176 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1163 HP1163 Helicobacter pylori 210 -11539748 7000690389 hypothetical protein hp1163 (db:pir2.dat) C64665 C64665 Helicobacter pylori 210 -11539748 7500959175 hp1163 h. pylori predicted coding region hp1163 (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1845) (re:2036) (di:direct) HPAE000622 AE000622 g2314326 Helicobacter pylori 210 -11539748 7502853630 fixs putative component of cation transport for (db:genpept) (de:helicobacter pylori, strain j99 section 97 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1163) (le:9113) (re:9304) (di:direct) AE001536 AE001536 g4155676 Helicobacter pylori J99 85963 -11539748 6500735890 hp1163 h. pylori predicted coding region hp1163 (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1845) (re:2036) (di:direct) HPAE000622 AE000622 g2314326 Helicobacter pylori 26695 85962 -11539748

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913874	18564	40720	2310	769

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913897	18565	40721	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913913	18566	40722	255	84

Description

GTC ORF with score 142 to: (sr:n.crassa (strain 74a) dna, clones psv50-5:4g) (db:genpept-pln1) (de:n.crassa tryptophan synthetase (trp3) alpha-2 subunit gene,complete cds.) (nt:tryptophan synthetase) (le:483:608:838) (re:530:766:2757) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913921	18567	40723	1344	447

Description

GTC ORF with score 1625 to: (sr:n.crassa (strain 74a) dna, clones psv50-5:4g) (db:genpept-pln1) (de:n.crassa tryptophan synthetase (trp3) alpha-2 subunit gene,complete cds.) (nt:tryptophan synthetase) (le:483:608:838) (re:530:766:2757) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913932	18568	40724	528	175

Description

6500735891 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1167 HP1167 Helicobacter pylori 210 -11539749 7000690390 hypothetical protein hp1167 (db:pir2.dat) G64665 G64665 Helicobacter pylori 210 -11539749 7500959177 hp1167 h. pylori predicted coding region hp1167 (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6209) (re:7624) (di:direct) HPAE000622 AE000622 g2314325 Helicobacter pylori 210 -11539749 7502853631 hp1167 h. pylori predicted coding region hp1167 (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6209) (re:7624) (di:direct) HPAE000622 AE000622 g2314325 Helicobacter pylori 26695 85962 -11539749

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913933	18569	40725	483	160

Description

GTC ORF with score 451 to: (sr:n.crassa (strain 74a) dna) (db:genpept-pln1) (de:n.crassa vacuolar atpase 57-kd subunit (vma-2) gene, complete cds.) (nt:vacuolar atpase vma-2) (le:1000:1155:1311:1390) (re:1098:1239:1330:1425) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913939	18570	40726	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913942	18571	40727	1041	346

Description

6500735892 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1173 HP1173 Helicobacter pylori 210 -11539750 7000690391 hypothetical protein hp1173 (db:pir2.dat) E64666 E64666 Helicobacter pylori 210 -11539750 7500959178 hp1173 h. pylori predicted coding region hp1173 (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3215) (re:3766) (di:direct) HPAE000623 AE000623 g2314338 Helicobacter pylori 210 -11539750 7502853632 hp1173 h. pylori predicted coding region hp1173 (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3215) (re:3766) (di:direct) HPAE000623 AE000623 g2314338 Helicobacter pylori 26695 85962 -11539750

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913943	18572	40728	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913944	18573	40729	318	105

Description

GTC ORF with score 120 to: (sr:n.crassa (strain 74a) dna) (db:genpept-pln1) (de:n.crassa vacuolar atpase 57-kd subunit (vma-2) gene, complete cds.) (nt:vacuolar atpase vma-2) (le:1000:1155:1311:1390) (re:1098:1239:1330:1425) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913945	18574	40730	255	84

Description

GTC ORF with score 265 to: (sr:n.crassa (strain 74a) dna) (db:genpept-pln1) (de:n.crassa vacuolar atpase 57-kd subunit (vma-2) gene, complete cds.) (nt:vacuolar atpase vma-2) (le:1000:1155:1311:1390) (re:1098:1239:1330:1425) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913950	18575	40731	735	244

Description

6500735893 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1176 HP1176 Helicobacter pylori 210 -11539751 7000690392 hypothetical protein hp1176 (db:pir2.dat) H64666 H64666 Helicobacter pylori 210 -11539751 7500959179 hp1176 h. pylori predicted coding region hp1176 (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6943) (re:7047) (di:complement) HPAE000623 AE000623 g2314339 Helicobacter pylori 210 -11539751 7502853633 hp1176 h. pylori predicted coding region hp1176 (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6943) (re:7047) (di:complement) HPAE000623 AE000623 g2314339 Helicobacter pylori 26695 85962 -11539751

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913953	18576	40732	897	298

Description

6500735894 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1187 HP1187 Helicobacter pylori 210 -11539752 7000690393 hypothetical protein hp1187 (db:pir2.dat) C64668 C64668 Helicobacter pylori 210 -11539752 7500959180 hp1187 h. pylori predicted coding region hp1187 (db:genpept-bct1) (de:helicobacter pylori section 102 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7551) (re:8708) (di:complement) HPAE000624 AE000624 g2314347 Helicobacter pylori 210 -11539752 7502853634 hp1187 h. pylori predicted coding region hp1187 (db:genpept) (de:helicobacter pylori 26695 section 102 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7551) (re:8708) (di:complement) HPAE000624 AE000624 g2314347 Helicobacter pylori 26695 85962 -11539752

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913959	18577	40733	297	98

Description

GTC ORF with score 328 to: (sr:n.crassa (strain 74a) dna) (db:genpept-pln1) (de:n.crassa vacuolar atpase 57-kd subunit (vma-2) gene, complete cds.) (nt:vacuolar atpase vma-2) (le:1000:1155:1311:1390) (re:1098:1239:1330:1425) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913967	18578	40734	1692	563

Description

6500735895 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1188 HP1188 Helicobacter pylori 210 -11539753 7000690394 hypothetical protein hp1188 (db:pir2.dat) D64668 D64668 Helicobacter pylori 210 -11539753 7500959181 hp1188 h. pylori predicted coding region hp1188 (db:genpept-bct1) (de:helicobacter pylori section 102 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9055) (re:9864) (di:complement) HPAE000624 AE000624 g2314348 Helicobacter pylori 210 -11539753 7502853635 hp1188 h. pylori predicted coding region hp1188 (db:genpept) (de:helicobacter pylori 26695 section 102 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9055) (re:9864) (di:complement) HPAE000624 AE000624 g2314348 Helicobacter pylori 26695 85962 -11539753

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913976	18579	40735	330	109

Description

6500735896 aldo-keto reductase:putative (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1193 HP1193 Helicobacter pylori 210 -11539754 7000690641 probable aldo-keto reductase (cl:conserved hypothetical protein ypl088w) (ec:1.-.-.-) (db:pir2.dat) A64669 A64669 Helicobacter pylori 210 -11539754 7500959418 hp1193 aldo-keto reductase:putative (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:similar to sp:p40691 percent identity: 46.55;) (le:4466) (re:5455) (di:direct) HPAE000625 AE000625 g2314358 Helicobacter pylori 210 -11539754 7502853636 hp1193 aldo-keto reductase:putative (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:similar to sp:p40691 percent identity: 46.55;) (le:4466) (re:5455) (di:direct) HPAE000625 AE000625 g2314358 Helicobacter pylori 26695 85962 -11539754

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913978	18580	40736	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501913983	18581	40737	216	71

Description

6500735897 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1194 HP1194 Helicobacter pylori 210 -11539755 7000690395 hypothetical protein hp1194 (db:pir2.dat) B64669 B64669 Helicobacter pylori 210 -11539755 7500959182 hp1194 h. pylori predicted coding region hp1194 (db:genpept-bct1) (de:helicobacter pylori section 103 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5626) (re:5712) (di:complement) HPAE000625 AE000625 g2314359 Helicobacter pylori 210 -11539755 7502853637 hp1194 h. pylori predicted coding region hp1194 (db:genpept) (de:helicobacter pylori 26695 section 103 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5626) (re:5712) (di:complement) HPAE000625 AE000625 g2314359 Helicobacter pylori 26695 85962 -11539755

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914013	18582	40738	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914014	18583	40739	726	241

Description

6500735898 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1207 HP1207 Helicobacter pylori 210 -11539756 7000690396 hypothetical protein hp1207 (db:pir2.dat) G64670 G64670 Helicobacter pylori 210 -11539756 7500959183 hp1207 h. pylori predicted coding region hp1207 (db:genpept-bct1) (de:helicobacter pylori section 104 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7193) (re:7861) (di:complement) HPAE000626 AE000626 g2314372 Helicobacter pylori 210 -11539756 7502853638 hp1207 h. pylori predicted coding region hp1207 (db:genpept) (de:helicobacter pylori 26695 section 104 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7193) (re:7861) (di:complement) HPAE000626 AE000626 g2314372 Helicobacter pylori 26695 85962 -11539756

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914030	18584	40740	864	287

Description

6500735899 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1211 HP1211 Helicobacter pylori 210 -11539757 7000690397 hypothetical protein hp1211 (db:pir2.dat) C64671 C64671 Helicobacter pylori 210 -11539757 7500959184 hp1211 h. pylori predicted coding region hp1211 (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:181) (re:426) (di:direct) HPAE000627 AE000627 g2314384 Helicobacter pylori 210 -11539757 7502853639 hp1211 h. pylori predicted coding region hp1211 (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:181) (re:426) (di:direct) HPAE000627 AE000627 g2314384 Helicobacter pylori 26695 85962 -11539757

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914031	18585	40741	540	179

Description

6500735900 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1215 HP1215 Helicobacter pylori 210 -11539758 7000690398 hypothetical protein hp1215 (db:pir2.dat) G64671 G64671 Helicobacter pylori 210 -11539758 7500959185 hp1215 h. pylori predicted coding region hp1215 (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3721) (re:3963) (di:complement) HPAE000627 AE000627 g2314382 Helicobacter pylori 210 -11539758 7502853640 hp1215 h. pylori predicted coding region hp1215 (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3721) (re:3963) (di:complement) HPAE000627 AE000627 g2314382 Helicobacter pylori 26695 85962 -11539758

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914032	18586	40742	228	75

Description

6500735901 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1217 HP1217 Helicobacter pylori 210 -11539759 7000690399 hypothetical protein hp1217 (db:pir2.dat) A64672 A64672 Helicobacter pylori 210 -11539759 7500959186 hp1217 h. pylori predicted coding region hp1217 (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5984) (re:6463) (di:complement) HPAE000627 AE000627 g2314383 Helicobacter pylori 210 -11539759 7502853641 hp1217 h. pylori predicted coding region hp1217 (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5984) (re:6463) (di:complement) HPAE000627 AE000627 g2314383 Helicobacter pylori 26695 85962 -11539759

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914054	18587	40743	1566	521

Description

GTC ORF with score 171 to: (db:genpept) (de:streptomyces fradiae dipeptidil carboxypeptidase (ddca), tylosinresistance protein (tlrb), glycosyltransferase (tyln),methyltransferase (tyle), 4-ketoreductase (tyld), ferredoxin(tylh2), cytochrome p450 ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914060	18588	40744	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914068	18589	40745	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914076	18590	40746	564	187

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914105	18591	40747	1623	540

Description

6500735902 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1219 HP1219 Helicobacter pylori 210 -11539760 7000690400 hypothetical protein hp1219 (db:pir2.dat) C64672 C64672 Helicobacter pylori 210 -11539760 7500959187 hp1219 h. pylori predicted coding region hp1219 (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7906) (re:8097) (di:direct) HPAE000627 AE000627 g2314385 Helicobacter pylori 210 -11539760 7502853642 hp1219 h. pylori predicted coding region hp1219 (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7906) (re:8097) (di:direct) HPAE000627 AE000627 g2314385 Helicobacter pylori 26695 85962 -11539760

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914106	18592	40748	495	164

Description

6500735903 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1223 HP1223 Helicobacter pylori 210 -11539761 7000690401 hypothetical protein hp1223 (db:pir2.dat) G64672 G64672 Helicobacter pylori 210 -11539761 7500959188 hp1223 h. pylori predicted coding region hp1223 (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:63) (re:395) (di:direct) HPAE000628 AE000628 g2314397 Helicobacter pylori 210 -11539761 7502853643 hp1223 h. pylori predicted coding region hp1223 (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:63) (re:395) (di:direct) HPAE000628 AE000628 g2314397 Helicobacter pylori 26695 85962 -11539761

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914107	18593	40749	3507	1168

Description

6500735904 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1230 HP1230 Helicobacter pylori 210 -11539762 7000690402 hypothetical protein hp1230 (db:pir2.dat) F64673 F64673 Helicobacter pylori 210 -11539762 7500959189 hp1230 h. pylori predicted coding region hp1230 (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4825) (re:5367) (di:direct) HPAE000628 AE000628 g2314398 Helicobacter pylori 210 -11539762 7502853644 hp1230 h. pylori predicted coding region hp1230 (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4825) (re:5367) (di:direct) HPAE000628 AE000628 g2314398 Helicobacter pylori 26695 85962 -11539762

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914118	18594	40750	351	116

Description

6500735905 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1233 HP1233 Helicobacter pylori 210 -11539763 7000690403 hypothetical protein hp1233 (db:pir2.dat) A64674 A64674 Helicobacter pylori 210 -11539763 7500959190 hp1233 h. pylori predicted coding region hp1233 (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7254) (re:7715) (di:complement) HPAE000628 AE000628 g2314399 Helicobacter pylori 210 -11539763 7502853645 hp1233 h. pylori predicted coding region hp1233 (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7254) (re:7715) (di:complement) HPAE000628 AE000628 g2314399 Helicobacter pylori 26695 85962 -11539763

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914119	18595	40751	366	121

Description

6500735906 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1236 HP1236 Helicobacter pylori 210 -11539764 7000690404 hypothetical protein hp1236 (db:pir2.dat) D64674 D64674 Helicobacter pylori 210 -11539764 7500959191 hp1236 h. pylori predicted coding region hp1236 (db:genpept-bct1) (de:helicobacter pylori section 107 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:70) (re:621) (di:direct) HPAE000629 AE000629 g2314406 Helicobacter pylori 210 -11539764 7502853646 hp1236 h. pylori predicted coding region hp1236 (db:genpept) (de:helicobacter pylori 26695 section 107 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:70) (re:621) (di:direct) HPAE000629 AE000629 g2314406 Helicobacter pylori 26695 85962 -11539764

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914133	18596	40752	411	136

Description

6500735907 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1239 HP1239 Helicobacter pylori 210 -11539765 7000690405 hypothetical protein hp1239 (db:pir2.dat) G64674 G64674 Helicobacter pylori 210 -11539765 7500959192 hp1239 h. pylori predicted coding region hp1239 (db:genpept-bct1) (de:helicobacter pylori section 107 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3170) (re:3259) (di:complement) HPAE000629 AE000629 g2314408 Helicobacter pylori 210 -11539765 7502853647 hp1239 h. pylori predicted coding region hp1239 (db:genpept) (de:helicobacter pylori 26695 section 107 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3170) (re:3259) (di:complement) HPAE000629 AE000629 g2314408 Helicobacter pylori 26695 85962 -11539765

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914144	18597	40753	423	140

Description

6500735908 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1247 HP1247 Helicobacter pylori 210 -11539766 7000690406 hypothetical protein hp1247 (db:pir2.dat) G64675 G64675 Helicobacter pylori 210 -11539766 7500959193 hp1247 h. pylori predicted coding region hp1247 (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1591) (re:2613) (di:complement) HPAE000630 AE000630 g2314419 Helicobacter pylori 210 -11539766 7502853648 hp1247 h. pylori predicted coding region hp1247 (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1591) (re:2613) (di:complement) HPAE000630 AE000630 g2314419 Helicobacter pylori 26695 85962 -11539766

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914145	18598	40754	222	73

Description

6500735909 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1250 HP1250 Helicobacter pylori 210 -11539767 7000690407 hypothetical protein hp1250 (db:pir2.dat) B64676 B64676 Helicobacter pylori 210 -11539767 7500959194 hp1250 h. pylori predicted coding region hp1250 (db:genpept-bct1) (de:helicobacter pylori section 108 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5336) (re:5914) (di:complement) HPAE000630 AE000630 g2314420 Helicobacter pylori 210 -11539767 7502853649 hp1250 h. pylori predicted coding region hp1250 (db:genpept) (de:helicobacter pylori 26695 section 108 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5336) (re:5914) (di:complement) HPAE000630 AE000630 g2314420 Helicobacter pylori 26695 85962 -11539767

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914149	18599	40755	429	142

Description

6500735910 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1264 HP1264 Helicobacter pylori 210 -11539768 7000690408 hypothetical protein hp1264 (db:pir2.dat) H64677 H64677 Helicobacter pylori 210 -11539768 7500959195 hp1264 h. pylori predicted coding region hp1264 (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6008) (re:6238) (di:direct) HPAE000631 AE000631 g2314442 Helicobacter pylori 210 -11539768 7502853650 hp1264 h. pylori predicted coding region hp1264 (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6008) (re:6238) (di:direct) HPAE000631 AE000631 g2314442 Helicobacter pylori 26695 85962 -11539768

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914157	18600	40756	789	262

Description

6500735911 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1265 HP1265 Helicobacter pylori 210 -11539769 7000690409 hypothetical protein hp1265 (db:pir2.dat) A64678 A64678 Helicobacter pylori 210 -11539769 7500959196 hp1265 h. pylori predicted coding region hp1265 (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6241) (re:7227) (di:direct) HPAE000631 AE000631 g2314441 Helicobacter pylori 210 -11539769 7502853651 hp1265 h. pylori predicted coding region hp1265 (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6241) (re:7227) (di:direct) HPAE000631 AE000631 g2314441 Helicobacter pylori 26695 85962 -11539769

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914161	18601	40757	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914162	18602	40758	405	134

Description

6500735912 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1276 HP1276 Helicobacter pylori 210 -11539770 7000690410 hypothetical protein hp1276 (db:pir2.dat) D64679 D64679 Helicobacter pylori 210 -11539770 7500959197 hp1276 h. pylori predicted coding region hp1276 (db:genpept-bct1) (de:helicobacter pylori section 110 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:103) (re:387) (di:direct) HPAE000632 AE000632 g2314450 Helicobacter pylori 210 -11539770 7502853652 hp1276 h. pylori predicted coding region hp1276 (db:genpept) (de:helicobacter pylori 26695 section 110 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:103) (re:387) (di:direct) HPAE000632 AE000632 g2314450 Helicobacter pylori 26695 85962 -11539770

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914166	18603	40759	702	233

Description

6500735913 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1283 HP1283 Helicobacter pylori 210 -11539771 7000690411 hypothetical protein hp1283 (db:pir2.dat) C64680 C64680 Helicobacter pylori 210 -11539771 7500959198 hp1283 h. pylori predicted coding region hp1283 (db:genpept-bct1) (de:helicobacter pylori section 110 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7364) (re:8821) (di:complement) HPAE000632 AE000632 g2314451 Helicobacter pylori 210 -11539771 7502853653 hp1283 h. pylori predicted coding region hp1283 (db:genpept) (de:helicobacter pylori 26695 section 110 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7364) (re:8821) (di:complement) HPAE000632 AE000632 g2314451 Helicobacter pylori 26695 85962 -11539771

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914169	18604	40760	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914170	18605	40761	1077	358

Description

6500735914 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1288 HP1288 Helicobacter pylori 210 -11539772 7000690412 hypothetical protein hp1288 (db:pir2.dat) H64680 H64680 Helicobacter pylori 210 -11539772 7500959199 hp1288 h. pylori predicted coding region hp1288 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2716) (re:3114) (di:direct) HPAE000633 AE000633 g2314487 Helicobacter pylori 210 -11539772 7502853654 hp1288 h. pylori predicted coding region hp1288 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2716) (re:3114) (di:direct) HPAE000633 AE000633 g2314487 Helicobacter pylori 26695 85962 -11539772

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914174	18606	40762	1056	351

Description

6500735915 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1289 HP1289 Helicobacter pylori 210 -11539773 7000690413 hypothetical protein hp1289 (db:pir2.dat) A64681 A64681 Helicobacter pylori 210 -11539773 7500959200 hp1289 h. pylori predicted coding region hp1289 (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3138) (re:3623) (di:direct) HPAE000633 AE000633 g2314488 Helicobacter pylori 210 -11539773 7502853655 hp1289 h. pylori predicted coding region hp1289 (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3138) (re:3623) (di:direct) HPAE000633 AE000633 g2314488 Helicobacter pylori 26695 85962 -11539773

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914175	18607	40763	324	107

Description

6500735916 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1322 HP1322 Helicobacter pylori 210 -11539774 7000690414 hypothetical protein hp1322 (db:pir2.dat) B64685 B64685 Helicobacter pylori 210 -11539774 7500959201 hp1322 h. pylori predicted coding region hp1322 (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1452) (re:2057) (di:direct) HPAE000634 AE000634 g2314498 Helicobacter pylori 210 -11539774 7502853656 hp1322 h. pylori predicted coding region hp1322 (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1452) (re:2057) (di:direct) HPAE000634 AE000634 g2314498 Helicobacter pylori 26695 85962 -11539774

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914187	18608	40764	864	287

Description

6500735917 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1324 HP1324 Helicobacter pylori 210 -11539775 7000690415 hypothetical protein hp1324 (db:pir2.dat) D64685 D64685 Helicobacter pylori 210 -11539775 7500959202 hp1324 h. pylori predicted coding region hp1324 (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2676) (re:2927) (di:complement) HPAE000634 AE000634 g2314499 Helicobacter pylori 210 -11539775 7502853657 hp1324 h. pylori predicted coding region hp1324 (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2676) (re:2927) (di:complement) HPAE000634 AE000634 g2314499 Helicobacter pylori 26695 85962 -11539775

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914188	18609	40765	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914190	18610	40766	1215	404

Description

6500735918 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1326 HP1326 Helicobacter pylori 210 -11539776 7000690416 hypothetical protein hp1326 (db:pir2.dat) F64685 F64685 Helicobacter pylori 210 -11539776 7500959203 hp1326 h. pylori predicted coding region hp1326 (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4515) (re:4892) (di:direct) HPAE000634 AE000634 g2314500 Helicobacter pylori 210 -11539776 7502853658 hp1326 h. pylori predicted coding region hp1326 (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4515) (re:4892) (di:direct) HPAE000634 AE000634 g2314500 Helicobacter pylori 26695 85962 -11539776

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914209	18611	40767	312	103

Description

6500735919 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1327 HP1327 Helicobacter pylori 210 -11539777 7000690417 hypothetical protein hp1327 (db:pir2.dat) G64685 G64685 Helicobacter pylori 210 -11539777 7500959204 hp1327 h. pylori predicted coding region hp1327 (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4897) (re:6135) (di:direct) HPAE000634 AE000634 g2314501 Helicobacter pylori 210 -11539777 7502853659 hp1327 h. pylori predicted coding region hp1327 (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4897) (re:6135) (di:direct) HPAE000634 AE000634 g2314501 Helicobacter pylori 26695 85962 -11539777

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914212	18612	40768	1977	658

Description

6500735920 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1333 HP1333 Helicobacter pylori 210 -11539778 7000690536 myosin-like protein (db:pir2.dat) E64686 E64686 Helicobacter pylori 210 -11539778 7500959323 hp1333 h. pylori predicted coding region hp1333 (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:93) (re:1241) (di:direct) HPAE000635 AE000635 g2314513 Helicobacter pylori 210 -11539778 7502853660 hp1333 h. pylori predicted coding region hp1333 (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:93) (re:1241) (di:direct) HPAE000635 AE000635 g2314513 Helicobacter pylori 26695 85962 -11539778

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914222	18613	40769	294	97

Description

6500735921 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1334 HP1334 Helicobacter pylori 210 -11539779 7000690418 hypothetical protein hp1334 (db:pir2.dat) F64686 F64686 Helicobacter pylori 210 -11539779 7500959205 hp1334 h. pylori predicted coding region hp1334 (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1450) (re:2124) (di:direct) HPAE000635 AE000635 g2314514 Helicobacter pylori 210 -11539779 7502853661 hp1334 h. pylori predicted coding region hp1334 (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1450) (re:2124) (di:direct) HPAE000635 AE000635 g2314514 Helicobacter pylori 26695 85962 -11539779

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914224	18614	40770	477	158

Description

6500735922 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1336 HP1336 Helicobacter pylori 210 -11539780 7000690419 hypothetical protein hp1336 (db:pir2.dat) H64686 H64686 Helicobacter pylori 210 -11539780 7500959206 hp1336 h. pylori predicted coding region hp1336 (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3355) (re:4116) (di:direct) HPAE000635 AE000635 g2314515 Helicobacter pylori 210 -11539780 7502853662 hp1336 h. pylori predicted coding region hp1336 (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3355) (re:4116) (di:direct) HPAE000635 AE000635 g2314515 Helicobacter pylori 26695 85962 -11539780

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914242	18615	40771	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914243	18616	40772	591	196

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914253	18617	40773	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914254	18618	40774	393	130

Description

6500735923 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1349 HP1349 Helicobacter pylori 210 -11539781 7000690420 hypothetical protein hp1349 (db:pir2.dat) E64688 E64688 Helicobacter pylori 210 -11539781 7500959207 hp1349 h. pylori predicted coding region hp1349 (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1482) (re:2645) (di:complement) HPAE000636 AE000636 g2314532 Helicobacter pylori 210 -11539781 7502853663 hp1349 h. pylori predicted coding region hp1349 (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1482) (re:2645) (di:complement) HPAE000636 AE000636 g2314532 Helicobacter pylori 26695 85962 -11539781

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914262	18619	40775	507	168

Description

6500735924 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1351 HP1351 Helicobacter pylori 210 -11539782 7000690421 hypothetical protein hp1351 (db:pir2.dat) G64688 G64688 Helicobacter pylori 210 -11539782 7500959208 hp1351 h. pylori predicted coding region hp1351 (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4241) (re:5113) (di:complement) HPAE000636 AE000636 g2314533 Helicobacter pylori 210 -11539782 7502853664 hp1351 h. pylori predicted coding region hp1351 (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4241) (re:5113) (di:complement) HPAE000636 AE000636 g2314533 Helicobacter pylori 26695 85962 -11539782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914265	18620	40776	276	91

Description

6500735925 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1358 HP1358 Helicobacter pylori 210 -11539783 7000690423 hypothetical protein hp1358 (db:pir2.dat) F64689 F64689 Helicobacter pylori 210 -11539783 7500959209 hp1358 h. pylori predicted coding region hp1358 (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:12581) (re:13087) (di:complement) HPAE000636 AE000636 g2314534 Helicobacter pylori 210 -11539783 7502853665 hp1358 h. pylori predicted coding region hp1358 (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:12581) (re:13087) (di:complement) HPAE000636 AE000636 g2314534 Helicobacter pylori 26695 85962 -11539783

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914266	18621	40777	258	85

Description

6500735926 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1359 HP1359 Helicobacter pylori 210 -11539784 7000690424 hypothetical protein hp1359 (db:pir2.dat) G64689 G64689 Helicobacter pylori 210 -11539784 7500959210 hp1359 h. pylori predicted coding region hp1359 (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13100) (re:13651) (di:complement) HPAE000636 AE000636 g2314535 Helicobacter pylori 210 -11539784 7502853666 hp1359 h. pylori predicted coding region hp1359 (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:13100) (re:13651) (di:complement) HPAE000636 AE000636 g2314535 Helicobacter pylori 26695 85962 -11539784

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914288	18622	40778	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914289	18623	40779	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914294	18624	40780	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914319	18625	40781	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914331	18626	40782	429	142

Description

6500735927 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1377 HP1377 Helicobacter pylori 210 -11539785 7000689479 hypothetical protein hp1377 (cl:hypothetical protein hp1154) (db:pir2.dat) A64692 A64692 Helicobacter pylori 210 -11539785 7500955777 hp1377 h. pylori predicted coding region hp1377 (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:116) (re:556) (di:complement) HPAE000638 AE000638 g2314555 Helicobacter pylori 210 -11539785 7502853667 hp1377 h. pylori predicted coding region hp1377 (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:116) (re:556) (di:complement) HPAE000638 AE000638 g2314555 Helicobacter pylori 26695 85962 -11539785

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914340	18627	40783	300	99

Description

6500735928 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1381 HP1381 Helicobacter pylori 210 -11539786 7000690425 hypothetical protein hp1381 (db:pir2.dat) E64692 E64692 Helicobacter pylori 210 -11539786 7500959211 hp1381 h. pylori predicted coding region hp1381 (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5013) (re:5246) (di:direct) HPAE000638 AE000638 g2314556 Helicobacter pylori 210 -11539786 7502853668 hp1381 h. pylori predicted coding region hp1381 (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5013) (re:5246) (di:direct) HPAE000638 AE000638 g2314556 Helicobacter pylori 26695 85962 -11539786

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914341	18628	40784	891	296

Description

6500735929 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1382 HP1382 Helicobacter pylori 210 -11539787 7000690426 hypothetical protein hp1382 (db:pir2.dat) F64692 F64692 Helicobacter pylori 210 -11539787 7500959212 hp1382 h. pylori predicted coding region hp1382 (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5305) (re:5697) (di:complement) HPAE000638 AE000638 g2314557 Helicobacter pylori 210 -11539787 7502853669 hp1382 h. pylori predicted coding region hp1382 (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5305) (re:5697) (di:complement) HPAE000638 AE000638 g2314557 Helicobacter pylori 26695 85962 -11539787

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914342	18629	40785	276	91

Description

6500735930 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1384 HP1384 Helicobacter pylori 210 -11539788 7000690427 hypothetical protein hp1384 (db:pir2.dat) H64692 H64692 Helicobacter pylori 210 -11539788 7500959213 hp1384 h. pylori predicted coding region hp1384 (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6173) (re:6379) (di:complement) HPAE000638 AE000638 g2314559 Helicobacter pylori 210 -11539788 7502853670 hp1384 h. pylori predicted coding region hp1384 (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6173) (re:6379) (di:complement) HPAE000638 AE000638 g2314559 Helicobacter pylori 26695 85962 -11539788

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914349	18630	40786	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914351	18631	40787	558	185

Description

6500735931 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1388 HP1388 Helicobacter pylori 210 -11539789 7000690428 hypothetical protein hp1388 (db:pir2.dat) D64693 D64693 Helicobacter pylori 210 -11539789 7500959214 hp1388 h. pylori predicted coding region hp1388 (db:genpept-bct1) (de:helicobacter pylori section 116 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9408) (re:9857) (di:direct) HPAE000638 AE000638 g2314558 Helicobacter pylori 210 -11539789 7502853671 hp1388 h. pylori predicted coding region hp1388 (db:genpept) (de:helicobacter pylori 26695 section 116 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9408) (re:9857) (di:direct) HPAE000638 AE000638 g2314558 Helicobacter pylori 26695 85962 -11539789

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914352	18632	40788	633	210

Description

6500735932 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1389 HP1389 Helicobacter pylori 210 -11539790 7000690429 hypothetical protein hp1389 (db:pir2.dat) E64693 E64693 Helicobacter pylori 210 -11539790 7500959215 hp1389 h. pylori predicted coding region hp1389 (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:102) (re:284) (di:direct) HPAE000639 AE000639 g2314566 Helicobacter pylori 210 -11539790 7502853672 hp1389 h. pylori predicted coding region hp1389 (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:102) (re:284) (di:direct) HPAE000639 AE000639 g2314566 Helicobacter pylori 26695 85962 -11539790

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914353	18633	40789	462	153

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914368	18634	40790	1047	348

Description

6500735933 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1390 HP1390 Helicobacter pylori 210 -11539791 7000690430 hypothetical protein hp1390 (db:pir2.dat) F64693 F64693 Helicobacter pylori 210 -11539791 7500959216 hp1390 h. pylori predicted coding region hp1390 (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:326) (re:826) (di:complement) HPAE000639 AE000639 g2314567 Helicobacter pylori 210 -11539791 7502853673 hp1390 h. pylori predicted coding region hp1390 (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:326) (re:826) (di:complement) HPAE000639 AE000639 g2314567 Helicobacter pylori 26695 85962 -11539791

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914371	18635	40791	2865	954

Description

6500735934 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1391 HP1391 Helicobacter pylori 210 -11539792 7000690431 hypothetical protein hp1391 (db:pir2.dat) G64693 G64693 Helicobacter pylori 210 -11539792 7500959217 hp1391 h. pylori predicted coding region hp1391 (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1079) (re:1375) (di:complement) HPAE000639 AE000639 g2314568 Helicobacter pylori 210 -11539792 7502853674 hp1391 h. pylori predicted coding region hp1391 (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1079) (re:1375) (di:complement) HPAE000639 AE000639 g2314568 Helicobacter pylori 26695 85962 -11539792

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914376	18636	40792	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914377	18637	40793	1284	427

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914407	18638	40794	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914415	18639	40795	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914425	18640	40796	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914426	18641	40797	936	311

Description

6500735935 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1396 HP1396 Helicobacter pylori 210 -11539793 7000690432 hypothetical protein hp1396 (db:pir2.dat) D64694 D64694 Helicobacter pylori 210 -11539793 7500959218 hp1396 h. pylori predicted coding region hp1396 (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6100) (re:6966) (di:complement) HPAE000639 AE000639 g2314570 Helicobacter pylori 210 -11539793 7502853675 hp1396 h. pylori predicted coding region hp1396 (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6100) (re:6966) (di:complement) HPAE000639 AE000639 g2314570 Helicobacter pylori 26695 85962 -11539793

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914429	18642	40798	579	192

Description

6500735936 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1397 HP1397 Helicobacter pylori 210 -11539794 7000690433 hypothetical protein hp1397 (db:pir2.dat) E64694 E64694 Helicobacter pylori 210 -11539794 7500959219 hp1397 h. pylori predicted coding region hp1397 (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6974) (re:7789) (di:complement) HPAE000639 AE000639 g2314571 Helicobacter pylori 210 -11539794 7502853676 hp1397 h. pylori predicted coding region hp1397 (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6974) (re:7789) (di:complement) HPAE000639 AE000639 g2314571 Helicobacter pylori 26695 85962 -11539794

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914433	18643	40799	438	145

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914434	18644	40800	513	170

Description

6500735937 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1405 HP1405 Helicobacter pylori 210 -11539795 7000690434 hypothetical protein hp1405 (db:pir2.dat) E64695 E64695 Helicobacter pylori 210 -11539795 7500959220 hp1405 h. pylori predicted coding region hp1405 (db:genpept-bct1) (de:helicobacter pylori section 118 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9716) (re:9820) (di:direct) HPAE000640 AE000640 g2314580 Helicobacter pylori 210 -11539795 7502853677 hp1405 h. pylori predicted coding region hp1405 (db:genpept) (de:helicobacter pylori 26695 section 118 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9716) (re:9820) (di:direct) HPAE000640 AE000640 g2314580 Helicobacter pylori 26695 85962 -11539795

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914435	18645	40801	471	156

Description

6500735938 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1410 HP1410 Helicobacter pylori 210 -11539796 7000690435 hypothetical protein hp1410 (db:pir2.dat) B64696 B64696 Helicobacter pylori 210 -11539796 7500959221 hp1410 h. pylori predicted coding region hp1410 (db:genpept-bct1) (de:helicobacter pylori section 119 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6534) (re:7718) (di:direct) HPAE000641 AE000641 g2314586 Helicobacter pylori 210 -11539796 7502853678 hp1410 h. pylori predicted coding region hp1410 (db:genpept) (de:helicobacter pylori 26695 section 119 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6534) (re:7718) (di:direct) HPAE000641 AE000641 g2314586 Helicobacter pylori 26695 85962 -11539796

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914436	18646	40802	231	76

Description

6500735939 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1424 HP1424 Helicobacter pylori 210 -11539797 7000690436 hypothetical protein hp1424 (db:pir2.dat) H64697 H64697 Helicobacter pylori 210 -11539797 7500959222 hp1424 h. pylori predicted coding region hp1424 (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:81) (re:701) (di:direct) HPAE000643 AE000643 g2314606 Helicobacter pylori 210 -11539797 7502853679 hp1424 h. pylori predicted coding region hp1424 (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:81) (re:701) (di:direct) HPAE000643 AE000643 g2314606 Helicobacter pylori 26695 85962 -11539797

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914438	18647	40803	507	168

Description

GTC ORF with score 104 to: (de:(ylr332w) (pn:mating process protein mid2:serine-rich protein sms1:mating process protein) (gn:sms1:l8543:mid2) (gtcfc:12.8:12.9) (ec:) (mid2_yeast) (keggfc:11.2) (sgdfc:3.3.0:3.8.0) (db:gtc-saccharomyces cerevisiae))

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914439	18648	40804	570	189

Description

6500735940 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1425 HP1425 Helicobacter pylori 210 -11539798 7000690437 hypothetical protein hp1425 (db:pir2.dat) A64698 A64698 Helicobacter pylori 210 -11539798 7500959223 hp1425 h. pylori predicted coding region hp1425 (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:829) (re:1056) (di:complement) HPAE000643 AE000643 g2314607 Helicobacter pylori 210 -11539798 7502853680 hp1425 h. pylori predicted coding region hp1425 (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:829) (re:1056) (di:complement) HPAE000643 AE000643 g2314607 Helicobacter pylori 26695 85962 -11539798

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914459	18649	40805	3078	1025

Description

6500735941 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1433 HP1433 Helicobacter pylori 210 -11539799 7000690438 hypothetical protein hp1433 (db:pir2.dat) A64699 A64699 Helicobacter pylori 210 -11539799 7500959224 hp1433 h. pylori predicted coding region hp1433 (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8455) (re:11025) (di:complement) HPAE000643 AE000643 g2314608 Helicobacter pylori 210 -11539799 7502853681 hp1433 h. pylori predicted coding region hp1433 (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8455) (re:11025) (di:complement) HPAE000643 AE000643 g2314608 Helicobacter pylori 26695 85962 -11539799

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914467	18650	40806	486	161

Description

6500735942 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1436 HP1436 Helicobacter pylori 210 -11539800 7000690439 hypothetical protein hp1436 (db:pir2.dat) D64699 D64699 Helicobacter pylori 210 -11539800 7500959225 hp1436 h. pylori predicted coding region hp1436 (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1918) (re:2166) (di:direct) HPAE000644 AE000644 g2314622 Helicobacter pylori 210 -11539800 7502853682 hp1436 h. pylori predicted coding region hp1436 (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1918) (re:2166) (di:direct) HPAE000644 AE000644 g2314622 Helicobacter pylori 26695 85962 -11539800

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914468	18651	40807	366	121

Description

GTC ORF with score 113 to: (fn:putative oxygen activation and/or lignin) (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana uclacyanin 3 (ucc3) mrna, complete cds.) (nt:member of a strictly plant-specific family of) (le:29) (re:697) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914477	18652	40808	420	139

Description

6500735943 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1437 HP1437 Helicobacter pylori 210 -11539801 7000690440 hypothetical protein hp1437 (db:pir2.dat) E64699 E64699 Helicobacter pylori 210 -11539801 7500959226 hp1437 h. pylori predicted coding region hp1437 (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2400) (re:3119) (di:direct) HPAE000644 AE000644 g2314619 Helicobacter pylori 210 -11539801 7502853683 hp1437 h. pylori predicted coding region hp1437 (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2400) (re:3119) (di:direct) HPAE000644 AE000644 g2314619 Helicobacter pylori 26695 85962 -11539801

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914491	18653	40809	1305	434

Description

6500735944 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1439 HP1439 Helicobacter pylori 210 -11539802 7000690441 hypothetical protein hp1439 (db:pir2.dat) G64699 G64699 Helicobacter pylori 210 -11539802 7500959227 hp1439 h. pylori predicted coding region hp1439 (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4156) (re:4401) (di:direct) HPAE000644 AE000644 g2314620 Helicobacter pylori 210 -11539802 7502853684 hp1439 h. pylori predicted coding region hp1439 (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4156) (re:4401) (di:direct) HPAE000644 AE000644 g2314620 Helicobacter pylori 26695 85962 -11539802

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914515	18654	40810	216	71

Description

6500735945 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1440 HP1440 Helicobacter pylori 210 -11539803 7000690442 hypothetical protein hp1440 (db:pir2.dat) H64699 H64699 Helicobacter pylori 210 -11539803 7500959228 hp1440 h. pylori predicted coding region hp1440 (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7111) (re:7890) (di:complement) HPAE000644 AE000644 g2314621 Helicobacter pylori 210 -11539803 7502853685 hp1440 h. pylori predicted coding region hp1440 (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7111) (re:7890) (di:complement) HPAE000644 AE000644 g2314621 Helicobacter pylori 26695 85962 -11539803

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914516	18655	40811	366	121

Description

6500735946 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1451 HP1451 Helicobacter pylori 210 -11539804 7000690443 hypothetical protein hp1451 (db:pir2.dat) C64701 C64701 Helicobacter pylori 210 -11539804 7500959229 hp1451 h. pylori predicted coding region hp1451 (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2634) (re:3428) (di:direct) HPAE000645 AE000645 g2314631 Helicobacter pylori 210 -11539804 7502853686 hp1451 h. pylori predicted coding region hp1451 (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2634) (re:3428) (di:direct) HPAE000645 AE000645 g2314631 Helicobacter pylori 26695 85962 -11539804

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914517	18656	40812	1074	357

Description

6500735947 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1454 HP1454 Helicobacter pylori 210 -11539805 7000690444 hypothetical protein hp1454 (db:pir2.dat) F64701 F64701 Helicobacter pylori 210 -11539805 7500959230 hp1454 h. pylori predicted coding region hp1454 (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8034) (re:8945) (di:complement) HPAE000645 AE000645 g2314632 Helicobacter pylori 210 -11539805 7502853687 hp1454 h. pylori predicted coding region hp1454 (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8034) (re:8945) (di:complement) HPAE000645 AE000645 g2314632 Helicobacter pylori 26695 85962 -11539805

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914518	18657	40813	1635	544

Description

6500735948 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1455 HP1455 Helicobacter pylori 210 -11539806 7500975645 hp1455 h. pylori predicted coding region hp1455 (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8955) (re:9347) (di:complement) HPAE000645 AE000645 g2314633 Helicobacter pylori 210 -11539806 7502853688 hp1455 h. pylori predicted coding region hp1455 (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8955) (re:9347) (di:complement) HPAE000645 AE000645 g2314633 Helicobacter pylori 26695 85962 -11539806

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914533	18658	40814	489	162

Description

6500735949 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1457 HP1457 Helicobacter pylori 210 -11539807 7000690446 hypothetical protein hp1457 (db:pir2.dat) A64702 A64702 Helicobacter pylori 210 -11539807 7500959231 hp1457 h. pylori predicted coding region hp1457 (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9855) (re:10487) (di:complement) HPAE000645 AE000645 g2314634 Helicobacter pylori 210 -11539807 7502853689 hp1457 h. pylori predicted coding region hp1457 (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9855) (re:10487) (di:complement) HPAE000645 AE000645 g2314634 Helicobacter pylori 26695 85962 -11539807

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914538	18659	40815	402	133

Description

6500735950 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1463 HP1463 Helicobacter pylori 210 -11539808 7000690447 hypothetical protein hp1463 (db:pir2.dat) G64702 G64702 Helicobacter pylori 210 -11539808 7500959232 hp1463 h. pylori predicted coding region hp1463 (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6972) (re:7649) (di:complement) HPAE000646 AE000646 g2314644 Helicobacter pylori 210 -11539808 7502853690 hp1463 h. pylori predicted coding region hp1463 (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6972) (re:7649) (di:complement) HPAE000646 AE000646 g2314644 Helicobacter pylori 26695 85962 -11539808

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914543	18660	40816	573	190

Description

6500735951 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1467 HP1467 Helicobacter pylori 210 -11539809 7000690448 hypothetical protein hp1467 (db:pir2.dat) C64703 C64703 Helicobacter pylori 210 -11539809 7500959233 hp1467 h. pylori predicted coding region hp1467 (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:98) (re:793) (di:direct) HPAE000647 AE000647 g2314663 Helicobacter pylori 210 -11539809 7502853691 hp1467 h. pylori predicted coding region hp1467 (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:98) (re:793) (di:direct) HPAE000647 AE000647 g2314663 Helicobacter pylori 26695 85962 -11539809

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914544	18661	40817	252	83

Description

6500735952 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1473 HP1473 Helicobacter pylori 210 -11539810 7000690449 hypothetical protein hp1473 (db:pir2.dat) A64704 A64704 Helicobacter pylori 210 -11539810 7500959234 hp1473 h. pylori predicted coding region hp1473 (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8808) (re:9383) (di:complement) HPAE000647 AE000647 g2314665 Helicobacter pylori 210 -11539810 7502853692 hp1473 h. pylori predicted coding region hp1473 (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8808) (re:9383) (di:complement) HPAE000647 AE000647 g2314665 Helicobacter pylori 26695 85962 -11539810

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914555	18662	40818	810	269

Description

6500735953 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1477 HP1477 Helicobacter pylori 210 -11539811 7000689897 distal basal body ring component protein (db:pir2.dat) E64704 E64704 Helicobacter pylori 210 -11539811 7500958694 hp1477 h. pylori predicted coding region hp1477 (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:10994) (re:11650) (di:complement) HPAE000647 AE000647 g2314666 Helicobacter pylori 210 -11539811 7502853693 hp1477 h. pylori predicted coding region hp1477 (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:10994) (re:11650) (di:complement) HPAE000647 AE000647 g2314666 Helicobacter pylori 26695 85962 -11539811

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914556	18663	40819	615	204

Description

6500735954 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1479 HP1479 Helicobacter pylori 210 -11539812 7000690450 hypothetical protein hp1479 (db:pir2.dat) G64704 G64704 Helicobacter pylori 210 -11539812 7500959235 hp1479 h. pylori predicted coding region hp1479 (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:13692) (re:16226) (di:complement) HPAE000647 AE000647 g2314667 Helicobacter pylori 210 -11539812 7502853694 hp1479 h. pylori predicted coding region hp1479 (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:13692) (re:16226) (di:complement) HPAE000647 AE000647 g2314667 Helicobacter pylori 26695 85962 -11539812

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914562	18664	40820	471	156

Description

GTC ORF with score 280 to: (sr:aspergillus niger (strain:wu-2223l) cdna to mrna, clone_lib:lambd) (db:genpept-pln1) (de:aspergillus niger mrna for nadp-dependent isocitrate dehydrogenaseprecursor, complete cds.) (le:288) (re:1784) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914563	18665	40821	705	234

Description

GTC ORF with score 805 to: (sr:aspergillus niger (strain:wu-2223l) cdna to mrna, clone_lib:lambd) (db:genpept-pln1) (de:aspergillus niger mrna for nadp-dependent isocitrate dehydrogenaseprecursor, complete cds.) (le:288) (re:1784) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914564	18666	40822	2463	820

Description

6500735955 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1481 HP1481 Helicobacter pylori 210 -11539813 7000690451 hypothetical protein hp1481 (db:pir2.dat) A64705 A64705 Helicobacter pylori 210 -11539813 7500959236 hp1481 h. pylori predicted coding region hp1481 (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:17484) (re:18281) (di:complement) HPAE000647 AE000647 g2314668 Helicobacter pylori 210 -11539813 7502853695 hp1481 h. pylori predicted coding region hp1481 (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:17484) (re:18281) (di:complement) HPAE000647 AE000647 g2314668 Helicobacter pylori 26695 85962 -11539813

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914568	18667	40823	438	145

Description

GTC ORF with score 685 to: (sr:aspergillus niger (strain:wu-2223l) cdna to mrna, clone_lib:lambd) (db:genpept-pln1) (de:aspergillus niger mrna for nadp-dependent isocitrate dehydrogenaseprecursor, complete cds.) (le:288) (re:1784) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914572	18668	40824	195	64

Description

6500735956 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1482 HP1482 Helicobacter pylori 210 -11539814 7000690452 hypothetical protein hp1482 (db:pir2.dat) B64705 B64705 Helicobacter pylori 210 -11539814 7500959237 hp1482 h. pylori predicted coding region hp1482 (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:18285) (re:18545) (di:complement) HPAE000647 AE000647 g2314669 Helicobacter pylori 210 -11539814 7502853696 hp1482 h. pylori predicted coding region hp1482 (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:18285) (re:18545) (di:complement) HPAE000647 AE000647 g2314669 Helicobacter pylori 26695 85962 -11539814

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914576	18669	40825	213	70

Description

GTC ORF with score 230 to: (sr:aspergillus niger (strain:wu-22231) cdna to mrna, clone_lib:lambd) (db:genpept-pln1) (de:aspergillus niger mrna for nadp-dependent isocitrate dehydrogenaseprecursor, complete cds.) (le:288) (re:1784) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914595	18670	40826	345	114

Description

6500735957 lipase-like protein (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1489 HP1489 Helicobacter pylori 210 -11539815 7000690499 lipase-like protein (db:pir2.dat) A64706 A64706 Helicobacter pylori 210 -11539815 7500959290 hp1489 lipase-like protein (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:40992 percent identity: 21.69;) (le:23575) (re:25107) (di:complement) HPAE000647 AE000647 g2314661 Helicobacter pylori 210 -11539815 7502853697 hp1489 lipase-like protein (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:40992 percent identity: 21.69;) (le:23575) (re:25107) (di:complement) HPAE000647 AE000647 g2314661 Helicobacter pylori 26695 85962 -11539815

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914607	18671	40827	411	136

Description

6500735958 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1493 HP1493 Helicobacter pylori 210 -11539816 7000690751 troponin c (db:pir2.dat) E64706 E64706 Helicobacter pylori 210 -11539816 7500959517 hp1493 h. pylori predicted coding region hp1493 (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:2103) (re:2714) (di:direct) HPAE000648 AE000648 g2314681 Helicobacter pylori 210 -11539816 7502853698 hp1493 h. pylori predicted coding region hp1493 (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:2103) (re:2714) (di:direct) HPAE000648 AE000648 g2314681 Helicobacter pylori 26695 85962 -11539816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914610	18672	40828	621	206

Description

6500735959 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1498 HP1498 Helicobacter pylori 210 -11539817 7000690453 hypothetical protein hp1498 (db:pir2.dat) B64707 B64707 Helicobacter pylori 210 -11539817 7500959238 hp1498 h. pylori predicted coding region hp1498 (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:6231) (re:7298) (di:direct) HPAE000648 AE000648 g2314682 Helicobacter pylori 210 -11539817 7502853699 hp1498 h. pylori predicted coding region hp1498 (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:6231) (re:7298) (di:direct) HPAE000648 AE000648 g2314682 Helicobacter pylori 26695 85962 -11539817

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914622	18673	40829	1434	477

Description

6500735960 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1499 HP1499 Helicobacter pylori 210 -11539818 7000690454 hypothetical protein hp1499 (db:pir2.dat) C64707 C64707 Helicobacter pylori 210 -11539818 7500959239 hp1499 h. pylori predicted coding region hp1499 (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7413) (re:8231) (di:direct) HPAE000648 AE000648 g2314683 Helicobacter pylori 210 -11539818 7502853700 hp1499 h. pylori predicted coding region hp1499 (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7413) (re:8231) (di:direct) HPAE000648 AE000648 g2314683 Helicobacter pylori 26695 85962 -11539818

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914623	18674	40830	195	64

Description

6500735961 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1500 HP1500 Helicobacter pylori 210 -11539819 7000690455 hypothetical protein hp1500 (db:pir2.dat) D64707 D64707 Helicobacter pylori 210 -11539819 7500959240 hp1500 h. pylori predicted coding region hp1500 (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8396) (re:8467) (di:complement) HPAE000648 AE000648 g2314686 Helicobacter pylori 210 -11539819 7502853701 hp1500 h. pylori predicted coding region hp1500 (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8396) (re:8467) (di:complement) HPAE000648 AE000648 g2314686 Helicobacter pylori 26695 85962 -11539819

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914624	18675	40831	723	241

Description

6500735962 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1502 HP1502 Helicobacter pylori 210 -11539820 7000690456 hypothetical protein hp1502 (db:pir2.dat) F64707 F64707 Helicobacter pylori 210 -11539820 7500959241 hp1502 h. pylori predicted coding region hp1502 (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9974) (re:10411) (di:direct) HPAE000648 AE000648 g2314685 Helicobacter pylori 210 -11539820 7502853702 hp1502 h. pylori predicted coding region hp1502 (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9974) (re:10411) (di:direct) HPAE000648 AE000648 g2314685 Helicobacter pylori 26695 85962 -11539820

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914626	18676	40832	720	239

Description

6500735963 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1511 HP1511 Helicobacter pylori 210 -11539821 7000690457 hypothetical protein hp1511 (db:pir2.dat) G64708 G64708 Helicobacter pylori 210 -11539821 7500959242 hp1511 h. pylori predicted coding region hp1511 (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3739) (re:4065) (di:direct) HPAE000649 AE000649 g2314696 Helicobacter pylori 210 -11539821 7502853703 hp1511 h. pylori predicted coding region hp1511 (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3739) (re:4065) (di:direct) HPAE000649 AE000649 g2314696 Helicobacter pylori 26695 85962 -11539821

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914628	18677	40833	1029	342

Description

6500735964 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1515 HP1515 Helicobacter pylori 210 -11539822 7000690458 hypothetical protein hp1515 (db:pir2.dat) C64709 C64709 Helicobacter pylori 210 -11539822 7500959243 hp1515 h. pylori predicted coding region hp1515 (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9728) (re:9820) (di:direct) HPAE000649 AE000649 g2314699 Helicobacter pylori 210 -11539822 7502853704 hp1515 h. pylori predicted coding region hp1515 (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9728) (re:9820) (di:direct) HPAE000649 AE000649 g2314699 Helicobacter pylori 26695 85962 -11539822

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914649	18678	40834	2136	711

Description

6500735965 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1516 HP1516 Helicobacter pylori 210 -11539823 7000690459 hypothetical protein hp1516 (db:pir2.dat) D64709 D64709 Helicobacter pylori 210 -11539823 7500959244 hp1516 h. pylori predicted coding region hp1516 (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9881) (re:10420) (di:complement) HPAE000649 AE000649 g2314697 Helicobacter pylori 210 -11539823 7502853705 hp1516 h. pylori predicted coding region hp1516 (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9881) (re:10420) (di:complement) HPAE000649 AE000649 g2314697 Helicobacter pylori 26695 85962 -11539823

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914650	18679	40835	2946	981

Description

6500735966 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1518 HP1518 Helicobacter pylori 210 -11539824 7000690460 hypothetical protein hp1518 (db:pir2.dat) F64709 F64709 Helicobacter pylori 210 -11539824 7500959245 hp1518 h. pylori predicted coding region hp1518 (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14262) (re:14549) (di:complement) HPAE000649 AE000649 g2314698 Helicobacter pylori 210 -11539824 7502853706 hp1518 h. pylori predicted coding region hp1518 (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:14262) (re:14549) (di:complement) HPAE000649 AE000649 g2314698 Helicobacter pylori 26695 85962 -11539824

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914676	18680	40836	651	216

Description

6500735967 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1519 HP1519 Helicobacter pylori 210 -11539825 7000690461 hypothetical protein hp1519 (db:pir2.dat) G64709 G64709 Helicobacter pylori 210 -11539825 7500959246 hp1519 h. pylori predicted coding region hp1519 (db:genpept-bct1) (de:helicobacter pylori section 128 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:96) (re:848) (di:complement) HPAE000650 AE000650 g2314704 Helicobacter pylori 210 -11539825 7502853707 hp1519 h. pylori predicted coding region hp1519 (db:genpept) (de:helicobacter pylori 26695 section 128 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:96) (re:848) (di:complement) HPAE000650 AE000650 g2314704 Helicobacter pylori 26695 85962 -11539825

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914682	18681	40837	1056	351

Description

6500735968 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1520 HP1520 Helicobacter pylori 210 -11539826 7000690462 hypothetical protein hp1520 (db:pir2.dat) H64709 H64709 Helicobacter pylori 210 -11539826 7500959247 hp1520 h. pylori predicted coding region hp1520 (db:genpept-bct1) (de:helicobacter pylori section 128 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:958) (re:2250) (di:complement) HPAE000650 AE000650 g2314705 Helicobacter pylori 210 -11539826 7502853708 hp1520 h. pylori predicted coding region hp1520 (db:genpept) (de:helicobacter pylori 26695 section 128 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:958) (re:2250) (di:complement) HPAE000650 AE000650 g2314705 Helicobacter pylori 26695 85962 -11539826

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914691	18682	40838	888	295

Description

6500735969 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1524 HP1524 Helicobacter pylori 210 -11539827 7000690463 hypothetical protein hp1524 (db:pir2.dat) D64710 D64710 Helicobacter pylori 210 -11539827 7500959248 hp1524 h. pylori predicted coding region hp1524 (db:genpept-bct1) (de:helicobacter pylori section 128 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9229) (re:9576) (di:direct) HPAE000650 AE000650 g2314706 Helicobacter pylori 210 -11539827 7502853709 hp1524 h. pylori predicted coding region hp1524 (db:genpept) (de:helicobacter pylori 26695 section 128 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9229) (re:9576) (di:direct) HPAE000650 AE000650 g2314706 Helicobacter pylori 26695 85962 -11539827

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914696	18683	40839	675	224

Description

6500735970 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1525 HP1525 Helicobacter pylori 210 -11539828 7000690464 hypothetical protein hp1525 (cl:hypothetical protein hp1066) (db:pir2.dat) E64710 E64710 Helicobacter pylori 210 -11539828 7500959249 hp1525 h. pylori predicted coding region hp1525 (db:genpept-bct1) (de:helicobacter pylori section 128 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9580) (re:10215) (di:direct) HPAE000650 AE000650 g2314707 Helicobacter pylori 210 -11539828 7502853710 hp1525 h. pylori predicted coding region hp1525 (db:genpept) (de:helicobacter pylori 26695 section 128 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9580) (re:10215) (di:direct) HPAE000650 AE000650 g2314707 Helicobacter pylori 26695 85962 -11539828

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914707	18684	40840	1077	358

Description

6500735971 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1527 HP1527 Helicobacter pylori 210 -11539829 7000690465 hypothetical protein hp1527 (db:pir2.dat) G64710 G64710 Helicobacter pylori 210 -11539829 7500959250 hp1527 h. pylori predicted coding region hp1527 (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:159) (re:1598) (di:complement) HPAE000651 AE000651 g2314715 Helicobacter pylori 210 -11539829 7502853711 hp1527 h. pylori predicted coding region hp1527 (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:159) (re:1598) (di:complement) HPAE000651 AE000651 g2314715 Helicobacter pylori 26695 85962 -11539829

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914712	18685	40841	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914721	18686	40842	231	76

Description

6500735972 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1528 HP1528 Helicobacter pylori 210 -11539830 7000690466 hypothetical protein hp1528 (db:pir2.dat) H64710 H64710 Helicobacter pylori 210 -11539830 7500959251 hp1528 h. pylori predicted coding region hp1528 (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:1597) (re:1674) (di:direct) HPAE000651 AE000651 g2314718 Helicobacter pylori 210 -11539830 7502853712 hp1528 h. pylori predicted coding region hp1528 (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:1597) (re:1674) (di:direct) HPAE000651 AE000651 g2314718 Helicobacter pylori 26695 85962 -11539830

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914736	18687	40843	342	113

Description

7500959253 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1531 HP1531 Helicobacter pylori 210 -11539831 7000690467 hypothetical protein hp1531 (db:pir2.dat) C64711 C64711 Helicobacter pylori 210 -11539831 7500959252 hp1531 h. pylori predicted coding region hp1531 (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3938) (re:4177) (di:direct) HPAE000651 AE000651 g2314716 Helicobacter pylori 210 -11539831 7502853713 jhp1419 putative (db:genpept) (de:helicobacter pylori, strain j99 section 125 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1531) (le:5757) (re:5996) (di:direct) AE001564 AE001564 g4156040 Helicobacter pylori J99 85963 -11539831 6500735973 hp1531 h. pylori predicted coding region hp1531 (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3938) (re:4177) (di:direct) HPAE000651 AE000651 g2314716 Helicobacter pylori 26695 85962 -11539831

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914737	18688	40844	993	330

Description

6500735974 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1536 HP1536 Helicobacter pylori 210 -11539832 7000690468 hypothetical protein hp1536 (db:pir2.dat) H64711 H64711 Helicobacter pylori 210 -11539832 7500959254 hp1536 h. pylori predicted coding region hp1536 (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9042) (re:9098) (di:complement) HPAE000651 AE000651 g2314719 Helicobacter pylori 210 -11539832 7502853714 hp1536 h. pylori predicted coding region hp1536 (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9042) (re:9098) (di:complement) HPAE000651 AE000651 g2314719 Helicobacter pylori 26695 85962 -11539832

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914739	18689	40845	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914751	18690	40846	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914792	18691	40847	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914794	18692	40848	336	111

Description

6500735975 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1537 HP1537 Helicobacter pylori 210 -11539833 7000690469 hypothetical protein hp1537 (db:pir2.dat) A64712 A64712 Helicobacter pylori 210 -11539833 7500959255 hp1537 h. pylori predicted coding region hp1537 (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9233) (re:9919) (di:direct) HPAE000651 AE000651 g2314717 Helicobacter pylori 210 -11539833 7502853715 hp1537 h. pylori predicted coding region hp1537 (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9233) (re:9919) (di:direct) HPAE000651 AE000651 g2314717 Helicobacter pylori 26695 85962 -11539833

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914801	18693	40849	651	216

Description

6500735976 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1542 HP1542 Helicobacter pylori 210 -11539834 7000690611 penicillin-binding protein 4 (db:pir2.dat) F64712 F64712 Helicobacter pylori 210 -11539834 7500959390 hp1542 h. pylori predicted coding region hp1542 (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5845) (re:6255) (di:complement) HPAE000652 AE000652 g2314731 Helicobacter pylori 210 -11539834 7502853716 hp1542 h. pylori predicted coding region hp1542 (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5845) (re:6255) (di:complement) HPAE000652 AE000652 g2314731 Helicobacter pylori 26695 85962 -11539834

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914808	18694	40850	270	89

Description

6500735977 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1546 HP1546 Helicobacter pylori 210 -11539835 7000690470 hypothetical protein hp1546 (db:pir2.dat) B64713 B64713 Helicobacter pylori 210 -11539835 7500959256 hp1546 h. pylori predicted coding region hp1546 (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9221) (re:9733) (di:complement) HPAE000652 AE000652 g2314732 Helicobacter pylori 210 -11539835 7502853717 hp1546 h. pylori predicted coding region hp1546 (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9221) (re:9733) (di:complement) HPAE000652 AE000652 g2314732 Helicobacter pylori 26695 85962 -11539835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914809	18695	40851	855	284

Description

6500735978 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1566 HP1566 Helicobacter pylori 210 -11539836 7000690471 hypothetical protein hp1566 (db:pir2.dat) F64715 F64715 Helicobacter pylori 210 -11539836 7500959257 hp1566 h. pylori predicted coding region hp1566 (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:7565) (re:8008) (di:complement) HPAE000654 AE000654 g2314754 Helicobacter pylori 210 -11539836 7502853718 hp1566 h. pylori predicted coding region hp1566 (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:7565) (re:8008) (di:complement) HPAE000654 AE000654 g2314754 Helicobacter pylori 26695 85962 -11539836

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914813	18696	40852	1650	549

Description

6500735979 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1568 HP1568 Helicobacter pylori 210 -11539837 7000690472 hypothetical protein hp1568 (db:pir2.dat) H64715 H64715 Helicobacter pylori 210 -11539837 7500959258 hp1568 h. pylori predicted coding region hp1568 (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:8644) (re:9195) (di:complement) HPAE000654 AE000654 g2314755 Helicobacter pylori 210 -11539837 7502853719 hp1568 h. pylori predicted coding region hp1568 (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:8644) (re:9195) (di:complement) HPAE000654 AE000654 g2314755 Helicobacter pylori 26695 85962 -11539837

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914824	18697	40853	447	149

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914833	18698	40854	417	138

Description

6500735980 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1569 HP1569 Helicobacter pylori 210 -11539838 7000690473 hypothetical protein hp1569 (db:pir2.dat) A64716 A64716 Helicobacter pylori 210 -11539838 7500959259 hp1569 h. pylori predicted coding region hp1569 (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:9195) (re:9788) (di:complement) HPAE000654 AE000654 g2314756 Helicobacter pylori 210 -11539838 7502853720 hp1569 h. pylori predicted coding region hp1569 (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:9195) (re:9788) (di:complement) HPAE000654 AE000654 g2314756 Helicobacter pylori 26695 85962 -11539838

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914846	18699	40855	612	203

Description

6500735981 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1579 HP1579 Helicobacter pylori 210 -11539839 7000690474 hypothetical protein hp1579 (db:pir2.dat) C64717 C64717 Helicobacter pylori 210 -11539839 7500959260 hp1579 h. pylori predicted coding region hp1579 (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:4659) (re:5087) (di:complement) HPAE000655 AE000655 g2314769 Helicobacter pylori 210 -11539839 7502853721 hp1579 h. pylori predicted coding region hp1579 (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:4659) (re:5087) (di:complement) HPAE000655 AE000655 g2314769 Helicobacter pylori 26695 85962 -11539839

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914847	18700	40856	369	122

Description

6500735982 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1580 HP1580 Helicobacter pylori 210 -11539840 7000690475 hypothetical protein hp1580 (db:pir2.dat) D64717 D64717 Helicobacter pylori 210 -11539840 7500959261 hp1580 h. pylori predicted coding region hp1580 (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5097) (re:5759) (di:complement) HPAE000655 AE000655 g2314770 Helicobacter pylori 210 -11539840 7502853722 hp1580 h. pylori predicted coding region hp1580 (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:5097) (re:5759) (di:complement) HPAE000655 AE000655 g2314770 Helicobacter pylori 26695 85962 -11539840

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914848	18701	40857	264	87

Description

6500735983 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1586 HP1586 Helicobacter pylori 210 -11539841 7000690476 hypothetical protein hp1586 (db:pir2.dat) B64718 B64718 Helicobacter pylori 210 -11539841 7500959262 hp1586 h. pylori predicted coding region hp1586 (db:genpept-bct1) (de:helicobacter pylori section 134 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:66) (re:404) (di:direct) HPAE000656 AE000656 g2314774 Helicobacter pylori 210 -11539841 7502853723 hp1586 h. pylori predicted coding region hp1586 (db:genpept) (de:helicobacter pylori 26695 section 134 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:66) (re:404) (di:direct) HPAE000656 AE000656 g2314774 Helicobacter pylori 26695 85962 -11539841

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914849	18702	40858	207	68

Description

6500735984 h (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-helicobacter pylori) HP1590 HP1590 Helicobacter pylori 210 -11539842 7000690477 hypothetical protein hp1590 (db:pir2.dat) F64718 F64718 Helicobacter pylori 210 -11539842 7500959263 hp1590 h. pylori predicted coding region hp1590 (db:genpept-bct1) (de:helicobacter pylori section 134 of 134 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:3297) (re:3416) (di:complement) HPAE000656 AE000656 g2314775 Helicobacter pylori 210 -11539842 7502853724 hp1590 h. pylori predicted coding region hp1590 (db:genpept) (de:helicobacter pylori 26695 section 134 of 134 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3297) (re:3416) (di:complement) HPAE000656 AE000656 g2314775 Helicobacter pylori 26695 85962 -11539842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914856	18703	40859	282	93

Description

6500735985 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0022 HP0022 Helicobacter pylori 210 -11539843 7000689730 conserved hypothetical integral membrane protein hp0022 (db:pir2.dat) F64522 F64522 Helicobacter pylori 210 -11539843 7500958537 hp0022 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 2 of 134 of the complete genome.) (nt:similar to egad:17681 percent identity: 30.82;) (le:8499) (re:10064) (di:complement) HPAE000524 AE000524 g2313094 Helicobacter pylori 210 -11539843 7502853725 hp0022 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 2 of 134 of the complete genome.) (nt:similar to egad:17681 percent identity: 30.82;) (le:8499) (re:10064) (di:complement) HPAE000524 AE000524 g2313094 Helicobacter pylori 26695 85962 -11539843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914857	18704	40860	768	255

Description

6500735986 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0028 HP0028 Helicobacter pylori 210 -11539844 7000689480 conserved hypothetical secreted protein hp0028 (cl:conserved hypothetical protein hi0453) (db:pir2.dat) D64523 D64523 Helicobacter pylori 210 -11539844 7500955778 hp0028 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to egad:29079 percent identity: 42.07;) (le:5772) (re:6305) (di:direct) HPAE000525 AE000525 g2313105 Helicobacter pylori 210 -11539844 7502853726 hp0028 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to egad:29079 percent identity: 42.07;) (le:5772) (re:6305) (di:direct) HPAE000525 AE000525 g2313105 Helicobacter pylori 26695 85962 -11539844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914858	18705	40861	531	176

Description

6500735987 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0032 HP0032 Helicobacter pylori 210 -11539845 5500686213 hp0032 (sr:,campylobacter pylori) (de:hypothetical protein hp0032) (db:swissprot) Y032_HELPY P56066 HELICOBACTER PYLORI 210 -11539845 7000687060 conserved hypothetical protein hp0032 (cl:hypothetical protein hp0032) (db:pir2.dat) H64523 H64523 Helicobacter pylori 210 -11539845 7500894559 hp0032 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to gp:1787108 percent identity: 37.04;) (le:9276) (re:9551) (di:direct) HPAE000525 AE000525 g2313107 Helicobacter pylori 210 -11539845 7502853727 hp0032 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to gp:1787108 percent identity: 37.04;) (le:9276) (re:9551) (di:direct) HPAE000525 AE000525 g2313107 Helicobacter pylori 26695 85962 -11539845

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914870	18706	40862	336	111

Description

6500735988 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0035 HP0035 Helicobacter pylori 210 -11539846 7000689771 conserved hypothetical protein hp0035 (db:pir2.dat) C64524 C64524 Helicobacter pylori 210 -11539846 7500958578 hp0035 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 3 of 134 of the complete genome.) (nt:similar to egad:14782 percent identity: 34.15;) (le:12122) (re:12415) (di:direct) HPAE000525 AE000525 g2313110 Helicobacter pylori 210 -11539846 7502853728 hp0035 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 3 of 134 of the complete genome.) (nt:similar to egad:14782 percent identity: 34.15;) (le:12122) (re:12415) (di:direct) HPAE000525 AE000525 g2313110 Helicobacter pylori 26695 85962 -11539846

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914872	18707	40863	450	149

Description

6500735989 conserved hypothetical atp-binding protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0066 HP0066 Helicobacter pylori 210 -11539847 7000689724 conserved hypothetical atp-binding protein hp0066 (db:pir2.dat) B64528 B64528 Helicobacter pylori 210 -11539847 7500958531 hp0066 conserved hypothetical atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 6 of 134 of the complete genome.) (nt:similar to gp:1665846 percent identity: 34.66;) (le:8040) (re:10535) (di:direct) HPAE000528 AE000528 g2313138 Helicobacter pylori 210 -11539847 7502853729 hp0066 conserved hypothetical atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 6 of 134 of the complete genome.) (nt:similar to gp:1665846 percent identity: 34.66;) (le:8040) (re:10535) (di:direct) HPAE000528 AE000528 g2313138 Helicobacter pylori 26695 85962 -11539847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914881	18708	40864	918	305

Description

6500735990 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0086 HP0086 Helicobacter pylori 210 -11539848 7000689772 conserved hypothetical protein hp0086 (db:pir2.dat) F64530 F64530 Helicobacter pylori 210 -11539848 7500958579 hp0086 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 8 of 134 of the complete genome.) (nt:similar to egad:9906 percent identity: 28.66;) (le:3907) (re:5259) (di:complement) HPAE000530 AE000530 g2313166 Helicobacter pylori 210 -11539848 7502853730 hp0086 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 8 of 134 of the complete genome.) (nt:similar to egad:9906 percent identity: 28.66;) (le:3907) (re:5259) (di:complement) HPAE000530 AE000530 g2313166 Helicobacter pylori 26695 85962 -11539848

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914882	18709	40865	1296	431

Description

GTC ORF with score 125 to: (fn:helicase, helicase-primase complex) (db:genpept-vrl) (de:human herpesvirus 6 serotype b putative major immediate-earlygenes.) (nt:similar to hhv6a u86, region ie-b) (le:16386) (re:19235) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914886	18710	40866	192	63

Description

6500735991 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0094 HP0094 Helicobacter pylori 210 -11539849 7000689773 conserved hypothetical protein hp0094 (db:pir2.dat) F64531 F64531 Helicobacter pylori 210 -11539849 7500958580 hp0094 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:similar to egad:34316 percent identity: 29.82;) (le:2511) (re:2978) (di:complement) HPAE000531 AE000531 g2313176 Helicobacter pylori 210 -11539849 7502853731 hp0094 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:similar to egad:34316 percent identity: 29.82;) (le:2511) (re:2978) (di:complement) HPAE000531 AE000531 g2313176 Helicobacter pylori 26695 85962 -11539849

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914899	18711	40867	636	211

Description

6500735992 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0100 HP0100 Helicobacter pylori 210 -11539850 7000689774 conserved hypothetical protein hp0100 (db:pir2.dat) D64532 D64532 Helicobacter pylori 210 -11539850 7500958581 hp0100 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 9 of 134 of the complete genome.) (nt:similar to egad:29365 percent identity: 32.02;) (le:9290) (re:10396) (di:direct) HPAE000531 AE000531 g2313180 Helicobacter pylori 210 -11539850 7502853732 hp0100 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 9 of 134 of the complete genome.) (nt:similar to egad:29365 percent identity: 32.02;) (le:9290) (re:10396) (di:direct) HPAE000531 AE000531 g2313180 Helicobacter pylori 26695 85962 -11539850

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914905	18712	40868	600	199

Description

6500735993 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0102 HP0102 Helicobacter pylori 210 -11539851 7000689775 conserved hypothetical protein hp0102 (db:pir2.dat) F64532 F64532 Helicobacter pylori 210 -11539851 7500958582 hp0102 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:similar to egad:34315 percent identity: 29.26;) (le:881) (re:1660) (di:complement) HPAE000532 AE000532 g2313185 Helicobacter pylori 210 -11539851 7502853733 hp0102 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:similar to egad:34315 percent identity: 29.26;) (le:881) (re:1660) (di:complement) HPAE000532 AE000532 g2313185 Helicobacter pylori 26695 85962 -11539851

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914911	18713	40869	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914921	18714	40870	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914934	18715	40871	681	226

Description

6500735994 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0105 HP0105 Helicobacter pylori 210 -11539852 7000689776 conserved hypothetical protein hp0105 (cl:conserved hypothetical protein hi0491) (db:pir2.dat) A64533 A64533 Helicobacter pylori 210 -11539852 7500958583 hp0105 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 10 of 134 of the complete genome.) (nt:similar to egad:29127 percent identity: 39.71;) (le:5494) (re:5961) (di:complement) HPAE000532 AE000532 g2313188 Helicobacter pylori 210 -11539852 7502853734 hp0105 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 10 of 134 of the complete genome.) (nt:similar to egad:29127 percent identity: 39.71;) (le:5494) (re:5961) (di:complement) HPAE000532 AE000532 g2313188 Helicobacter pylori 26695 85962 -11539852

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914942	18716	40872	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914948	18717	40873	792	263

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914953	18718	40874	255	84

Description

6500735995 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0117 HP0117 Helicobacter pylori 210 -11539853 5500686272 hp0117 (sr:,campylobacter pylori) (de:hypothetical protein hp0117) (db:swissprot) Y117_HELPY P56080 HELICOBACTER PYLORI 210 -11539853 7000687068 conserved hypothetical protein hp0117 (db:pir2.dat) E64534 E64534 Helicobacter pylori 210 -11539853 7500894732 hp0117 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 11 of 134 of the complete genome.) (nt:similar to egad:43921 percent identity: 34.23;) (le:7075) (re:8001) (di:direct) HPAE000533 AE000533 g2313199 Helicobacter pylori 210 -11539853 7502853735 hp0117 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 11 of 134 of the complete genome.) (nt:similar to egad:43921 percent identity: 34.23;) (le:7075) (re:8001) (di:direct) HPAE000533 AE000533 g2313199 Helicobacter pylori 26695 85962 -11539853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914965	18719	40875	654	217

Description

6500735996 conserved hypothetical iron-sulfur protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0138 HP0138 Helicobacter pylori 210 -11539854 7000689767 conserved hypothetical iron-sulfur protein hp0138 (cl:conserved hypothetical iron-sulfur protein hp0138) (db:pir2.dat) B64537 B64537 Helicobacter pylori 210 -11539854 7500958572 hp0138 conserved hypothetical iron-sulfur protein (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:similar to gp:1657506 percent identity: 41.19;) (le:6269) (re:7714) (di:complement) HPAE000535 AE000535 g2313222 Helicobacter pylori 210 -11539854 7502853736 hp0138 conserved hypothetical iron-sulfur protein (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:similar to gp:1657506 percent identity: 41.19;) (le:6269) (re:7714) (di:complement) HPAE000535 AE000535 g2313222 Helicobacter pylori 26695 85962 -11539854

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914967	18720	40876	330	109

Description

6500735997 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0139 HP0139 Helicobacter pylori 210 -11539855 7000689859 conserved hypothetical secreted protein hp0139 (cl:conserved hypothetical protein hp0139) (db:pir2.dat) C64537 C64537 Helicobacter pylori 210 -11539855 7500958660 hp0139 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 13 of 134 of the complete genome.) (nt:similar to gp:1657505 percent identity: 37.08;) (le:7743) (re:8471) (di:complement) HPAE000535 AE000535 g2313223 Helicobacter pylori 210 -11539855 7502853737 hp0139 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 13 of 134 of the complete genome.) (nt:similar to gp:1657505 percent identity: 37.08;) (le:7743) (re:8471) (di:complement) HPAE000535 AE000535 g2313223 Helicobacter pylori 26695 85962 -11539855

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914968	18721	40877	354	117

Description

6500735998 conserved hypothetical membrane protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0151 HP0151 Helicobacter pylori 210 -11539856 7000689769 conserved hypothetical membrane protein hp0151 (db:pir2.dat) G64538 G64538 Helicobacter pylori 210 -11539856 7500958574 hp0151 conserved hypothetical membrane protein (db:genpept-bct1) (de:helicobacter pylori section 14 of 134 of the complete genome.) (nt:similar to egad:45608 percent identity: 21.76;) (le:4938) (re:5750) (di:direct) HPAE000536 AE000536 g2313234 Helicobacter pylori 210 -11539856 7502853738 hp0151 conserved hypothetical membrane protein (db:genpept) (de:helicobacter pylori 26695 section 14 of 134 of the complete genome.) (nt:similar to egad:45608 percent identity: 21.76;) (le:4938) (re:5750) (di:direct) HPAE000536 AE000536 g2313234 Helicobacter pylori 26695 85962 -11539856

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914971	18722	40878	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914974	18723	40879	534	177

Description

6500735999 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0160 HP0160 Helicobacter pylori 210 -11539857 7000689469 conserved hypothetical secreted protein hp0160 (cl:conserved hypothetical secreted protein hp1098) (db:pir2.dat) H64539 H64539 Helicobacter pylori 210 -11539857 7500955765 hp0160 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 30.57;) (le:106) (re:1026) (di:direct) HPAE000537 AE000537 g2313248 Helicobacter pylori 210 -11539857 7502853739 hp0160 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 30.57;) (le:106) (re:1026) (di:direct) HPAE000537 AE000537 g2313248 Helicobacter pylori 26695 85962 -11539857

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914975	18724	40880	654	217

Description

6500736000 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0162 HP0162 Helicobacter pylori 210 -11539858 7000689777 conserved hypothetical protein hp0162 (cl:hypothetical protein mg332) (db:pir2.dat) B64540 B64540 Helicobacter pylori 210 -11539858 7500958584 hp0162 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 15 of 134 of the complete genome.) (nt:similar to egad:35798 percent identity: 36.65;) (le:1928) (re:2650) (di:complement) HPAE000537 AE000537 g2313249 Helicobacter pylori 210 -11539858 7502853740 hp0162 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 15 of 134 of the complete genome.) (nt:similar to egad:35798 percent identity: 36.65;) (le:1928) (re:2650) (di:complement) HPAE000537 AE000537 g2313249 Helicobacter pylori 26695 85962 -11539858

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501914980	18725	40881	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915009	18726	40882	507	168

Description

6500736001 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0189 HP0189 Helicobacter pylori 210 -11539859 7000689731 conserved hypothetical integral membrane protein hp0189 (cl:conserved hypothetical protein hi0507) (db:pir2.dat) E64543 E64543 Helicobacter pylori 210 -11539859 7500958538 hp0189 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:similar to egad:36550 percent identity: 43.14;) (le:2075) (re:2608) (di:direct) HPAE000539 AE000539 g2313276 Helicobacter pylori 210 -11539859 7502853741 hp0189 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:similar to egad:36550 percent identity: 43.14;) (le:2075) (re:2608) (di:direct) HPAE000539 AE000539 g2313276 Helicobacter pylori 26695 85962 -11539859

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915013	18727	40883	483	160

Description

6500736002 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0190 HP0190 Helicobacter pylori 210 -11539860 5500686288 hp0190 (sr:,campylobacter pylori) (de:hypothetical protein hp0190) (db:swissprot) Y190_HELPY P56117 HELICOBACTER PYLORI 210 -11539860 7000687078 conserved hypothetical secreted protein hp0190 (db:pir2.dat) F64543 F64543 Helicobacter pylori 210 -11539860 7500894850 hp0190 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 17 of 134 of the complete genome.) (nt:similar to gp:1787284 percent identity: 31.43;) (le:2614) (re:4122) (di:complement) HPAE000539 AE000539 g2313277 Helicobacter pylori 210 -11539860 7502853742 hp0190 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 17 of 134 of the complete genome.) (nt:similar to gp:1787284 percent identity: 31.43;) (le:2614) (re:4122) (di:complement) HPAE000539 AE000539 g2313277 Helicobacter pylori 26695 85962 -11539860

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915014	18728	40884	1233	410

Description

6500736003 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0211 HP0211 Helicobacter pylori 210 -11539861 7000689468 conserved hypothetical secreted protein hp0211 (cl:conserved hypothetical secreted protein hp1098) (db:pir2.dat) C64546 C64546 Helicobacter pylori 210 -11539861 7500955764 hp0211 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 24.31;) (le:3628) (re:4380) (di:complement) HPAE000541 AE000541 g2313301 Helicobacter pylori 210 -11539861 7502853743 hp0211 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 24.31;) (le:3628) (re:4380) (di:complement) HPAE000541 AE000541 g2313301 Helicobacter pylori 26695 85962 -11539861

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915017	18729	40885	582	193

Description

6500736004 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0216 HP0216 Helicobacter pylori 210 -11539862 5500686290 dxr:hp0216 (sr:,campylobacter pylori) (ec:1.1.1.-) (de:reductoisomerase)) (db:swissprot) DXR_HELPY P56139 HELICOBACTER PYLORI 210 -11539862 7000687082 conserved hypothetical protein hp0216 (cl:conserved hypothetical protein hi0807) (db:pir2.dat) H64546 H64546 Helicobacter pylori 210 -11539862 7500894895 hp0216 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 19 of 134 of the complete genome.) (nt:similar to gp:1786369 percent identity: 33.88;) (le:10054) (re:11160) (di:direct) HPAE000541 AE000541 g2313306 Helicobacter pylori 210 -11539862 7502853744 hp0216 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 19 of 134 of the complete genome.) (nt:similar to gp:1786369 percent identity: 33.88;) (le:10054) (re:11160) (di:direct) HPAE000541 AE000541 g2313306 Helicobacter pylori 26695 85962 -11539862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915061	18730	40886	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915074	18731	40887	1194	397

Description

6500736005 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0226 HP0226 Helicobacter pylori 210 -11539863 7000689732 conserved hypothetical integral membrane protein hp0226 (db:pir2.dat) B64548 B64548 Helicobacter pylori 210 -11539863 7500958539 hp0226 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:similar to egad:32187 percent identity: 27.64;) (le:6337) (re:7170) (di:complement) HPAE000542 AE000542 g2313315 Helicobacter pylori 210 -11539863 7502853745 hp0226 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:similar to egad:32187 percent identity: 27.64;) (le:6337) (re:7170) (di:complement) HPAE000542 AE000542 g2313315 Helicobacter pylori 26695 85962 -11539863

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915080	18732	40888	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915094	18733	40889	1416	471

Description

6500736006 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0228 HP0228 Helicobacter pylori 210 -11539864 7000689366 integral membrane protein hp0228 (cl:integral membrane protein hp0228) (db:pir2.dat) D64548 D64548 Helicobacter pylori 210 -11539864 7500955225 hp0228 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 20 of 134 of the complete genome.) (nt:similar to egad:45979 percent identity: 43.24;) (le:9705) (re:10877) (di:direct) HPAE000542 AE000542 g2313317 Helicobacter pylori 210 -11539864 7502853746 hp0228 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 20 of 134 of the complete genome.) (nt:similar to egad:45979 percent identity: 43.24;) (le:9705) (re:10877) (di:direct) HPAE000542 AE000542 g2313317 Helicobacter pylori 26695 85962 -11539864

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915103	18734	40890	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915137	18735	40891	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915151	18736	40892	1401	466

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915157	18737	40893	555	184

Description

6500736007 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0233 HP0233 Helicobacter pylori 210 -11539865 7000689778 conserved hypothetical protein hp0233 (db:pir2.dat) A64549 A64549 Helicobacter pylori 210 -11539865 7500958585 hp0233 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to egad:29412 percent identity: 30.53;) (le:4064) (re:5236) (di:direct) HPAE000543 AE000543 g2313325 Helicobacter pylori 210 -11539865 7502853747 hp0233 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to egad:29412 percent identity: 30.53;) (le:4064) (re:5236) (di:direct) HPAE000543 AE000543 g2313325 Helicobacter pylori 26695 85962 -11539865

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915160	18738	40894	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915161	18739	40895	783	260

Description

6500736008 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0234 HP0234 Helicobacter pylori 210 -11539866 7000689733 conserved hypothetical integral membrane protein hp0234 (db:pir2.dat) B64549 B64549 Helicobacter pylori 210 -11539866 7500958540 hp0234 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to egad:35687 percent identity: 32.40;) (le:5236) (re:5766) (di:direct) HPAE000543 AE000543 g2313326 Helicobacter pylori 210 -11539866 7502853748 hp0234 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to egad:35687 percent identity: 32.40;) (le:5236) (re:5766) (di:direct) HPAE000543 AE000543 g2313326 Helicobacter pylori 26695 85962 -11539866

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915171	18740	40896	456	151

Description

GTC ORF with score 150 to: (sr:schizosaccharomyces pombe (strain 972h-) dna, clone psprpb3-c2) (db:genpept-pln1) (de:fission yeast gene for rna polymerase ii third largest subunit(subunit 3), partial sequence.) (le:988:1111:1207) (re:1067:1160:1970) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915189	18741	40897	324	107

Description

GTC ORF with score 141 to: (db:genpept-pln1) (de:ustilago maydis mismatched base pair and cruciform dna recognitionprotein (hmp1) gene, complete cds.) (nt:mismatch base pair and cruciform dna recognition) (le:26:145) (re:52:414) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915192	18742	40898	936	311

Description

6500736009 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0235 HP0235 Helicobacter pylori 210 -11539867 7000689860 conserved hypothetical secreted protein hp0235 (db:pir2.dat) C64549 C64549 Helicobacter pylori 210 -11539867 7500958661 hp0235 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 21 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 31.53;) (le:6485) (re:7552) (di:complement) HPAE000543 AE000543 g2313327 Helicobacter pylori 210 -11539867 7502853749 hp0235 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 21 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 31.53;) (le:6485) (re:7552) (di:complement) HPAE000543 AE000543 g2313327 Helicobacter pylori 26695 85962 -11539867

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915195	18743	40899	186	61

Description

6500736010 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0248 HP0248 Helicobacter pylori 210 -11539868 7000689779 conserved hypothetical protein hp0248 (db:pir2.dat) H64550 H64550 Helicobacter pylori 210 -11539868 7500958586 hp0248 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 22 of 134 of the complete genome.) (nt:similar to gp:1652146 percent identity: 30.71;) (le:4305) (re:5393) (di:direct) HPAE000544 AE000544 g2313341 Helicobacter pylori 210 -11539868 7502853750 hp0248 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 22 of 134 of the complete genome.) (nt:similar to gp:1652146 percent identity: 30.71;) (le:4305) (re:5393) (di:direct) HPAE000544 AE000544 g2313341 Helicobacter pylori 26695 85962 -11539868

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915201	18744	40900	630	209

Description

6500736011 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0257 HP0257 Helicobacter pylori 210 -11539869 7000689861 conserved hypothetical secreted protein hp0257 (db:pir2.dat) A64552 A64552 Helicobacter pylori 210 -11539869 7500958662 hp0257 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to egad:20752 percent identity: 29.17;) (le:1733) (re:2392) (di:direct) HPAE000545 AE000545 g2313351 Helicobacter pylori 210 -11539869 7502853751 hp0257 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to egad:20752 percent identity: 29.17;) (le:1733) (re:2392) (di:direct) HPAE000545 AE000545 g2313351 Helicobacter pylori 26695 85962 -11539869

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915212	18745	40901	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915222	18746	40902	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915227	18747	40903	510	169

Description

6500736012 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0258 HP0258 Helicobacter pylori 210 -11539870 5500686292 hp0258 (sr:,campylobacter pylori) (de:hypothetical protein hp0258) (db:swissprot) Y258_HELPY P56136 HELICOBACTER PYLORI 210 -11539870 7000687084 conserved hypothetical integral membrane protein hp0258 (db:pir2.dat) B64552 B64552 Helicobacter pylori 210 -11539870 7500894984 hp0258 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 23 of 134 of the complete genome.) (nt:similar to egad:29391 percent identity: 32.66;) (le:2392) (re:3438) (di:direct) HPAE000545 AE000545 g2313352 Helicobacter pylori 210 -11539870 7502853752 hp0258 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 23 of 134 of the complete genome.) (nt:similar to egad:29391 percent identity: 32.66;) (le:2392) (re:3438) (di:direct) HPAE000545 AE000545 g2313352 Helicobacter pylori 26695 85962 -11539870

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915229	18748	40904	849	282

Description

6500736013 conserved hypothetical atp-binding protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0269 HP0269 Helicobacter pylori 210 -11539871 5500686293 hp0269 (sr:,campylobacter pylori) (de:hypothetical protein hp0269) (db:swissprot) Y269_HELPY P56131 HELICOBACTER PYLORI 210 -11539871 7000687085 conserved hypothetical atp-binding protein hp0269 (cl:conserved hypothetical protein hi0019) (db:pir2.dat) E64553 E64553 Helicobacter pylori 210 -11539871 7500895010 hp0269 conserved hypothetical atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:similar to egad:32922 percent identity: 37.67;) (le:313) (re:1626) (di:direct) HPAE000546 AE000546 g2313364 Helicobacter pylori 210 -11539871 7502853753 hp0269 conserved hypothetical atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:similar to egad:32922 percent identity: 37.67;) (le:313) (re:1626) (di:direct) HPAE000546 AE000546 g2313364 Helicobacter pylori 26695 85962 -11539871

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915236	18749	40905	216	71

Description

6500736014 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0274 HP0274 Helicobacter pylori 210 -11539872 5500686294 hp0274 (sr:,campylobacter pylori) (de:hypothetical protein hp0274) (db:swissprot) Y274_HELPY P56132 HELICOBACTER PYLORI 210 -11539872 7000687086 conserved hypothetical protein hp0274 (db:pir2.dat) B64554 B64554 Helicobacter pylori 210 -11539872 7500895043 hp0274 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 24 of 134 of the complete genome.) (nt:similar to egad:44828 percent identity: 38.46;) (le:4371) (re:4769) (di:direct) HPAE000546 AE000546 g2313365 Helicobacter pylori 210 -11539872 7502853754 hp0274 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 24 of 134 of the complete genome.) (nt:similar to egad:44828 percent identity: 38.46;) (le:4371) (re:4769) (di:direct) HPAE000546 AE000546 g2313365 Helicobacter pylori 26695 85962 -11539872

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915239	18750	40906	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915244	18751	40907	753	250

Description

6500736015 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0284 HP0284 Helicobacter pylori 210 -11539873 7000689734 conserved hypothetical integral membrane protein hp0284 (db:pir2.dat) D64555 D64555 Helicobacter pylori 210 -11539873 7500958541 hp0284 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:similar to egad:44867 percent identity: 29.18;) (le:3715) (re:5286) (di:direct) HPAE000547 AE000547 g2313380 Helicobacter pylori 210 -11539873 7502853755 hp0284 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:similar to egad:44867 percent identity: 29.18;) (le:3715) (re:5286) (di:direct) HPAE000547 AE000547 g2313380 Helicobacter pylori 26695 85962 -11539873

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915245	18752	40908	402	133

Description

6500736016 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0285 HP0285 Helicobacter pylori 210 -11539874 5500686295 hp0285 (sr:,campylobacter pylori) (de:hypothetical protein hp0285) (db:swissprot) Y285_HELPY P56130 HELICOBACTER PYLORI 210 -11539874 7000687087 conserved hypothetical protein hp0285 (db:pir2.dat) E64555 E64555 Helicobacter pylori 210 -11539874 7500895067 hp0285 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 25 of 134 of the complete genome.) (nt:similar to egad:45804 percent identity: 30.84;) (le:5283) (re:6539) (di:direct) HPAE000547 AE000547 g2313381 Helicobacter pylori 210 -11539874 7502853756 hp0285 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 25 of 134 of the complete genome.) (nt:similar to egad:45804 percent identity: 30.84;) (le:5283) (re:6539) (di:direct) HPAE000547 AE000547 g2313381 Helicobacter pylori 26695 85962 -11539874

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915249	18753	40909	276	91

Description

GTC ORF with score 122 to: (fn:krebs cycle) (db:genpept-pln2) (ec:1.1.1.41) (de:kluyveromyces lactis nad-dependent isocitrate dehydrogenase subunit2 (idh2) gene, nuclear gene encoding mitochondrial protein,complete cds.) (nt:idh2p) (le:294) (re:1400) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915254	18754	40910	1947	649

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915261	18755	40911	411	136

Description

6500736017 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0309 HP0309 Helicobacter pylori 210 -11539875 7000689780 conserved hypothetical protein hp0309 (cl:hypothetical protein ylr351c) (db:pir2.dat) E64558 E64558 Helicobacter pylori 210 -11539875 7500958587 hp0309 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:similar to egad:36723 percent identity: 31.27;) (le:2781) (re:3659) (di:direct) HPAE000549 AE000549 g2313405 Helicobacter pylori 210 -11539875 7502853757 hp0309 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:similar to egad:36723 percent identity: 31.27;) (le:2781) (re:3659) (di:direct) HPAE000549 AE000549 g2313405 Helicobacter pylori 26695 85962 -11539875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915278	18756	40912	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915282	18757	40913	786	261

Description

6500736018 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0310 HP0310 Helicobacter pylori 210 -11539876 7000689781 conserved hypothetical protein hp0310 (db:pir2.dat) F64558 F64558 Helicobacter pylori 210 -11539876 7500958588 hp0310 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:similar to egad:12469 percent identity: 33.66;) (le:3672) (re:4553) (di:direct) HPAE000549 AE000549 g2313406 Helicobacter pylori 210 -11539876 7502853758 hp0310 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:similar to egad:12469 percent identity: 33.66;) (le:3672) (re:4553) (di:direct) HPAE000549 AE000549 g2313406 Helicobacter pylori 26695 85962 -11539876

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915285	18758	40914	798	265

Description

6500736019 conserved hypothetical atp-binding protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0312 HP0312 Helicobacter pylori 210 -11539877 7000689725 conserved hypothetical atp-binding protein hp0312 (db:pir2.dat) H64558 H64558 Helicobacter pylori 210 -11539877 7500958532 hp0312 conserved hypothetical atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 27 of 134 of the complete genome.) (nt:similar to egad:36749 percent identity: 34.05;) (le:4967) (re:5932) (di:direct) HPAE000549 AE000549 g2313407 Helicobacter pylori 210 -11539877 7502853759 hp0312 conserved hypothetical atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 27 of 134 of the complete genome.) (nt:similar to egad:36749 percent identity: 34.05;) (le:4967) (re:5932) (di:direct) HPAE000549 AE000549 g2313407 Helicobacter pylori 26695 85962 -11539877

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915287	18759	40915	993	330

Description

6500736020 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0318 HP0318 Helicobacter pylori 210 -11539878 7000689464 conserved hypothetical protein hp0318 (cl:conserved hypothetical protein hp0318) (db:pir2.dat) F64559 F64559 Helicobacter pylori 210 -11539878 7500955759 hp0318 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:29339 percent identity: 47.18;) (le:179) (re:934) (di:complement) HPAE000550 AE000550 g2313418 Helicobacter pylori 210 -11539878 7502853760 hp0318 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:29339 percent identity: 47.18;) (le:179) (re:934) (di:complement) HPAE000550 AE000550 g2313418 Helicobacter pylori 26695 85962 -11539878

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915293	18760	40916	714	237

Description

6500736021 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0320 HP0320 Helicobacter pylori 210 -11539879 7000689470 conserved hypothetical secreted protein hp0320 (cl:conserved hypothetical secreted protein hp0320) (db:pir2.dat) H64559 H64559 Helicobacter pylori 210 -11539879 7500955766 hp0320 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:46186 percent identity: 36.36;) (le:2623) (re:2862) (di:complement) HPAE000550 AE000550 g2313428 Helicobacter pylori 210 -11539879 7502853761 hp0320 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:46186 percent identity: 36.36;) (le:2623) (re:2862) (di:complement) HPAE000550 AE000550 g2313428 Helicobacter pylori 26695 85962 -11539879

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915301	18761	40917	258	85

Description

6500736022 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0328 HP0328 Helicobacter pylori 210 -11539880 7000689782 conserved hypothetical protein hp0328 (db:pir2.dat) H64560 H64560 Helicobacter pylori 210 -11539880 7500958589 hp0328 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 28 of 134 of the complete genome.) (nt:similar to egad:27894 percent identity: 30.74;) (le:9379) (re:10317) (di:complement) HPAE000550 AE000550 g2313426 Helicobacter pylori 210 -11539880 7502853762 hp0328 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 28 of 134 of the complete genome.) (nt:similar to egad:27894 percent identity: 30.74;) (le:9379) (re:10317) (di:complement) HPAE000550 AE000550 g2313426 Helicobacter pylori 26695 85962 -11539880

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915302	18762	40918	210	69

Description

6500736023 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0334 HP0334 Helicobacter pylori 210 -11539881 7000689783 conserved hypothetical protein hp0334 (db:pir2.dat) F64561 F64561 Helicobacter pylori 210 -11539881 7500958590 hp0334 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:similar to egad:36516 percent identity: 30.77;) (le:3099) (re:3503) (di:direct) HPAE000551 AE000551 g2313435 Helicobacter pylori 210 -11539881 7502853763 hp0334 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:similar to egad:36516 percent identity: 30.77;) (le:3099) (re:3503) (di:direct) HPAE000551 AE000551 g2313435 Helicobacter pylori 26695 85962 -11539881

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915309	18763	40919	954	317

Description

6500736024 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0347 HP0347 Helicobacter pylori 210 -11539882 7502853764 hp0347 (sr:,campylobacter pylori) (de:hypothetical protein hp0347) (db:swissprot) Y347_HELPY O25114 HELICOBACTER PYLORI 210 -11539882 7000689784 conserved hypothetical protein hp0347 (db:pir2.dat) C64563 C64563 Helicobacter pylori 210 -11539882 7500958591 hp0347 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 29 of 134 of the complete genome.) (nt:similar to egad:31419 percent identity: 31.79;) (le:8678) (re:9574) (di:complement) HPAE000551 AE000551 g2313436 Helicobacter pylori 210 -11539882 7502853765 hp0347 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 29 of 134 of the complete genome.) (nt:similar to egad:31419 percent identity: 31.79;) (le:8678) (re:9574) (di:complement) HPAE000551 AE000551 g2313436 Helicobacter pylori 26695 85962 -11539882

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915313	18764	40920	468	155

Description

6500736025 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0362 HP0362 Helicobacter pylori 210 -11539883 7000689735 conserved hypothetical integral membrane protein hp0362 (db:pir2.dat) B64565 B64565 Helicobacter pylori 210 -11539883 7500958542 hp0362 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 31 of 134 of the complete genome.) (nt:similar to egad:28682 percent identity: 28.83;) (le:2289) (re:3326) (di:complement) HPAE000553 AE000553 g2313464 Helicobacter pylori 210 -11539883 7502853766 hp0362 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 31 of 134 of the complete genome.) (nt:similar to egad:28682 percent identity: 28.83;) (le:2289) (re:3326) (di:complement) HPAE000553 AE000553 g2313464 Helicobacter pylori 26695 85962 -11539883

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915321	18765	40921	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915324	18766	40922	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915347	18767	40923	1263	420

Description

6500736026 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0373 HP0373 Helicobacter pylori 210 -11539884 7000689785 conserved hypothetical protein hp0373 (db:pir2.dat) E64566 E64566 Helicobacter pylori 210 -11539884 7500958592 hp0373 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 31.40;) (le:823) (re:2925) (di:direct) HPAE000554 AE000554 g2313477 Helicobacter pylori 210 -11539884 7502853767 hp0373 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 31.40;) (le:823) (re:2925) (di:direct) HPAE000554 AE000554 g2313477 Helicobacter pylori 26695 85962 -11539884

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915349	18768	40924	2193	730

Description

6500736027 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0374 HP0374 Helicobacter pylori 210 -11539885 7000689786 conserved hypothetical protein hp0374 (db:pir2.dat) F64566 F64566 Helicobacter pylori 210 -11539885 7500958593 hp0374 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 32 of 134 of the complete genome.) (nt:similar to egad:28934 percent identity: 24.67;) (le:2949) (re:3629) (di:complement) HPAE000554 AE000554 g2313478 Helicobacter pylori 210 -11539885 7502853768 hp0374 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 32 of 134 of the complete genome.) (nt:similar to egad:28934 percent identity: 24.67;) (le:2949) (re:3629) (di:complement) HPAE000554 AE000554 g2313478 Helicobacter pylori 26695 85962 -11539885

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915359	18769	40925	363	120

Description

6500736028 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0388 HP0388 Helicobacter pylori 210 -11539886 7000689787 conserved hypothetical protein hp0388 (cl:conserved hypothetical protein hi0319) (db:pir2.dat) D64568 D64568 Helicobacter pylori 210 -11539886 7500958594 hp0388 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:28960 percent identity: 39.83;) (le:6172) (re:6903) (di:complement) HPAE000555 AE000555 g2313489 Helicobacter pylori 210 -11539886 7502853769 hp0388 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:28960 percent identity: 39.83;) (le:6172) (re:6903) (di:complement) HPAE000555 AE000555 g2313489 Helicobacter pylori 26695 85962 -11539886

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915368	18770	40926	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915385	18771	40927	246	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915391	18772	40928	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915411	18773	40929	558	185

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915426	18774	40930	1011	336

Description

6500736029 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0395 HP0395 Helicobacter pylori 210 -11539887 7500895236 hp0395 (sr:,campylobacter pylori) (de:hypothetical protein hp0395) (db:swissprot) Y395_HELPY O25156 HELICOBACTER PYLORI 210 -11539887 7000689788 conserved hypothetical protein hp0395 (cl:conserved hypothetical protein hi0090) (db:pir2.dat) C64569 C64569 Helicobacter pylori 210 -11539887 7500895238 hp0395 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:28744 percent identity: 39.91;) (le:13239) (re:13907) (di:complement) HPAE000555 AE000555 g2313495 Helicobacter pylori 210 -11539887 7502853770 hp0395 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:28744 percent identity: 39.91;) (le:13239) (re:13907) (di:complement) HPAE000555 AE000555 g2313495 Helicobacter pylori 26695 85962 -11539887

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915455	18775	40931	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915468	18776	40932	987	328

Description

6500736030 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0396 HP0396 Helicobacter pylori 210 -11539888 7000689789 conserved hypothetical protein hp0396 (db:pir2.dat) D64569 D64569 Helicobacter pylori 210 -11539888 7500958595 hp0396 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 33 of 134 of the complete genome.) (nt:similar to egad:6056 percent identity: 33.70;) (le:13930) (re:15780) (di:complement) HPAE000555 AE000555 g2313496 Helicobacter pylori 210 -11539888 7502853771 hp0396 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 33 of 134 of the complete genome.) (nt:similar to egad:6056 percent identity: 33.70;) (le:13930) (re:15780) (di:complement) HPAE000555 AE000555 g2313496 Helicobacter pylori 26695 85962 -11539888

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915469	18777	40933	312	103

Description

6500736031 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0415 HP0415 Helicobacter pylori 210 -11539889 7000689736 conserved hypothetical integral membrane protein hp0415 (db:pir2.dat) G64571 G64571 Helicobacter pylori 210 -11539889 7500958543 hp0415 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to gp:1787591 percent identity: 44.44;) (le:6167) (re:8038) (di:direct) HPAE000557 AE000557 g2313519 Helicobacter pylori 210 -11539889 7502853772 hp0415 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to gp:1787591 percent identity: 44.44;) (le:6167) (re:8038) (di:direct) HPAE000557 AE000557 g2313519 Helicobacter pylori 26695 85962 -11539889

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915476	18778	40934	672	223

Description

6500736032 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0419 HP0419 Helicobacter pylori 210 -11539890 7000689485 conserved hypothetical protein hp0419 (cl:conserved hypothetical protein hp0419:bioc homology) (db:pir2.dat) C64572 C64572 Helicobacter pylori 210 -11539890 7500955784 hp0419 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 35 of 134 of the complete genome.) (nt:similar to egad:28355 percent identity: 45.56;) (le:12343) (re:13128) (di:direct) HPAE000557 AE000557 g2313522 Helicobacter pylori 210 -11539890 7502853773 hp0419 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 35 of 134 of the complete genome.) (nt:similar to egad:28355 percent identity: 45.56;) (le:12343) (re:13128) (di:direct) HPAE000557 AE000557 g2313522 Helicobacter pylori 26695 85962 -11539890

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915481	18779	40935	1809	602

Description

6500736033 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0447 HP0447 Helicobacter pylori 210 -11539891 7000689790 conserved hypothetical protein hp0447 (db:pir2.dat) G64575 G64575 Helicobacter pylori 210 -11539891 7500958596 hp0447 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 38 of 134 of the complete genome.) (nt:similar to egad:53922 percent identity: 38.22;) (le:1179) (re:2261) (di:direct) HPAE000560 AE000560 g2313555 Helicobacter pylori 210 -11539891 7502853774 hp0447 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 38 of 134 of the complete genome.) (nt:similar to egad:53922 percent identity: 38.22;) (le:1179) (re:2261) (di:direct) HPAE000560 AE000560 g2313555 Helicobacter pylori 26695 85962 -11539891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915486	18780	40936	483	160

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915497	18781	40937	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915507	18782	40938	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915510	18783	40939	1455	484

Description

6500736034 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0465 HP0465 Helicobacter pylori 210 -11539892 7000689791 conserved hypothetical protein hp0465 (db:pir2.dat) A64578 A64578 Helicobacter pylori 210 -11539892 7500958597 hp0465 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to gp:1800177 percent identity: 95.55;) (le:11831) (re:13726) (di:complement) HPAE000561 AE000561 g2313569 Helicobacter pylori 210 -11539892 7502853775 hp0465 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to gp:1800177 percent identity: 95.55;) (le:11831) (re:13726) (di:complement) HPAE000561 AE000561 g2313569 Helicobacter pylori 26695 85962 -11539892

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915532	18784	40940	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915535	18785	40941	414	137

Description

6500736035 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0466 HP0466 Helicobacter pylori 210 -11539893 7000689792 conserved hypothetical protein hp0466 (db:pir2.dat) B64578 B64578 Helicobacter pylori 210 -11539893 7500958598 hp0466 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to gp:1800178 percent identity: 95.69;) (le:13751) (re:14518) (di:complement) HPAE000561 AE000561 g2313570 Helicobacter pylori 210 -11539893 7502853776 hp0466 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to gp:1800178 percent identity: 95.69;) (le:13751) (re:14518) (di:complement) HPAE000561 AE000561 g2313570 Helicobacter pylori 26695 85962 -11539893

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915544	18786	40942	855	284

Description

5000696660 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0467 HP0467 Helicobacter pylori 210 -11539894 7000689737 conserved hypothetical integral membrane protein hp0467 (db:pir2.dat) C64578 C64578 Helicobacter pylori 210 -11539894 7500958544 hp0467 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to gp:1800179 percent identity: 100.00;) (le:14528) (re:14875) (di:complement) HPAE000561 AE000561 g2313571 Helicobacter pylori 210 -11539894 7502853777 jhp0419 putative (db:genpept) (de:helicobacter pylori, strain j99 section 37 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0467) (le:3065) (re:3412) (di:complement) AE001476 AE001476 g4154955 Helicobacter pylori J99 85963 -11539894 7502853778 hp0467 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to gp:1800179 percent identity: 100.00;) (le:14528) (re:14875) (di:complement) HPAE000561 AE000561 g2313571 Helicobacter pylori 26695 85962 -11539894 243467 orf28 (db:genpept-bct1) (de:h. pylori chromosomal fragment ~38.5kb, complete sequence.) (nt:orf28 - similar to yeast 64.6 kd protein in) (le:29410) (re:29757) (di:complement) HPAC000108 AC000108 g1800179 Helicobacter pylori 210 -11539894 6500736036 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0467 HP0467 Helicobacter pylori 210 -11539894 7500958545 (de:unknown (h. pylori specific with no known function)) (sr:strain j99) JHP419 JHP419 Helicobacter pylori 210 -11539894

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915563	18787	40943	1092	363

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915570	18788	40944	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915571	18789	40945	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915589	18790	40946	1503	500

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915623	18791	40947	2127	708

Description

6500736037 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0468 HP0468 Helicobacter pylori 210 -11539895 7000689793 conserved hypothetical protein hp0468 (db:pir2.dat) D64578 D64578 Helicobacter pylori 210 -11539895 7500958599 hp0468 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to gp:1800180 percent identity: 97.14;) (le:14844) (re:16331) (di:complement) HPAE000561 AE000561 g2313572 Helicobacter pylori 210 -11539895 7502853779 hp0468 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to gp:1800180 percent identity: 97.14;) (le:14844) (re:16331) (di:complement) HPAE000561 AE000561 g2313572 Helicobacter pylori 26695 85962 -11539895

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915625	18792	40948	1323	440

Description

6500736038 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0469 HP0469 Helicobacter pylori 210 -11539896 7000689794 conserved hypothetical protein hp0469 (db:pir2.dat) E64578 E64578 Helicobacter pylori 210 -11539896 7500958600 hp0469 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 39 of 134 of the complete genome.) (nt:similar to gp:1800181 percent identity: 95.06;) (le:16343) (re:16831) (di:complement) HPAE000561 AE000561 g2313573 Helicobacter pylori 210 -11539896 7502853780 hp0469 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 39 of 134 of the complete genome.) (nt:similar to gp:1800181 percent identity: 95.06;) (le:16343) (re:16831) (di:complement) HPAE000561 AE000561 g2313573 Helicobacter pylori 26695 85962 -11539896

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915626	18793	40949	891	297

Description

6500736039 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0496 HP0496 Helicobacter pylori 210 -11539897 7000689795 conserved hypothetical protein hp0496 (db:pir2.dat) H64581 H64581 Helicobacter pylori 210 -11539897 7500958601 hp0496 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 42 of 134 of the complete genome.) (nt:similar to gp:1763299 percent identity: 99.25;) (le:5352) (re:5753) (di:complement) HPAE000564 AE000564 g2313606 Helicobacter pylori 210 -11539897 7502853781 hp0496 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 42 of 134 of the complete genome.) (nt:similar to gp:1763299 percent identity: 99.25;) (le:5352) (re:5753) (di:complement) HPAE000564 AE000564 g2313606 Helicobacter pylori 26695 85962 -11539897

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915627	18794	40950	1125	374

Description

6500736040 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0506 HP0506 Helicobacter pylori 210 -11539898 7000689862 conserved hypothetical secreted protein hp0506 (db:pir2.dat) B64583 B64583 Helicobacter pylori 210 -11539898 7500958663 hp0506 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:similar to egad:29045 percent identity: 29.81;) (le:1760) (re:2971) (di:direct) HPAE000565 AE000565 g2313617 Helicobacter pylori 210 -11539898 7502853782 hp0506 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:similar to egad:29045 percent identity: 29.81;) (le:1760) (re:2971) (di:direct) HPAE000565 AE000565 g2313617 Helicobacter pylori 26695 85962 -11539898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915631	18795	40951	885	294

Description

6500736041 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0507 HP0507 Helicobacter pylori 210 -11539899 7000689796 conserved hypothetical protein hp0507 (db:pir2.dat) C64583 C64583 Helicobacter pylori 210 -11539899 7500958602 hp0507 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 43 of 134 of the complete genome.) (nt:similar to gp:1262938 percent identity: 37.21;) (le:2971) (re:3609) (di:direct) HPAE000565 AE000565 g2313618 Helicobacter pylori 210 -11539899 7502853783 hp0507 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 43 of 134 of the complete genome.) (nt:similar to gp:1262938 percent identity: 37.21;) (le:2971) (re:3609) (di:direct) HPAE000565 AE000565 g2313618 Helicobacter pylori 26695 85962 -11539899

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915646	18796	40952	438	145

Description

6500736042 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0518 HP0518 Helicobacter pylori 210 -11539900 7000689863 conserved hypothetical secreted protein hp0518 (db:pir2.dat) F64584 F64584 Helicobacter pylori 210 -11539900 7500958664 hp0518 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800155 percent identity: 96.88;) (le:3292) (re:4284) (di:direct) HPAE000566 AE000566 g2313633 Helicobacter pylori 210 -11539900 7502853784 hp0518 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800155 percent identity: 96.88;) (le:3292) (re:4284) (di:direct) HPAE000566 AE000566 g2313633 Helicobacter pylori 26695 85962 -11539900

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915648	18797	40953	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915659	18798	40954	714	237

Description

6500736043 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0519 HP0519 Helicobacter pylori 210 -11539901 7000689797 conserved hypothetical protein hp0519 (db:pir2.dat) G64584 G64584 Helicobacter pylori 210 -11539901 7500958603 hp0519 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 44 of 134 of the complete genome.) (nt:similar to gp:1800156 percent identity: 95.32;) (le:4373) (re:5203) (di:complement) HPAE000566 AE000566 g2313634 Helicobacter pylori 210 -11539901 7502853785 hp0519 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 44 of 134 of the complete genome.) (nt:similar to gp:1800156 percent identity: 95.32;) (le:4373) (re:5203) (di:complement) HPAE000566 AE000566 g2313634 Helicobacter pylori 26695 85962 -11539901

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915660	18799	40955	276	91

Description

6500736044 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0552 HP0552 Helicobacter pylori 210 -11539902 7000687090 hp0552 (sr:,campylobacter pylori) (de:hypothetical protein hp0552) (db:swissprot) Y552_HELPY P56204 HELICOBACTER PYLORI 210 -11539902 7000687091 conserved hypothetical protein hp0552 (db:pir2.dat) H64588 H64588 Helicobacter pylori 210 -11539902 7500895399 hp0552 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 47 of 134 of the complete genome.) (nt:similar to egad:29798 percent identity: 37.78;) (le:7722) (re:8585) (di:direct) HPAE000569 AE000569 g2313668 Helicobacter pylori 210 -11539902 7502853786 hp0552 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 47 of 134 of the complete genome.) (nt:similar to egad:29798 percent identity: 37.78;) (le:7722) (re:8585) (di:direct) HPAE000569 AE000569 g2313668 Helicobacter pylori 26695 85962 -11539902

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915663	18800	40956	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915680	18801	40957	786	261

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915686	18802	40958	438	145

Description

6500736045 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0553 HP0553 Helicobacter pylori 210 -11539903 7000689798 conserved hypothetical protein hp0553 (db:pir2.dat) A64589 A64589 Helicobacter pylori 210 -11539903 7500958604 hp0553 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 47 of 134 of the complete genome.) (nt:similar to egad:29345 percent identity: 30.04;) (le:8598) (re:9281) (di:direct) HPAE000569 AE000569 g2313669 Helicobacter pylori 210 -11539903 7502853787 hp0553 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 47 of 134 of the complete genome.) (nt:similar to egad:29345 percent identity: 30.04;) (le:8598) (re:9281) (di:direct) HPAE000569 AE000569 g2313669 Helicobacter pylori 26695 85962 -11539903

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915692	18803	40959	291	96

Description

6500736046 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0571 HP0571 Helicobacter pylori 210 -11539904 7000689738 conserved hypothetical integral membrane protein hp0571 (db:pir2.dat) C64591 C64591 Helicobacter pylori 210 -11539904 7500958546 hp0571 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to egad:6152 percent identity: 29.51;) (le:2738) (re:3316) (di:complement) HPAE000571 AE000571 g2313691 Helicobacter pylori 210 -11539904 7502853788 hp0571 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to egad:6152 percent identity: 29.51;) (le:2738) (re:3316) (di:complement) HPAE000571 AE000571 g2313691 Helicobacter pylori 26695 85962 -11539904

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915701	18804	40960	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915708	18805	40961	585	194

Description

6500736047 conserved hypothetical membrane protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0575 HP0575 Helicobacter pylori 210 -11539905 7000689770 conserved hypothetical membrane protein hp0575 (db:pir2.dat) G64591 G64591 Helicobacter pylori 210 -11539905 7500958575 hp0575 conserved hypothetical membrane protein (db:genpept-bct1) (de:helicobacter pylori section 49 of 134 of the complete genome.) (nt:similar to gp:1565238 percent identity: 38.83;) (le:4788) (re:5486) (di:complement) HPAE000571 AE000571 g2313694 Helicobacter pylori 210 -11539905 7502853789 hp0575 conserved hypothetical membrane protein (db:genpept) (de:helicobacter pylori 26695 section 49 of 134 of the complete genome.) (nt:similar to gp:1565238 percent identity: 38.83;) (le:4788) (re:5486) (di:complement) HPAE000571 AE000571 g2313694 Helicobacter pylori 26695 85962 -11539905

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915719	18806	40962	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915720	18807	40963	348	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915723	18808	40964	555	184

Description

6500736048 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0639 HP0639 Helicobacter pylori 210 -11539906 7000689799 conserved hypothetical protein hp0639 (cl:conserved hypothetical protein hi1191) (db:pir2.dat) G64599 G64599 Helicobacter pylori 210 -11539906 7500958605 hp0639 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:28204 percent identity: 41.01;) (le:2086) (re:2766) (di:complement) HPAE000578 AE000578 g2313760 Helicobacter pylori 210 -11539906 7502853790 hp0639 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:28204 percent identity: 41.01;) (le:2086) (re:2766) (di:complement) HPAE000578 AE000578 g2313760 Helicobacter pylori 26695 85962 -11539906

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915731	18809	40965	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915742	18810	40966	270	89

Description

6500736049 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0644 HP0644 Helicobacter pylori 210 -11539907 7000689739 conserved hypothetical integral membrane protein hp0644 (db:pir2.dat) D64600 D64600 Helicobacter pylori 210 -11539907 7500958547 hp0644 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 56 of 134 of the complete genome.) (nt:similar to egad:6912 percent identity: 30.26;) (le:6414) (re:6707) (di:direct) HPAE000578 AE000578 g2313764 Helicobacter pylori 210 -11539907 7502853791 hp0644 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 56 of 134 of the complete genome.) (nt:similar to egad:6912 percent identity: 30.26;) (le:6414) (re:6707) (di:direct) HPAE000578 AE000578 g2313764 Helicobacter pylori 26695 85962 -11539907

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915765	18811	40967	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915770	18812	40968	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915787	18813	40969	294	97

Description

6500736050 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0654 HP0654 Helicobacter pylori 210 -11539908 7000689800 conserved hypothetical protein hp0654 (cl:hypothetical protein af0390) (db:pir2.dat) F64601 F64601 Helicobacter pylori 210 -11539908 7500955910 hp0654 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:44035 percent identity: 32.01;) (le:179) (re:1261) (di:direct) HPAE000579 AE000579 g2313779 Helicobacter pylori 210 -11539908 7502853792 hp0654 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:44035 percent identity: 32.01;) (le:179) (re:1261) (di:direct) HPAE000579 AE000579 g2313779 Helicobacter pylori 26695 85962 -11539908

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915792	18814	40970	1662	553

Description

6500736051 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0656 HP0656 Helicobacter pylori 210 -11539909 7000689801 conserved hypothetical protein hp0656 (cl:hypothetical protein af0390) (db:pir2.dat) H64601 H64601 Helicobacter pylori 210 -11539909 7500955909 hp0656 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 57 of 134 of the complete genome.) (nt:similar to egad:44035 percent identity: 35.99;) (le:4006) (re:5157) (di:direct) HPAE000579 AE000579 g2313781 Helicobacter pylori 210 -11539909 7502853793 hp0656 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 57 of 134 of the complete genome.) (nt:similar to egad:44035 percent identity: 35.99;) (le:4006) (re:5157) (di:direct) HPAE000579 AE000579 g2313781 Helicobacter pylori 26695 85962 -11539909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915794	18815	40971	702	234

Description

GTC ORF with score 130 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c18.) (nt:spcc18.10, len:340, similarity:saccharomyces) (le:26200:26299:26550:26948) (re:26253:26407:26856:27500) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915803	18816	40972	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915808	18817	40973	399	132

Description

6500736052 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0677 HP0677 Helicobacter pylori 210 -11539910 7000689740 conserved hypothetical integral membrane protein hp0677 (db:pir2.dat) E64604 E64604 Helicobacter pylori 210 -11539910 7500958548 hp0677 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 59 of 134 of the complete genome.) (nt:similar to egad:44611 percent identity: 28.46;) (le:571) (re:1338) (di:complement) HPAE000581 AE000581 g2313804 Helicobacter pylori 210 -11539910 7502853794 hp0677 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 59 of 134 of the complete genome.) (nt:similar to egad:44611 percent identity: 28.46;) (le:571) (re:1338) (di:complement) HPAE000581 AE000581 g2313804 Helicobacter pylori 26695 85962 -11539910

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915822	18818	40974	714	237

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915833	18819	40975	753	250

Description

6500736053 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0693 HP0693 Helicobacter pylori 210 -11539911 7000689465 conserved hypothetical integral membrane protein hp0693 (cl:conserved hypothetical integral membrane protein hp0693) (db:pir2.dat) E64606 E64606 Helicobacter pylori 210 -11539911 7500955760 hp0693 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 60 of 134 of the complete genome.) (nt:similar to egad:27939 percent identity: 46.68;) (le:5843) (re:7207) (di:direct) HPAE000582 AE000582 g2313817 Helicobacter pylori 210 -11539911 7502853795 hp0693 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 60 of 134 of the complete genome.) (nt:similar to egad:27939 percent identity: 46.68;) (le:5843) (re:7207) (di:direct) HPAE000582 AE000582 g2313817 Helicobacter pylori 26695 85962 -11539911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915865	18820	40976	1128	375

Description

6500736054 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0707 HP0707 Helicobacter pylori 210 -11539912 7000689802 yabc protein homolog hp0707 (cl:escherichia coli yabc protein) (db:pir2.dat) C64608 C64608 Helicobacter pylori 210 -11539912 7500958606 hp0707 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:similar to gp:1122760 percent identity: 40.13;) (le:120) (re:1046) (di:direct) HPAE000584 AE000584 g2313835 Helicobacter pylori 210 -11539912 7502853796 hp0707 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:similar to gp:1122760 percent identity: 40.13;) (le:120) (re:1046) (di:direct) HPAE000584 AE000584 g2313835 Helicobacter pylori 26695 85962 -11539912

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915870	18821	40977	759	252

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915871	18822	40978	2121	707

Description

6500736055 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0709 HP0709 Helicobacter pylori 210 -11539913 7000689803 conserved hypothetical protein hp0709 (db:pir2.dat) E64608 E64608 Helicobacter pylori 210 -11539913 7500958607 hp0709 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:similar to egad:44254 percent identity: 49.64;) (le:1657) (re:2559) (di:direct) HPAE000584 AE000584 g2313836 Helicobacter pylori 210 -11539913 7502853797 hp0709 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:similar to egad:44254 percent identity: 49.64;) (le:1657) (re:2559) (di:direct) HPAE000584 AE000584 g2313836 Helicobacter pylori 26695 85962 -11539913

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915921	18823	40979	432	143

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915925	18824	40980	1353	450

Description

6500736056 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0710 HP0710 Helicobacter pylori 210 -11539914 7000689804 conserved hypothetical protein hp0710 (db:pir2.dat) F64608 F64608 Helicobacter pylori 210 -11539914 7500958608 hp0710 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 33.71;) (le:2830) (re:4812) (di:direct) HPAE000584 AE000584 g2313837 Helicobacter pylori 210 -11539914 7502853798 hp0710 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 33.71;) (le:2830) (re:4812) (di:direct) HPAE000584 AE000584 g2313837 Helicobacter pylori 26695 85962 -11539914

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915927	18825	40981	678	225

Description

6500736057 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0716 HP0716 Helicobacter pylori 210 -11539915 7000689806 conserved hypothetical protein hp0716 (db:pir2.dat) D64609 D64609 Helicobacter pylori 210 -11539915 7500958609 hp0716 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 62 of 134 of the complete genome.) (nt:similar to egad:27900 percent identity: 30.21;) (le:8919) (re:9320) (di:complement) HPAE000584 AE000584 g2313840 Helicobacter pylori 210 -11539915 7502853799 hp0716 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 62 of 134 of the complete genome.) (nt:similar to egad:27900 percent identity: 30.21;) (le:8919) (re:9320) (di:complement) HPAE000584 AE000584 g2313840 Helicobacter pylori 26695 85962 -11539915

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915949	18826	40982	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915966	18827	40983	579	192

Description

GTC ORF with score 115 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome 1 bac f5f19 sequence, completesequence.) (nt:similar to gb|y09437 myrosinase binding protein) (le:24840:25635:27045) (re:25550:26972:27188) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915972	18828	40984	315	104

Description

6500736058 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0718 HP0718 Helicobacter pylori 210 -11539916 7000689741 conserved hypothetical integral membrane protein hp0718 (db:pir2.dat) F64609 F64609 Helicobacter pylori 210 -11539916 7500958549 hp0718 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 63 of 134 of the complete genome.) (nt:similar to gp:1519238 percent identity: 33.52;) (le:65) (re:697) (di:complement) HPAE000585 AE000585 g2313846 Helicobacter pylori 210 -11539916 7502853800 hp0718 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 63 of 134 of the complete genome.) (nt:similar to gp:1519238 percent identity: 33.52;) (le:65) (re:697) (di:complement) HPAE000585 AE000585 g2313846 Helicobacter pylori 26695 85962 -11539916

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915977	18829	40985	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915981	18830	40986	966	321

Description

6500736059 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0728 HP0728 Helicobacter pylori 210 -11539917 7000689807 conserved hypothetical protein hp0728 (db:pir2.dat) H64610 H64610 Helicobacter pylori 210 -11539917 7500958610 hp0728 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:18381 percent identity: 29.28;) (le:77) (re:1087) (di:complement) HPAE000586 AE000586 g2313855 Helicobacter pylori 210 -11539917 7502853801 hp0728 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:18381 percent identity: 29.28;) (le:77) (re:1087) (di:complement) HPAE000586 AE000586 g2313855 Helicobacter pylori 26695 85962 -11539917

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915987	18831	40987	1278	426

Description

6500736060 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0734 HP0734 Helicobacter pylori 210 -11539918 7000689808 conserved hypothetical protein hp0734 (cl:conserved hypothetical protein hi0019) (db:pir2.dat) F64611 F64611 Helicobacter pylori 210 -11539918 7500958611 hp0734 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:45804 percent identity: 30.99;) (le:6303) (re:7622) (di:complement) HPAE000586 AE000586 g2313856 Helicobacter pylori 210 -11539918 7502853802 hp0734 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:45804 percent identity: 30.99;) (le:6303) (re:7622) (di:complement) HPAE000586 AE000586 g2313856 Helicobacter pylori 26695 85962 -11539918

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501915991	18832	40988	324	107

Description

6500736061 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0737 HP0737 Helicobacter pylori 210 -11539919 7000689742 conserved hypothetical integral membrane protein hp0737 (db:pir2.dat) A64612 A64612 Helicobacter pylori 210 -11539919 7500958550 hp0737 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:28303 percent identity: 33.33;) (le:9350) (re:9826) (di:direct) HPAE000586 AE000586 g2313859 Helicobacter pylori 210 -11539919 7502853803 hp0737 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:28303 percent identity: 33.33;) (le:9350) (re:9826) (di:direct) HPAE000586 AE000586 g2313859 Helicobacter pylori 26695 85962 -11539919

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916004	18833	40989	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916010	18834	40990	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916026	18835	40991	921	307

Description

6500736062 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0741 HP0741 Helicobacter pylori 210 -11539920 7000689809 conserved hypothetical protein hp0741 (cl:protein kinase c inhibitor:histidine triad homology) (db:pir2.dat) E64612 E64612 Helicobacter pylori 210 -11539920 7500958612 hp0741 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:45029 percent identity: 30.23;) (le:13150) (re:13635) (di:direct) HPAE000586 AE000586 g2313863 Helicobacter pylori 210 -11539920 7502853804 hp0741 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:45029 percent identity: 30.23;) (le:13150) (re:13635) (di:direct) HPAE000586 AE000586 g2313863 Helicobacter pylori 26695 85962 -11539920

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916033	18836	40992	771	256

Description

GTC ORF with score 304 to: (sr:yeast (s.cerevisiae, strain ab 320 -(m.olson)) dna, clones a(0-6)) (db:genpept-pln1) (de:yeast (s.cerevisiae) rna polymerase a(i) large subunit gene,complete cds.) (nt:rna polymerase a(i) large subunit) (le:887) (re:5881)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916036	18837	40993	669	223

Description

6500736063 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0745 HP0745 Helicobacter pylori 210 -11539921 7502853805 hp0745 (sr:,campylobacter pylori) (de:hypothetical protein hp0745) (db:swissprot) Y745_HELPY O25441 HELICOBACTER PYLORI 210 -11539921 7000689810 conserved hypothetical protein hp0745 (db:pir2.dat) A64613 A64613 Helicobacter pylori 210 -11539921 7500958613 hp0745 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:similar to egad:31419 percent identity: 33.68;) (le:3619) (re:4602) (di:direct) HPAE000587 AE000587 g2313872 Helicobacter pylori 210 -11539921 7502853806 hp0745 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:similar to egad:31419 percent identity: 33.68;) (le:3619) (re:4602) (di:direct) HPAE000587 AE000587 g2313872 Helicobacter pylori 26695 85962 -11539921

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916039	18838	40994	330	109

Description

6500736064 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0747 HP0747 Helicobacter pylori 210 -11539922 7000689811 conserved hypothetical protein hp0747 (db:pir2.dat) C64613 C64613 Helicobacter pylori 210 -11539922 7500958614 hp0747 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 65 of 134 of the complete genome.) (nt:similar to egad:28979 percent identity: 32.35;) (le:5823) (re:7004) (di:direct) HPAE000587 AE000587 g2313873 Helicobacter pylori 210 -11539922 7502853807 hp0747 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 65 of 134 of the complete genome.) (nt:similar to egad:28979 percent identity: 32.35;) (le:5823) (re:7004) (di:direct) HPAE000587 AE000587 g2313873 Helicobacter pylori 26695 85962 -11539922

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916047	18839	40995	2943	980

Description

6500736065 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0758 HP0758 Helicobacter pylori 210 -11539923 7000689367 conserved hypothetical integral membrane protein hp0758 (cl:conserved integral membrane protein hp0758) (db:pir2.dat) F64614 F64614 Helicobacter pylori 210 -11539923 7500955226 hp0758 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:similar to egad:28966 percent identity: 47.58;) (le:2554) (re:3867) (di:direct) HPAE000588 AE000588 g2313884 Helicobacter pylori 210 -11539923 7502853808 hp0758 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:similar to egad:28966 percent identity: 47.58;) (le:2554) (re:3867) (di:direct) HPAE000588 AE000588 g2313884 Helicobacter pylori 26695 85962 -11539923

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916048	18840	40996	351	116

Description

6500736066 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0759 HP0759 Helicobacter pylori 210 -11539924 7000689743 conserved hypothetical integral membrane protein hp0759 (db:pir2.dat) G64614 G64614 Helicobacter pylori 210 -11539924 7500958551 hp0759 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:similar to egad:36821 percent identity: 31.08;) (le:3930) (re:5183) (di:direct) HPAE000588 AE000588 g2313885 Helicobacter pylori 210 -11539924 7502853809 hp0759 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:similar to egad:36821 percent identity: 31.08;) (le:3930) (re:5183) (di:direct) HPAE000588 AE000588 g2313885 Helicobacter pylori 26695 85962 -11539924

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916049	18841	40997	507	168

Description

6500736067 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0760 HP0760 Helicobacter pylori 210 -11539925 7000689812 conserved hypothetical protein hp0760 (cl:hypothetical protein ymda) (db:pir2.dat) H64614 H64614 Helicobacter pylori 210 -11539925 7500955922 hp0760 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 66 of 134 of the complete genome.) (nt:similar to egad:11562 percent identity: 36.10;) (le:5184) (re:6572) (di:complement) HPAE000588 AE000588 g2313886 Helicobacter pylori 210 -11539925 7502853810 hp0760 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 66 of 134 of the complete genome.) (nt:similar to egad:11562 percent identity: 36.10;) (le:5184) (re:6572) (di:complement) HPAE000588 AE000588 g2313886 Helicobacter pylori 26695 85962 -11539925

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916050	18842	40998	318	105

Description

6500736068 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0785 HP0785 Helicobacter pylori 210 -11539926 7000689864 conserved hypothetical secreted protein hp0785 (db:pir2.dat) A64618 A64618 Helicobacter pylori 210 -11539926 7500958665 hp0785 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:similar to egad:18896 percent identity: 26.60;) (le:7850) (re:8404) (di:complement) HPAE000590 AE000590 g2313909 Helicobacter pylori 210 -11539926 7502853811 hp0785 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:similar to egad:18896 percent identity: 26.60;) (le:7850) (re:8404) (di:complement) HPAE000590 AE000590 g2313909 Helicobacter pylori 26695 85962 -11539926

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916053	18843	40999	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916054	18844	41000	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916055	18845	41001	399	132

Description

6500736069 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0787 HP0787 Helicobacter pylori 210 -11539927 7000689744 conserved hypothetical integral membrane protein hp0787 (db:pir2.dat) C64618 C64618 Helicobacter pylori 210 -11539927 7500958552 hp0787 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 68 of 134 of the complete genome.) (nt:similar to egad:28549 percent identity: 25.19;) (le:11139) (re:12371) (di:direct) HPAE000590 AE000590 g2313911 Helicobacter pylori 210 -11539927 7502853812 hp0787 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 68 of 134 of the complete genome.) (nt:similar to egad:28549 percent identity: 25.19;) (le:11139) (re:12371) (di:direct) HPAE000590 AE000590 g2313911 Helicobacter pylori 26695 85962 -11539927

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916056	18846	41002	333	110

Description

6500736070 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0810 HP0810 Helicobacter pylori 210 -11539928 7000689813 conserved hypothetical protein hp0810 (db:pir2.dat) B64621 B64621 Helicobacter pylori 210 -11539928 7500958615 hp0810 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 70 of 134 of the complete genome.) (nt:similar to egad:7463 percent identity: 31.02;) (le:9709) (re:10311) (di:complement) HPAE000592 AE000592 g2313938 Helicobacter pylori 210 -11539928 7502853813 hp0810 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 70 of 134 of the complete genome.) (nt:similar to egad:7463 percent identity: 31.02;) (le:9709) (re:10311) (di:complement) HPAE000592 AE000592 g2313938 Helicobacter pylori 26695 85962 -11539928

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916066	18847	41003	1314	437

Description

6500736071 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0813 HP0813 Helicobacter pylori 210 -11539929 7000689814 conserved hypothetical protein hp0813 (cl:glyoxalase) (db:pir2.dat) E64621 E64621 Helicobacter pylori 210 -11539929 7500958616 hp0813 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:24313 percent identity: 32.47;) (le:1400) (re:2017) (di:direct) HPAE000593 AE000593 g2313945 Helicobacter pylori 210 -11539929 7502853814 hp0813 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:24313 percent identity: 32.47;) (le:1400) (re:2017) (di:direct) HPAE000593 AE000593 g2313945 Helicobacter pylori 26695 85962 -11539929

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916105	18848	41004	912	303

Description

6500736072 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0823 HP0823 Helicobacter pylori 210 -11539930 7000689815 conserved hypothetical protein hp0823 (db:pir2.dat) G64622 G64622 Helicobacter pylori 210 -11539930 7500958617 hp0823 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 71 of 134 of the complete genome.) (nt:similar to egad:46247 percent identity: 27.84;) (le:10874) (re:11218) (di:direct) HPAE000593 AE000593 g2313953 Helicobacter pylori 210 -11539930 7502853815 hp0823 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 71 of 134 of the complete genome.) (nt:similar to egad:46247 percent identity: 27.84;) (le:10874) (re:11218) (di:direct) HPAE000593 AE000593 g2313953 Helicobacter pylori 26695 85962 -11539930

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916110	18849	41005	1554	517

Description

GTC ORF with score 214 to: (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe nuclear envelope protein cut11p (cut11+)mrna, complete cds.) (nt:membrane protein; associated with nuclear pore) (le:24) (re:1829) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916126	18850	41006	1005	334

Description

6500736073 conserved hypothetical atp binding protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0831 HP0831 Helicobacter pylori 210 -11539931 7000689723 conserved hypothetical atp binding protein hp0831 (cl:conserved hypothetical protein ydr196c) (db:pir2.dat) G64623 G64623 Helicobacter pylori 210 -11539931 7500958530 hp0831 conserved hypothetical atp binding protein (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:10585 percent identity: 32.26;) (le:6828) (re:7418) (di:complement) HPAE000594 AE000594 g2313965 Helicobacter pylori 210 -11539931 7502853816 hp0831 conserved hypothetical atp binding protein (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:10585 percent identity: 32.26;) (le:6828) (re:7418) (di:complement) HPAE000594 AE000594 g2313965 Helicobacter pylori 26695 85962 -11539931

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916128	18851	41007	519	172

Description

6500736074 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0851 HP0851 Helicobacter pylori 210 -11539932 7000689745 conserved hypothetical integral membrane protein hp0851 (db:pir2.dat) C64626 C64626 Helicobacter pylori 210 -11539932 7500958553 hp0851 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:44548 percent identity: 37.25;) (le:3317) (re:4000) (di:direct) HPAE000596 AE000596 g2313985 Helicobacter pylori 210 -11539932 7502853817 hp0851 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:44548 percent identity: 37.25;) (le:3317) (re:4000) (di:direct) HPAE000596 AE000596 g2313985 Helicobacter pylori 26695 85962 -11539932

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916142	18852	41008	519	172

Description

6500736075 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0860 HP0860 Helicobacter pylori 210 -11539933 7000689508 conserved hypothetical protein hp0860 (cl:lmbk protein) (db:pir2.dat) D64627 D64627 Helicobacter pylori 210 -11539933 7500955809 hp0860 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 74 of 134 of the complete genome.) (nt:similar to egad:27863 percent identity: 52.05;) (le:13734) (re:14255) (di:complement) HPAE000596 AE000596 g2313992 Helicobacter pylori 210 -11539933 7502853818 hp0860 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 74 of 134 of the complete genome.) (nt:similar to egad:27863 percent identity: 52.05;) (le:13734) (re:14255) (di:complement) HPAE000596 AE000596 g2313992 Helicobacter pylori 26695 85962 -11539933

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916146	18853	41009	210	69

Description

6500736076 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0890 HP0890 Helicobacter pylori 210 -11539934 7000689816 conserved hypothetical protein hp0890 (cl:retinol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) B64631 B64631 Helicobacter pylori 210 -11539934 7500958618 hp0890 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 76 of 134 of the complete genome.) (nt:similar to gp:1786701 percent identity: 32.17;) (le:11644) (re:12414) (di:complement) HPAE000598 AE000598 g2314026 Helicobacter pylori 210 -11539934 7502853819 hp0890 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 76 of 134 of the complete genome.) (nt:similar to gp:1786701 percent identity: 32.17;) (le:11644) (re:12414) (di:complement) HPAE000598 AE000598 g2314026 Helicobacter pylori 26695 85962 -11539934

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916151	18854	41010	345	114

Description

7500894014 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0891 HP0891 Helicobacter pylori 210 -11539935 5500686160 vdld:hp0891 (sr:,campylobacter pylori) (de:protein vdld) (db:swissprot) VDLD_HELPY O05729 HELICOBACTER PYLORI 210 -11539935 7000686943 conserved hypothetical protein hp0891 (db:pir2.dat) C64631 C64631 Helicobacter pylori 210 -11539935 7500894013 hp0891 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:similar to egad:37639 percent identity: 33.80;) (le:139) (re:663) (di:direct) HPAE000599 AE000599 g2314029 Helicobacter pylori 210 -11539935 7502853820 jhp0824 putative (db:genpept) (de:helicobacter pylori, strain j99 section 73 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp0891) (le:122) (re:646) (di:direct) AE001512 AE001512 g4155401 Helicobacter pylori J99 85963 -11539935 6500736077 hp0891 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:similar to egad:37639 percent identity: 33.80;) (le:139) (re:663) (di:direct) HPAE000599 AE000599 g2314029 Helicobacter pylori 26695 85962 -11539935

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916152	18855	41011	765	254

Description

GTC ORF with score 312 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana dna chromosome 4, bac clone f22k18 (essaiiproject).) (nt:similarity to hpv16 e1 protein binding protein,) (le:32267:32473:32671:33059) (re:32390:32565:32745:33125) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916155	18856	41012	381	126

Description

6500736078 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0892 HP0892 Helicobacter pylori 210 -11539936 7000689817 conserved hypothetical protein hp0892 (cl:conserved hypothetical protein hi0711) (db:pir2.dat) D64631 D64631 Helicobacter pylori 210 -11539936 7500958619 hp0892 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:similar to egad:37579 percent identity: 39.08;) (le:755) (re:1027) (di:complement) HPAE000599 AE000599 g2314030 Helicobacter pylori 210 -11539936 7502853821 hp0892 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:similar to egad:37579 percent identity: 39.08;) (le:755) (re:1027) (di:complement) HPAE000599 AE000599 g2314030 Helicobacter pylori 26695 85962 -11539936

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916167	18857	41013	288	95

Description

6500736079 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0894 HP0894 Helicobacter pylori 210 -11539937 7000689818 conserved hypothetical protein hp0894 (cl:conserved hypothetical protein hi0711) (db:pir2.dat) F64631 F64631 Helicobacter pylori 210 -11539937 7500958620 hp0894 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 77 of 134 of the complete genome.) (nt:similar to egad:29478 percent identity: 39.77;) (le:1409) (re:1675) (di:complement) HPAE000599 AE000599 g2314031 Helicobacter pylori 210 -11539937 7502853822 hp0894 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 77 of 134 of the complete genome.) (nt:similar to egad:29478 percent identity: 39.77;) (le:1409) (re:1675) (di:complement) HPAE000599 AE000599 g2314031 Helicobacter pylori 26695 85962 -11539937

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916185	18858	41014	1230	409

Description

6500736080 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0920 HP0920 Helicobacter pylori 210 -11539938 7000689746 conserved hypothetical integral membrane protein hp0920 (cl:escherichia coli ybhl protein) (db:pir2.dat) H64634 H64634 Helicobacter pylori 210 -11539938 7500958554 hp0920 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 79 of 134 of the complete genome.) (nt:similar to egad:6204 percent identity: 36.31;) (le:8761) (re:9453) (di:complement) HPAE000601 AE000601 g2314055 Helicobacter pylori 210 -11539938 7502853823 hp0920 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 79 of 134 of the complete genome.) (nt:similar to egad:6204 percent identity: 36.31;) (le:8761) (re:9453) (di:complement) HPAE000601 AE000601 g2314055 Helicobacter pylori 26695 85962 -11539938

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916193	18859	41015	396	131

Description

6500736081 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0926 HP0926 Helicobacter pylori 210 -11539939 5500686448 hp0926 (sr:,campylobacter pylori) (de:hypothetical protein hp0926) (db:swissprot) Y926_HELPY P55985 HELICOBACTER PYLORI 210 -11539939 7000687098 conserved hypothetical protein hp0926 (db:pir2.dat) F64635 F64635 Helicobacter pylori 210 -11539939 7500895690 hp0926 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:29470 percent identity: 30.72;) (le:9821) (re:10966) (di:direct) HPAE000602 AE000602 g2314063 Helicobacter pylori 210 -11539939 7502853824 hp0926 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:29470 percent identity: 30.72;) (le:9821) (re:10966) (di:direct) HPAE000602 AE000602 g2314063 Helicobacter pylori 26695 85962 -11539939

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916194	18860	41016	372	123

Description

6500736082 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0934 HP0934 Helicobacter pylori 210 -11539940 7000689819 conserved hypothetical protein hp0934 (db:pir2.dat) F64636 F64636 Helicobacter pylori 210 -11539940 7500958621 hp0934 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:36608 percent identity: 33.63;) (le:15417) (re:16172) (di:direct) HPAE000602 AE000602 g2314068 Helicobacter pylori 210 -11539940 7502853825 hp0934 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:36608 percent identity: 33.63;) (le:15417) (re:16172) (di:direct) HPAE000602 AE000602 g2314068 Helicobacter pylori 26695 85962 -11539940

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916195	18861	41017	255	84

Description

GTC ORF with score 99 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f18e5 (essaiiproject).) (nt:similarity to pig3 homo sapiens, patchx:g2754812;) (le:80680:81288:81659:81819) (re:80931:81467:81740:82085) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916202	18862	41018	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916209	18863	41019	1059	352

Description

6500736083 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0946 HP0946 Helicobacter pylori 210 -11539941 7000689747 conserved hypothetical integral membrane protein hp0946 (db:pir2.dat) B64638 B64638 Helicobacter pylori 210 -11539941 7500958555 hp0946 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:28568 percent identity: 35.88;) (le:408) (re:1898) (di:direct) HPAE000604 AE000604 g2314087 Helicobacter pylori 210 -11539941 7502853826 hp0946 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:28568 percent identity: 35.88;) (le:408) (re:1898) (di:direct) HPAE000604 AE000604 g2314087 Helicobacter pylori 26695 85962 -11539941

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916210	18864	41020	315	104

Description

6500736084 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0949 HP0949 Helicobacter pylori 210 -11539942 7000689865 conserved hypothetical secreted protein hp0949 (db:pir2.dat) E64638 E64638 Helicobacter pylori 210 -11539942 7500958666 hp0949 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:37660 percent identity: 39.66;) (le:3965) (re:4417) (di:complement) HPAE000604 AE000604 g2314088 Helicobacter pylori 210 -11539942 7502853827 hp0949 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:37660 percent identity: 39.66;) (le:3965) (re:4417) (di:complement) HPAE000604 AE000604 g2314088 Helicobacter pylori 26695 85962 -11539942

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916222	18865	41021	270	89

Description

6500736085 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0952 HP0952 Helicobacter pylori 210 -11539943 7000689748 conserved hypothetical integral membrane protein hp0952 (cl:conserved hypothetical protein aq_1996) (db:pir2.dat) H64638 H64638 Helicobacter pylori 210 -11539943 7500958556 hp0952 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:36867 percent identity: 38.46;) (le:6006) (re:6662) (di:direct) HPAE000604 AE000604 g2314090 Helicobacter pylori 210 -11539943 7502853828 hp0952 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:36867 percent identity: 38.46;) (le:6006) (re:6662) (di:direct) HPAE000604 AE000604 g2314090 Helicobacter pylori 26695 85962 -11539943

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916224	18866	41022	231	76

Description

6500736086 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0956 HP0956 Helicobacter pylori 210 -11539944 7502853829 hp0956 (sr:,campylobacter pylori) (de:hypothetical protein hp0956) (db:swissprot) Y956_HELPY O25610 HELICOBACTER PYLORI 210 -11539944 7000689820 conserved hypothetical protein hp0956 (db:pir2.dat) D64639 D64639 Helicobacter pylori 210 -11539944 7500958622 hp0956 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:46219 percent identity: 36.19;) (le:8789) (re:9517) (di:complement) HPAE000604 AE000604 g2314093 Helicobacter pylori 210 -11539944 7502853830 hp0956 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:46219 percent identity: 36.19;) (le:8789) (re:9517) (di:complement) HPAE000604 AE000604 g2314093 Helicobacter pylori 26695 85962 -11539944

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916226	18867	41023	516	171

Description

6500736087 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0959 HP0959 Helicobacter pylori 210 -11539945 7000689821 conserved hypothetical protein hp0959 (db:pir2.dat) G64639 G64639 Helicobacter pylori 210 -11539945 7500958623 hp0959 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 82 of 134 of the complete genome.) (nt:similar to egad:43548 percent identity: 31.10;) (le:11485) (re:12216) (di:complement) HPAE000604 AE000604 g2314095 Helicobacter pylori 210 -11539945 7502853831 hp0959 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 82 of 134 of the complete genome.) (nt:similar to egad:43548 percent identity: 31.10;) (le:11485) (re:12216) (di:complement) HPAE000604 AE000604 g2314095 Helicobacter pylori 26695 85962 -11539945

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916228	18868	41024	264	87

Description

6500736088 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0966 HP0966 Helicobacter pylori 210 -11539946 7000689822 conserved hypothetical protein hp0966 (db:pir2.dat) F64640 F64640 Helicobacter pylori 210 -11539946 7500958624 hp0966 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 83 of 134 of the complete genome.) (nt:similar to egad:20215 percent identity: 29.07;) (le:4219) (re:5868) (di:complement) HPAE000605 AE000605 g2314105 Helicobacter pylori 210 -11539946 7502853832 hp0966 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 83 of 134 of the complete genome.) (nt:similar to egad:20215 percent identity: 29.07;) (le:4219) (re:5868) (di:complement) HPAE000605 AE000605 g2314105 Helicobacter pylori 26695 85962 -11539946

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916235	18869	41025	474	157

Description

6500736089 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0975 HP0975 Helicobacter pylori 210 -11539947 7000689823 conserved hypothetical protein hp0975 (db:pir2.dat) G64641 G64641 Helicobacter pylori 210 -11539947 7500958625 hp0975 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:similar to egad:34580 percent identity: 25.00;) (le:2650) (re:2931) (di:direct) HPAE000606 AE000606 g2314117 Helicobacter pylori 210 -11539947 7502853833 hp0975 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:similar to egad:34580 percent identity: 25.00;) (le:2650) (re:2931) (di:direct) HPAE000606 AE000606 g2314117 Helicobacter pylori 26695 85962 -11539947

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916239	18870	41026	525	174

Description

6500736090 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0977 HP0977 Helicobacter pylori 210 -11539948 7000689866 conserved hypothetical secreted protein hp0977 (db:pir2.dat) A64642 A64642 Helicobacter pylori 210 -11539948 7500958667 hp0977 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:similar to egad:36840 percent identity: 29.41;) (le:4490) (re:5953) (di:direct) HPAE000606 AE000606 g2314119 Helicobacter pylori 210 -11539948 7502853834 hp0977 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:similar to egad:36840 percent identity: 29.41;) (le:4490) (re:5953) (di:direct) HPAE000606 AE000606 g2314119 Helicobacter pylori 26695 85962 -11539948

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916242	18871	41027	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916244	18872	41028	387	128

Description

6500736091 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0980 HP0980 Helicobacter pylori 210 -11539949 7000689867 conserved hypothetical secreted protein hp0980 (db:pir2.dat) D64642 D64642 Helicobacter pylori 210 -11539949 7500958668 hp0980 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 84 of 134 of the complete genome.) (nt:similar to egad:8229 percent identity: 57.38;) (le:9893) (re:10195) (di:direct) HPAE000606 AE000606 g2314122 Helicobacter pylori 210 -11539949 7502853835 hp0980 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 84 of 134 of the complete genome.) (nt:similar to egad:8229 percent identity: 57.38;) (le:9893) (re:10195) (di:direct) HPAE000606 AE000606 g2314122 Helicobacter pylori 26695 85962 -11539949

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916250	18873	41029	282	93

Description

GTC ORF with score 308 to: (or:Homo sapiens) (sr:human placenta, cdna to mrna, (library of clontech)) (db:genpept-pri1) (de:human isovaleryl-coa dehydrogenase (ivd) mrna, complete cds.) (nt:isovaleryl-coa dehydrogenase (ivd)) (le:16) (re:1287) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916251	18874	41030	426	141

Description

GTC ORF with score 426 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c02b10.) (nt:similar to acyl-coa dehydrogenase; coded for by c.) (le:22488:23069:23434:23984) (re:22622:23380:23931:24298) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916258	18875	41031	276	91

Description

GTC ORF with score 265 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c02b10.) (nt:similar to acyl-coa dehydrogenase; coded for by c.) (le:22488:23069:23434:23984) (re:22622:23380:23931:24298) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916267	18876	41032	213	70

Description

6500736092 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP0983 HP0983 Helicobacter pylori 210 -11539950 7000689749 conserved hypothetical integral membrane protein hp0983 (db:pir2.dat) G64642 G64642 Helicobacter pylori 210 -11539950 7500958557 hp0983 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 85 of 134 of the complete genome.) (nt:similar to egad:6287 percent identity: 32.82;) (le:1734) (re:2558) (di:direct) HPAE000607 AE000607 g2314126 Helicobacter pylori 210 -11539950 7502853836 hp0983 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 85 of 134 of the complete genome.) (nt:similar to egad:6287 percent identity: 32.82;) (le:1734) (re:2558) (di:direct) HPAE000607 AE000607 g2314126 Helicobacter pylori 26695 85962 -11539950

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916271	18877	41033	1146	381

Description

6500736093 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1020 HP1020 Helicobacter pylori 210 -11539951 7000689824 conserved hypothetical protein hp1020 (db:pir2.dat) D64647 D64647 Helicobacter pylori 210 -11539951 7500958626 hp1020 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:similar to egad:22730 percent identity: 31.52;) (le:4283) (re:5503) (di:direct) HPAE000610 AE000610 g2314164 Helicobacter pylori 210 -11539951 7502853837 hp1020 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:similar to egad:22730 percent identity: 31.52;) (le:4283) (re:5503) (di:direct) HPAE000610 AE000610 g2314164 Helicobacter pylori 26695 85962 -11539951

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916275	18878	41034	309	102

Description

6500736094 conserved hypothetical helicase-like protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1026 HP1026 Helicobacter pylori 210 -11539952 7000689729 conserved hypothetical helicase-like protein hp1026 (db:pir2.dat) B64648 B64648 Helicobacter pylori 210 -11539952 7500958536 hp1026 conserved hypothetical helicase-like protein (db:genpept-bct1) (de:helicobacter pylori section 88 of 134 of the complete genome.) (nt:similar to egad:28582 percent identity: 35.20;) (le:10270) (re:11445) (di:direct) HPAE000610 AE000610 g2314168 Helicobacter pylori 210 -11539952 7502853838 hp1026 conserved hypothetical helicase-like protein (db:genpept) (de:helicobacter pylori 26695 section 88 of 134 of the complete genome.) (nt:similar to egad:28582 percent identity: 35.20;) (le:10270) (re:11445) (di:direct) HPAE000610 AE000610 g2314168 Helicobacter pylori 26695 85962 -11539952

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916293	18879	41035	525	174

Description

6500736095 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1037 HP1037 Helicobacter pylori 210 -11539953 7000689825 probable x-pro dipeptidase::conserved hypothetical protein hp1037:hypothetical protein 2 aroq 3-region (cl:x-pro aminopeptidase) (ec:3.4.13.9) (db:pir2.dat) E64649 E64649 Helicobacter pylori 210 -11539953 7500958627 hp1037 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to gp:1806001 percent identity: 95.89;) (le:7373) (re:8446) (di:complement) HPAE000611 AE000611 g2314181 Helicobacter pylori 210 -11539953 7502853839 hp1037 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to gp:1806001 percent identity: 95.89;) (le:7373) (re:8446) (di:complement) HPAE000611 AE000611 g2314181 Helicobacter pylori 26695 85962 -11539953

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916300	18880	41036	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916310	18881	41037	309	102

Description

GTC ORF with score 178 to: (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae putative acyltransferase (slc1) gene andputative la homolog (yla1) gene, complete cds.) (nt:complements e.coli mutant defective in) (le:1430) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916312	18882	41038	300	99

Description

6500736096 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1044 HP1044 Helicobacter pylori 210 -11539954 7000689750 probable membrane-bound phosphoesterase:hp1044:conserved hypothetical integral membrane protein hp1044 (cl:probable membrane-bound phosphoesterase hp1044:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) D64650 D64650 Helicobacter pylori 210 -11539954 7500954193 hp1044 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to gp:1132531 percent identity: 30.63;) (le:4947) (re:6059) (di:complement) HPAE000612 AE000612 g2314191 Helicobacter pylori 210 -11539954 7502853840 hp1044 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to gp:1132531 percent identity: 30.63;) (le:4947) (re:6059) (di:complement) HPAE000612 AE000612 g2314191 Helicobacter pylori 26695 85962 -11539954

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916317	18883	41039	1296	431

Description

6500736097 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1046 HP1046 Helicobacter pylori 210 -11539955 7000689826 conserved hypothetical protein hp1046 (db:pir2.dat) F64650 F64650 Helicobacter pylori 210 -11539955 7500958628 hp1046 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to egad:7067 percent identity: 32.58;) (le:8353) (re:8793) (di:complement) HPAE000612 AE000612 g2314193 Helicobacter pylori 210 -11539955 7502853841 hp1046 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to egad:7067 percent identity: 32.58;) (le:8353) (re:8793) (di:complement) HPAE000612 AE000612 g2314193 Helicobacter pylori 26695 85962 -11539955

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916327	18884	41040	375	124

Description

6500736098 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1049 HP1049 Helicobacter pylori 210 -11539956 7000689827 conserved hypothetical protein hp1049 (db:pir2.dat) A64651 A64651 Helicobacter pylori 210 -11539956 7500958629 hp1049 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 90 of 134 of the complete genome.) (nt:similar to egad:33081 percent identity: 39.68;) (le:11952) (re:12221) (di:complement) HPAE000612 AE000612 g2314196 Helicobacter pylori 210 -11539956 7502853842 hp1049 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 90 of 134 of the complete genome.) (nt:similar to egad:33081 percent identity: 39.68;) (le:11952) (re:12221) (di:complement) HPAE000612 AE000612 g2314196 Helicobacter pylori 26695 85962 -11539956

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916345	18885	41041	2484	827

Description

6500736099 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1061 HP1061 Helicobacter pylori 210 -11539957 7000689751 conserved hypothetical integral membrane protein hp1061 (cl:conserved hypothetical protein hi0188) (db:pir2.dat) E64652 E64652 Helicobacter pylori 210 -11539957 7500958558 hp1061 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:similar to egad:28835 percent identity: 34.96;) (le:7894) (re:8655) (di:direct) HPAE000613 AE000613 g2314204 Helicobacter pylori 210 -11539957 7502853843 hp1061 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:similar to egad:28835 percent identity: 34.96;) (le:7894) (re:8655) (di:direct) HPAE000613 AE000613 g2314204 Helicobacter pylori 26695 85962 -11539957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916347	18886	41042	915	304

Description

6500736100 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1066 HP1066 Helicobacter pylori 210 -11539958 7000689828 conserved hypothetical protein hp1066 (cl:hypothetical protein hp1066) (db:pir2.dat) B64653 B64653 Helicobacter pylori 210 -11539958 7500958630 hp1066 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 91 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 41.27;) (le:10993) (re:11595) (di:complement) HPAE000613 AE000613 g2314207 Helicobacter pylori 210 -11539958 7502853844 jhp0359 putative outer membrane protein (db:genpept) (de:helicobacter pylori, strain j99 section 32 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1066) (le:7096) (re:7698) (di:direct) AE001471 AE001471 g4154895 Helicobacter pylori J99 85963 -11539958 7502853845 hp1066 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 91 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 41.27;) (le:10993) (re:11595) (di:complement) HPAE000613 AE000613 g2314207 Helicobacter pylori 26695 85962 -11539958

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916348	18887	41043	606	201

Description

6500736101 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1075 HP1075 Helicobacter pylori 210 -11539959 7000689868 conserved hypothetical secreted protein hp1075 (db:pir2.dat) C64654 C64654 Helicobacter pylori 210 -11539959 7500958669 hp1075 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 92 of 134 of the complete genome.) (nt:similar to egad:18312 percent identity: 42.86;) (le:7843) (re:9159) (di:complement) HPAE000614 AE000614 g2314222 Helicobacter pylori 210 -11539959 7502853846 hp1075 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 92 of 134 of the complete genome.) (nt:similar to egad:18312 percent identity: 42.86;) (le:7843) (re:9159) (di:complement) HPAE000614 AE000614 g2314222 Helicobacter pylori 26695 85962 -11539959

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916353	18888	41044	450	149

Description

GTC ORF with score 277 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f18e5 (essaiiproject).) (nt:strong similarity to nadh dehydrogenase) (le:41353:41539:41790) (re:41440:41658:41911) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916361	18889	41045	942	313

Description

6500736102 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1080 HP1080 Helicobacter pylori 210 -11539960 7000689752 conserved hypothetical integral membrane protein hp1080 (db:pir2.dat) H64654 H64654 Helicobacter pylori 210 -11539960 7500958559 hp1080 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 93 of 134 of the complete genome.) (nt:similar to gp:1653086 percent identity: 44.00;) (le:86) (re:655) (di:complement) HPAE000615 AE000615 g2314231 Helicobacter pylori 210 -11539960 7502853847 hp1080 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 93 of 134 of the complete genome.) (nt:similar to gp:1653086 percent identity: 44.00;) (le:86) (re:655) (di:complement) HPAE000615 AE000615 g2314231 Helicobacter pylori 26695 85962 -11539960

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916369	18890	41046	774	257

Description

6500736103 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1098 HP1098 Helicobacter pylori 210 -11539961 7000689467 conserved hypothetical secreted protein hp1098 (cl:conserved hypothetical secreted protein hp1098) (db:pir2.dat) B64657 B64657 Helicobacter pylori 210 -11539961 7500955763 hp1098 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 94 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 27.01;) (le:5203) (re:6075) (di:complement) HPAE000616 AE000616 g2314247 Helicobacter pylori 210 -11539961 7502853848 hp1098 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 94 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 27.01;) (le:5203) (re:6075) (di:complement) HPAE000616 AE000616 g2314247 Helicobacter pylori 26695 85962 -11539961

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916383	18891	41047	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916384	18892	41048	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916385	18893	41049	201	66

Description

6500736104 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1117 HP1117 Helicobacter pylori 210 -11539962 7000689869 conserved hypothetical secreted protein hp1117 (db:pir2.dat) E64659 E64659 Helicobacter pylori 210 -11539962 7500958670 hp1117 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 96 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 32.34;) (le:4048) (re:4818) (di:complement) HPAE000618 AE000618 g2314269 Helicobacter pylori 210 -11539962 7502853849 hp1117 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 96 of 134 of the complete genome.) (nt:similar to gp:1786864 percent identity: 32.34;) (le:4048) (re:4818) (di:complement) HPAE000618 AE000618 g2314269 Helicobacter pylori 26695 85962 -11539962

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916386	18894	41050	234	77

Description

6500736105 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1149 HP1149 Helicobacter pylori 210 -11539963 7000689829 conserved hypothetical protein hp1149 (db:pir2.dat) E64663 E64663 Helicobacter pylori 210 -11539963 7500958631 hp1149 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 99 of 134 of the complete genome.) (nt:similar to egad:10765 percent identity: 24.68;) (le:2873) (re:3427) (di:complement) HPAE000621 AE000621 g2314304 Helicobacter pylori 210 -11539963 7502853850 hp1149 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 99 of 134 of the complete genome.) (nt:similar to egad:10765 percent identity: 24.68;) (le:2873) (re:3427) (di:complement) HPAE000621 AE000621 g2314304 Helicobacter pylori 26695 85962 -11539963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916387	18895	41051	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916390	18896	41052	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916391	18897	41053	339	112

Description

6500736106 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1160 HP1160 Helicobacter pylori 210 -11539964 7000689830 conserved hypothetical protein hp1160 (db:pir2.dat) H64664 H64664 Helicobacter pylori 210 -11539964 7500958632 hp1160 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:similar to egad:27821 percent identity: 34.65;) (le:76) (re:498) (di:complement) HPAE000622 AE000622 g2314318 Helicobacter pylori 210 -11539964 7502853851 hp1160 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:similar to egad:27821 percent identity: 34.65;) (le:76) (re:498) (di:complement) HPAE000622 AE000622 g2314318 Helicobacter pylori 26695 85962 -11539964

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916394	18898	41054	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916397	18899	41055	231	76

Description

6500736107 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1162 HP1162 Helicobacter pylori 210 -11539965 7000689753 conserved hypothetical integral membrane protein hp1162 (db:pir2.dat) B64665 B64665 Helicobacter pylori 210 -11539965 7500958560 hp1162 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 100 of 134 of the complete genome.) (nt:similar to egad:6152 percent identity: 27.62;) (le:1137) (re:1751) (di:complement) HPAE000622 AE000622 g2314320 Helicobacter pylori 210 -11539965 7502853852 hp1162 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 100 of 134 of the completegenome.) (nt:similar to egad:6152 percent identity: 27.62;) (le:1137) (re:1751) (di:complement) HPAE000622 AE000622 g2314320 Helicobacter pylori 26695 85962 -11539965

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916398	18900	41056	549	182

Description

6500736108 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1175 HP1175 Helicobacter pylori 210 -11539966 7000689754 conserved hypothetical integral membrane protein hp1175 (cl:conserved hypothetical protein hi0125) (db:pir2.dat) G64666 G64666 Helicobacter pylori 210 -11539966 7500958561 hp1175 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 101 of 134 of the complete genome.) (nt:similar to egad:44500 percent identity: 40.61;) (le:5390) (re:6697) (di:complement) HPAE000623 AE000623 g2314333 Helicobacter pylori 210 -11539966 7502853853 hp1175 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 101 of 134 of the completegenome.) (nt:similar to egad:44500 percent identity: 40.61;) (le:5390) (re:6697) (di:complement) HPAE000623 AE000623 g2314333 Helicobacter pylori 26695 85962 -11539966

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916403	18901	41057	567	188

Description

6500736109 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1182 HP1182 Helicobacter pylori 210 -11539967 7000689831 conserved hypothetical protein hp1182 (cl:hypothetical protein hp1182) (db:pir2.dat) F64667 F64667 Helicobacter pylori 210 -11539967 7500958633 hp1182 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 102 of 134 of the complete genome.) (nt:similar to egad:27870 percent identity: 34.55;) (le:1643) (re:2404) (di:direct) HPAE000624 AE000624 g2314342 Helicobacter pylori 210 -11539967 7502853854 hp1182 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 102 of 134 of the completegenome.) (nt:similar to egad:27870 percent identity: 34.55;) (le:1643) (re:2404) (di:direct) HPAE000624 AE000624 g2314342 Helicobacter pylori 26695 85962 -11539967

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916405	18902	41058	1338	445

Description

6500736110 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1184 HP1184 Helicobacter pylori 210 -11539968 7000689755 conserved hypothetical integral membrane protein hp1184 (db:pir2.dat) H64667 H64667 Helicobacter pylori 210 -11539968 7500958562 hp1184 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 102 of 134 of the complete genome.) (nt:similar to egad:44875 percent identity: 23.50;) (le:3590) (re:4969) (di:complement) HPAE000624 AE000624 g2314344 Helicobacter pylori 210 -11539968 7502853855 hp1184 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 102 of 134 of the completegenome.) (nt:similar to egad:44875 percent identity: 23.50;) (le:3590) (re:4969) (di:complement) HPAE000624 AE000624 g2314344 Helicobacter pylori 26695 85962 -11539968

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916424	18903	41059	1692	563

Description

6500736111 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1185 HP1185 Helicobacter pylori 210 -11539969 7000689506 chloramphenicol resistance protein homolog hp1185 (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) A64668 A64668 Helicobacter pylori 210 -11539969 7500955808 hp1185 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 102 of 134 of the complete genome.) (nt:similar to egad:28788 percent identity: 55.53;) (le:5130) (re:6305) (di:complement) HPAE000624 AE000624 g2314345 Helicobacter pylori 210 -11539969 7502853856 hp1185 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 102 of 134 of the completegenome.) (nt:similar to egad:28788 percent identity: 55.53;) (le:5130) (re:6305) (di:complement) HPAE000624 AE000624 g2314345 Helicobacter pylori 26695 85962 -11539969

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916425	18904	41060	300	99

Description

6500736112 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1214 HP1214 Helicobacter pylori 210 -11539970 7000689832 conserved hypothetical protein hp1214 (db:pir2.dat) F64671 F64671 Helicobacter pylori 210 -11539970 7500958634 hp1214 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:similar to egad:38966 percent identity: 21.46;) (le:3002) (re:3724) (di:complement) HPAE000627 AE000627 g2314376 Helicobacter pylori 210 -11539970 7502853857 hp1214 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:similar to egad:38966 percent identity: 21.46;) (le:3002) (re:3724) (di:complement) HPAE000627 AE000627 g2314376 Helicobacter pylori 26695 85962 -11539970

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916433	18905	41061	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916447	18906	41062	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916449	18907	41063	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916452	18908	41064	795	264

Description

6500736113 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1216 HP1216 Helicobacter pylori 210 -11539971 7000689870 conserved hypothetical secreted protein hp1216 (db:pir2.dat) H64671 H64671 Helicobacter pylori 210 -11539971 7500958671 hp1216 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:similar to egad:29496 percent identity: 31.91;) (le:3999) (re:5981) (di:complement) HPAE000627 AE000627 g2314377 Helicobacter pylori 210 -11539971 7502853858 hp1216 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:similar to egad:29496 percent identity: 31.91;) (le:3999) (re:5981) (di:complement) HPAE000627 AE000627 g2314377 Helicobacter pylori 26695 85962 -11539971

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916484	18909	41065	960	319

Description

6500736114 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1221 HP1221 Helicobacter pylori 210 -11539972 5500686486 hp1221 (sr:,campylobacter pylori) (de:hypothetical protein hp1221) (db:swissprot) YC21_HELPY P55984 HELICOBACTER PYLORI 210 -11539972 7000687392 conserved hypothetical protein hp1221 (cl:conserved hypothetical protein ybr002c) (db:pir2.dat) E64672 E64672 Helicobacter pylori 210 -11539972 7500921443 hp1221 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 105 of 134 of the complete genome.) (nt:similar to egad:29403 percent identity: 42.36;) (le:8779) (re:9483) (di:complement) HPAE000627 AE000627 g2314380 Helicobacter pylori 210 -11539972 7502853859 hp1221 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 105 of 134 of the completegenome.) (nt:similar to egad:29403 percent identity: 42.36;) (le:8779) (re:9483) (di:complement) HPAE000627 AE000627 g2314380 Helicobacter pylori 26695 85962 -11539972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916488	18910	41066	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916507	18911	41067	654	217

Description

6500736115 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1225 HP1225 Helicobacter pylori 210 -11539973 7000689756 conserved hypothetical integral membrane protein hp1225 (cl:hypothetical protein mj1523) (db:pir2.dat) A64673 A64673 Helicobacter pylori 210 -11539973 7500958563 hp1225 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to egad:44127 percent identity: 31.62;) (le:1126) (re:1518) (di:direct) HPAE000628 AE000628 g2314388 Helicobacter pylori 210 -11539973 7502853860 hp1225 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to egad:44127 percent identity: 31.62;) (le:1126) (re:1518) (di:direct) HPAE000628 AE000628 g2314388 Helicobacter pylori 26695 85962 -11539973

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916508	18912	41068	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916511	18913	41069	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916512	18914	41070	960	319

Description

6500736116 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1234 HP1234 Helicobacter pylori 210 -11539974 7000689757 conserved hypothetical integral membrane protein hp1234 (db:pir2.dat) B64674 B64674 Helicobacter pylori 210 -11539974 7500958564 hp1234 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to gp:1314584 percent identity: 29.03;) (le:8108) (re:9004) (di:direct) HPAE000628 AE000628 g2314395 Helicobacter pylori 210 -11539974 7502853861 hp1234 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to gp:1314584 percent identity: 29.03;) (le:8108) (re:9004) (di:direct) HPAE000628 AE000628 g2314395 Helicobacter pylori 26695 85962 -11539974

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916515	18915	41071	1023	340

Description

GTC ORF with score 319 to: (db:genpept-bct1) (de:streptomyces lividans amplifiable element aud4: putativetranscriptional regulator, putative ferredoxin, putative cytochromep450 oxidoreductase, and putative oxidoreductase genes, completecds; and unknown...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916528	18916	41072	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916541	18917	41073	1992	663

Description

6500736117 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1235 HP1235 Helicobacter pylori 210 -11539975 7000689758 conserved hypothetical integral membrane protein hp1235 (db:pir2.dat) C64674 C64674 Helicobacter pylori 210 -11539975 7500958565 hp1235 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 106 of 134 of the complete genome.) (nt:similar to gp:1788047 percent identity: 30.86;) (le:9008) (re:10255) (di:direct) HPAE000628 AE000628 g2314396 Helicobacter pylori 210 -11539975 7502853862 hp1235 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 106 of 134 of the completegenome.) (nt:similar to gp:1788047 percent identity: 30.86;) (le:9008) (re:10255) (di:direct) HPAE000628 AE000628 g2314396 Helicobacter pylori 26695 85962 -11539975

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916546	18918	41074	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916554	18919	41075	405	134

Description

6500736118 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1240 HP1240 Helicobacter pylori 210 -11539976 7000689833 conserved hypothetical protein hp1240 (db:pir2.dat) H64674 H64674 Helicobacter pylori 210 -11539976 7500958635 hp1240 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 107 of 134 of the complete genome.) (nt:similar to egad:10567 percent identity: 22.54;) (le:3372) (re:3944) (di:complement) HPAE000629 AE000629 g2314403 Helicobacter pylori 210 -11539976 7502853863 hp1240 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 107 of 134 of the completegenome.) (nt:similar to egad:10567 percent identity: 22.54;) (le:3372) (re:3944) (di:complement) HPAE000629 AE000629 g2314403 Helicobacter pylori 26695 85962 -11539976

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916563	18920	41076	1638	545

Description

6500736119 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1242 HP1242 Helicobacter pylori 210 -11539977 7000689834 conserved hypothetical protein hp1242 (cl:hypothetical protein hp1242) (db:pir2.dat) B64675 B64675 Helicobacter pylori 210 -11539977 7500958636 hp1242 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 107 of 134 of the complete genome.) (nt:similar to egad:30116 percent identity: 42.31;) (le:6609) (re:6839) (di:direct) HPAE000629 AE000629 g2314405 Helicobacter pylori 210 -11539977 7502853864 hp1242 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 107 of 134 of the completegenome.) (nt:similar to egad:30116 percent identity: 42.31;) (le:6609) (re:6839) (di:direct) HPAE000629 AE000629 g2314405 Helicobacter pylori 26695 85962 -11539977

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916574	18921	41077	489	162

Description

6500736120 conserved hypothetical mitochondrial protein 4 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1258 HP1258 Helicobacter pylori 210 -11539978 7500958637 conserved hypothetical protein hp1258 (db:pir2.dat) B64677 B64677 Helicobacter pylori 210 -11539978 7500958638 hp1258 conserved hypothetical mitochondrial protein 4 (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to pir:e22845 percent identity: 23.20;) (le:1850) (re:2314) (di:direct) HPAE000631 AE000631 g2314425 Helicobacter pylori 210 -11539978 7502853865 hp1258 conserved hypothetical mitochondrial protein 4 (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to pir:e22845 percent identity: 23.20;) (le:1850) (re:2314) (di:direct) HPAE000631 AE000631 g2314425 Helicobacter pylori 26695 85962 -11539978

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916578	18922	41078	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916579	18923	41079	564	187

Description

6500736121 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1259 HP1259 Helicobacter pylori 210 -11539979 7000689835 conserved hypothetical protein hp1259 (db:pir2.dat) C64677 C64677 Helicobacter pylori 210 -11539979 7500958639 hp1259 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 109 of 134 of the complete genome.) (nt:similar to gp:1787364 percent identity: 44.58;) (le:2384) (re:3001) (di:direct) HPAE000631 AE000631 g2314426 Helicobacter pylori 210 -11539979 7502853866 hp1259 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 109 of 134 of the completegenome.) (nt:similar to gp:1787364 percent identity: 44.58;) (le:2384) (re:3001) (di:direct) HPAE000631 AE000631 g2314426 Helicobacter pylori 26695 85962 -11539979

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916580	18924	41080	2019	673

Description

6500736122 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1284 HP1284 Helicobacter pylori 210 -11539980 7000689836 conserved hypothetical protein hp1284 (db:pir2.dat) D64680 D64680 Helicobacter pylori 210 -11539980 7500958640 hp1284 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 110 of 134 of the complete genome.) (nt:similar to egad:29149 percent identity: 36.78;) (le:8919) (re:9959) (di:complement) HPAE000632 AE000632 g2314449 Helicobacter pylori 210 -11539980 7502853867 hp1284 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 110 of 134 of the completegenome.) (nt:similar to egad:29149 percent identity: 36.78;) (le:8919) (re:9959) (di:complement) HPAE000632 AE000632 g2314449 Helicobacter pylori 26695 85962 -11539980

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916593	18925	41081	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916594	18926	41082	576	191

Description

6500736123 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1285 HP1285 Helicobacter pylori 210 -11539981 7000689871 conserved hypothetical secreted protein hp1285 (db:pir2.dat) E64680 E64680 Helicobacter pylori 210 -11539981 7500958672 hp1285 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:17331 percent identity: 38.05;) (le:65) (re:757) (di:complement) HPAE000633 AE000633 g2314453 Helicobacter pylori 210 -11539981 7502853868 hp1285 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:17331 percent identity: 38.05;) (le:65) (re:757) (di:complement) HPAE000633 AE000633 g2314453 Helicobacter pylori 26695 85962 -11539981

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916602	18927	41083	411	137

Description

6500736124 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1286 HP1286 Helicobacter pylori 210 -11539982 7000689872 conserved hypothetical secreted protein hp1286 (db:pir2.dat) F64680 F64680 Helicobacter pylori 210 -11539982 7500958673 hp1286 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to egad:7494 percent identity: 37.50;) (le:927) (re:1475) (di:direct) HPAE000633 AE000633 g2314454 Helicobacter pylori 210 -11539982 7502853869 hp1286 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to egad:7494 percent identity: 37.50;) (le:927) (re:1475) (di:direct) HPAE000633 AE000633 g2314454 Helicobacter pylori 26695 85962 -11539982

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916609	18928	41084	2112	703

Description

6500736125 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1291 HP1291 Helicobacter pylori 210 -11539983 7000689837 conserved hypothetical protein hp1291 (db:pir2.dat) C64681 C64681 Helicobacter pylori 210 -11539983 7500958641 hp1291 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 111 of 134 of the complete genome.) (nt:similar to sp:p30636 percent identity: 26.35;) (le:4459) (re:5073) (di:direct) HPAE000633 AE000633 g2314457 Helicobacter pylori 210 -11539983 7502853870 hp1291 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 111 of 134 of the completegenome.) (nt:similar to sp:p30636 percent identity: 26.35;) (le:4459) (re:5073) (di:direct) HPAE000633 AE000633 g2314457 Helicobacter pylori 26695 85962 -11539983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916610	18929	41085	834	277

Description

6500736126 conserved hypothetical atp-binding protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1321 HP1321 Helicobacter pylori 210 -11539984 7000689726 conserved hypothetical atp-binding protein hp1321 (db:pir2.dat) A64685 A64685 Helicobacter pylori 210 -11539984 7500958533 hp1321 conserved hypothetical atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:similar to egad:44148 percent identity: 30.81;) (le:113) (re:1246) (di:direct) HPAE000634 AE000634 g2314490 Helicobacter pylori 210 -11539984 7502853871 hp1321 conserved hypothetical atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:similar to egad:44148 percent identity: 30.81;) (le:113) (re:1246) (di:direct) HPAE000634 AE000634 g2314490 Helicobacter pylori 26695 85962 -11539984

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916611	18930	41086	369	122

Description

6500736127 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1330 HP1330 Helicobacter pylori 210 -11539985 7500922080 hp1330 (sr:,campylobacter pylori) (de:hypothetical protein hp1330) (db:swissprot) YD30_HELPY O25888 HELICOBACTER PYLORI 210 -11539985 7000689472 branched-chain amino acid transport protein azld homolog hp1330 (cl:branched-chain amino acid transport protein azld) (db:pir2.dat) B64686 B64686 Helicobacter pylori 210 -11539985 7500922082 hp1330 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:similar to egad:28717 percent identity: 41.75;) (le:10259) (re:10606) (di:complement) HPAE000634 AE000634 g2314495 Helicobacter pylori 210 -11539985 7502853872 hp1330 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:similar to egad:28717 percent identity: 41.75;) (le:10259) (re:10606) (di:complement) HPAE000634 AE000634 g2314495 Helicobacter pylori 26695 85962 -11539985

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916617	18931	41087	216	71

Description

6500736128 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1331 HP1331 Helicobacter pylori 210 -11539986 7500922083 hp1331 (sr:,campylobacter pylori) (de:hypothetical protein hp1331) (db:swissprot) YD31_HELPY O25889 HELICOBACTER PYLORI 210 -11539986 7000689759 conserved hypothetical integral membrane protein hp1331 (cl:hypothetical protein b2682) (db:pir2.dat) C64686 C64686 Helicobacter pylori 210 -11539986 7500922085 hp1331 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 112 of 134 of the complete genome.) (nt:similar to egad:28724 percent identity: 33.63;) (le:10600) (re:11286) (di:complement) HPAE000634 AE000634 g2314496 Helicobacter pylori 210 -11539986 7502853873 hp1331 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 112 of 134 of the completegenome.) (nt:similar to egad:28724 percent identity: 33.63;) (le:10600) (re:11286) (di:complement) HPAE000634 AE000634 g2314496 Helicobacter pylori 26695 85962 -11539986

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916633	18932	41088	705	235

Description

6500736129 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1335 HP1335 Helicobacter pylori 210 -11539987 7500893415 trmu:hp1335 (sr:,campylobacter pylori) (ec:2.1.1.61) (de:(ec 2.1.1.61)) (db:swissprot) TRMU_HELPY O25893 HELICOBACTER PYLORI 210 -11539987 7000689838 conserved hypothetical protein hp1335 (cl:probable membrane protein ydl033c) (db:pir2.dat) G64686 G64686 Helicobacter pylori 210 -11539987 7500893417 hp1335 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:31503 percent identity: 33.91;) (le:2188) (re:3270) (di:complement) HPAE000635 AE000635 g2314503 Helicobacter pylori 210 -11539987 7502853874 hp1335 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:31503 percent identity: 33.91;) (le:2188) (re:3270) (di:complement) HPAE000635 AE000635 g2314503 Helicobacter pylori 26695 85962 -11539987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916646	18933	41089	4965	1654

Description

6500736130 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1337 HP1337 Helicobacter pylori 210 -11539988 7000689839 conserved hypothetical protein hp1337 (db:pir2.dat) A64687 A64687 Helicobacter pylori 210 -11539988 7500958642 hp1337 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:45797 percent identity: 27.22;) (le:4113) (re:4637) (di:complement) HPAE000635 AE000635 g2314504 Helicobacter pylori 210 -11539988 7502853875 hp1337 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:45797 percent identity: 27.22;) (le:4113) (re:4637) (di:complement) HPAE000635 AE000635 g2314504 Helicobacter pylori 26695 85962 -11539988

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916657	18934	41090	501	166

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916665	18935	41091	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916666	18936	41092	756	251

Description

GTC ORF with score 143 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916678	18937	41093	561	186

Description

6500736131 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1338 HP1338 Helicobacter pylori 210 -11539989 7000689840 conserved hypothetical protein hp1338 (cl:conserved hypothetical protein mj0080) (db:pir2.dat) B64687 B64687 Helicobacter pylori 210 -11539989 7500958643 hp1338 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:44717 percent identity: 36.22;) (le:4621) (re:5067) (di:complement) HPAE000635 AE000635 g2314505 Helicobacter pylori 210 -11539989 7502853876 hp1338 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:44717 percent identity: 36.22;) (le:4621) (re:5067) (di:complement) HPAE000635 AE000635 g2314505 Helicobacter pylori 26695 85962 -11539989

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916691	18938	41094	792	263

Description

6500736132 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1343 HP1343 Helicobacter pylori 210 -11539990 7000689760 conserved hypothetical integral membrane protein hp1343 (cl:conserved hypothetical protein hi0056) (db:pir2.dat) G64687 G64687 Helicobacter pylori 210 -11539990 7500958566 hp1343 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 113 of 134 of the complete genome.) (nt:similar to egad:27891 percent identity: 49.11;) (le:9462) (re:10190) (di:complement) HPAE000635 AE000635 g2314509 Helicobacter pylori 210 -11539990 7502853877 hp1343 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 113 of 134 of the completegenome.) (nt:similar to egad:27891 percent identity: 49.11;) (le:9462) (re:10190) (di:complement) HPAE000635 AE000635 g2314509 Helicobacter pylori 26695 85962 -11539990

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916693	18939	41095	276	91

Description

6500736133 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1363 HP1363 Helicobacter pylori 210 -11539991 5500686511 hp1363 (sr:,campylobacter pylori) (de:hypothetical protein hp1363) (db:swissprot) YD63_HELPY P56176 HELICOBACTER PYLORI 210 -11539991 7000687509 conserved hypothetical integral membrane protein hp1363 (db:pir2.dat) C64690 C64690 Helicobacter pylori 210 -11539991 7500922102 hp1363 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 114 of 134 of the complete genome.) (nt:similar to egad:21908 percent identity: 33.07;) (le:17287) (re:18687) (di:complement) HPAE000636 AE000636 g2314529 Helicobacter pylori 210 -11539991 7502853878 hp1363 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 114 of 134 of the completegenome.) (nt:similar to egad:21908 percent identity: 33.07;) (le:17287) (re:18687) (di:complement) HPAE000636 AE000636 g2314529 Helicobacter pylori 26695 85962 -11539991

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916705	18940	41096	672	223

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916709	18941	41097	369	122

Description

6500736134 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1394 HP1394 Helicobacter pylori 210 -11539992 7000689841 conserved hypothetical protein hp1394 (db:pir2.dat) B64694 B64694 Helicobacter pylori 210 -11539992 7500958644 hp1394 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 117 of 134 of the complete genome.) (nt:similar to egad:43538 percent identity: 33.61;) (le:4287) (re:5141) (di:complement) HPAE000639 AE000639 g2314563 Helicobacter pylori 210 -11539992 7502853879 hp1394 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 117 of 134 of the completegenome.) (nt:similar to egad:43538 percent identity: 33.61;) (le:4287) (re:5141) (di:complement) HPAE000639 AE000639 g2314563 Helicobacter pylori 26695 85962 -11539992

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916710	18942	41098	906	301

Description

6500736135 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1401 HP1401 Helicobacter pylori 210 -11539993 7000689842 conserved hypothetical protein hp1401 (db:pir2.dat) A64695 A64695 Helicobacter pylori 210 -11539993 7500958645 hp1401 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 118 of 134 of the complete genome.) (nt:similar to egad:43824 percent identity: 27.47;) (le:2916) (re:3623) (di:complement) HPAE000640 AE000640 g2314574 Helicobacter pylori 210 -11539993 7502853880 hp1401 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 118 of 134 of the completegenome.) (nt:similar to egad:43824 percent identity: 27.47;) (le:2916) (re:3623) (di:complement) HPAE000640 AE000640 g2314574 Helicobacter pylori 26695 85962 -11539993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916716	18943	41099	420	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916758	18944	41100	2118	705

Description

6500736136 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1407 HP1407 Helicobacter pylori 210 -11539994 7000689761 conserved hypothetical integral membrane protein hp1407 (db:pir2.dat) G64695 G64695 Helicobacter pylori 210 -11539994 7500958567 hp1407 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 118 of 134 of the complete genome.) (nt:similar to egad:28919 percent identity: 22.36;) (le:10835) (re:11713) (di:direct) HPAE000640 AE000640 g2314579 Helicobacter pylori 210 -11539994 7502853881 hp1407 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 118 of 134 of the completegenome.) (nt:similar to egad:28919 percent identity: 22.36;) (le:10835) (re:11713) (di:direct) HPAE000640 AE000640 g2314579 Helicobacter pylori 26695 85962 -11539994

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916764	18945	41101	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916769	18946	41102	885	294

Description

6500736137 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1413 HP1413 Helicobacter pylori 210 -11539995 7000689843 conserved hypothetical protein hp1413 (cl:hypothetical protein ykvm) (db:pir2.dat) E64696 E64696 Helicobacter pylori 210 -11539995 7500955894 hp1413 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to egad:28298 percent identity: 41.60;) (le:94) (re:540) (di:complement) HPAE000642 AE000642 g2314588 Helicobacter pylori 210 -11539995 7502853882 hp1413 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to egad:28298 percent identity: 41.60;) (le:94) (re:540) (di:complement) HPAE000642 AE000642 g2314588 Helicobacter pylori 26695 85962 -11539995

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916813	18947	41103	564	187

Description

6500736138 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1414 HP1414 Helicobacter pylori 210 -11539996 7000689844 ybeb protein homolog (cl:escherichia coli ybeb protein) (db:pir2.dat) F64696 F64696 Helicobacter pylori 210 -11539996 7500958646 hp1414 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to egad:27850 percent identity: 27.37;) (le:600) (re:941) (di:direct) HPAE000642 AE000642 g2314589 Helicobacter pylori 210 -11539996 7502853883 hp1414 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to egad:27850 percent identity: 27.37;) (le:600) (re:941) (di:direct) HPAE000642 AE000642 g2314589 Helicobacter pylori 26695 85962 -11539996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916815	18948	41104	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916816	18949	41105	1356	451

Description

6500736139 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1423 HP1423 Helicobacter pylori 210 -11539997 7000689845 conserved hypothetical protein hp1423 (db:pir2.dat) G64697 G64697 Helicobacter pylori 210 -11539997 7500958648 hp1423 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 120 of 134 of the complete genome.) (nt:similar to egad:20009 percent identity: 40.28;) (le:10773) (re:11027) (di:complement) HPAE000642 AE000642 g2314597 Helicobacter pylori 210 -11539997 7502853884 hp1423 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 120 of 134 of the completegenome.) (nt:similar to egad:20009 percent identity: 40.28;) (le:10773) (re:11027) (di:complement) HPAE000642 AE000642 g2314597 Helicobacter pylori 26695 85962 -11539997

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916827	18950	41106	573	191

Description

6500736140 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1426 HP1426 Helicobacter pylori 210 -11539998 7000689846 conserved hypothetical protein hp1426 (db:pir2.dat) B64698 B64698 Helicobacter pylori 210 -11539998 7500958649 hp1426 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:similar to gp:1405463 percent identity: 40.00;) (le:1113) (re:1655) (di:complement) HPAE000643 AE000643 g2314599 Helicobacter pylori 210 -11539998 7502853885 hp1426 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:similar to gp:1405463 percent identity: 40.00;) (le:1113) (re:1655) (di:complement) HPAE000643 AE000643 g2314599 Helicobacter pylori 26695 85962 -11539998

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916838	18951	41107	414	137

Description

6500736141 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1428 HP1428 Helicobacter pylori 210 -11539999 7500922677 hp1428 (sr:,campylobacter pylori) (de:hypothetical protein hp1428) (db:swissprot) YE28_HELPY O25970 HELICOBACTER PYLORI 210 -11539999 7000689847 conserved hypothetical protein hp1428 (cl:conserved hypothetical protein hi0365) (db:pir2.dat) D64698 D64698 Helicobacter pylori 210 -11539999 7500922679 hp1428 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:similar to egad:39884 percent identity: 37.76;) (le:2384) (re:3457) (di:complement) HPAE000643 AE000643 g2314600 Helicobacter pylori 210 -11539999 7502853886 hp1428 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:similar to egad:39884 percent identity: 37.76;) (le:2384) (re:3457) (di:complement) HPAE000643 AE000643 g2314600 Helicobacter pylori 26695 85962 -11539999

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916861	18952	41108	462	153

Description

6500736142 conserved hypothetical atp-binding protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1430 HP1430 Helicobacter pylori 210 -11540000 5500686554 hp1430 (sr:,campylobacter pylori) (de:hypothetical protein hp1430) (db:swissprot) YE30_HELPY P56185 HELICOBACTER PYLORI 210 -11540000 7000687578 conserved hypothetical atp-binding protein hp1430 (db:pir2.dat) F64698 F64698 Helicobacter pylori 210 -11540000 7500922684 hp1430 conserved hypothetical atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 121 of 134 of the complete genome.) (nt:similar to gp:1377831 percent identity: 38.11;) (le:4427) (re:6496) (di:complement) HPAE000643 AE000643 g2314602 Helicobacter pylori 210 -11540000 7502853887 hp1430 conserved hypothetical atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 121 of 134 of the completegenome.) (nt:similar to gp:1377831 percent identity: 38.11;) (le:4427) (re:6496) (di:complement) HPAE000643 AE000643 g2314602 Helicobacter pylori 26695 85962 -11540000

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916862	18953	41109	522	173

Description

6500736143 conserved hypothetical lipoprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1438 HP1438 Helicobacter pylori 210 -11540001 7000689768 conserved hypothetical lipoprotein hp1438 (db:pir2.dat) F64699 F64699 Helicobacter pylori 210 -11540001 7500958573 hp1438 conserved hypothetical lipoprotein (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to egad:42146 percent identity: 32.00;) (le:3128) (re:4144) (di:direct) HPAE000644 AE000644 g2314612 Helicobacter pylori 210 -11540001 7502853888 hp1438 conserved hypothetical lipoprotein (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to egad:42146 percent identity: 32.00;) (le:3128) (re:4144) (di:direct) HPAE000644 AE000644 g2314612 Helicobacter pylori 26695 85962 -11540001

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916863	18954	41110	531	176

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916901	18955	41111	318	105

Description

6500736144 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1443 HP1443 Helicobacter pylori 210 -11540002 7000689848 conserved hypothetical protein hp1443 (db:pir2.dat) C64700 C64700 Helicobacter pylori 210 -11540002 7500958650 hp1443 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 122 of 134 of the complete genome.) (nt:similar to egad:19904 percent identity: 37.86;) (le:8749) (re:9555) (di:direct) HPAE000644 AE000644 g2314615 Helicobacter pylori 210 -11540002 7502853889 hp1443 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 122 of 134 of the completegenome.) (nt:similar to egad:19904 percent identity: 37.86;) (le:8749) (re:9555) (di:direct) HPAE000644 AE000644 g2314615 Helicobacter pylori 26695 85962 -11540002

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916921	18956	41112	2652	883

Description

6500736145 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1449 HP1449 Helicobacter pylori 210 -11540003 7000689849 conserved hypothetical protein hp1449 (cl:conserved hypothetical protein hi1000) (db:pir2.dat) A64701 A64701 Helicobacter pylori 210 -11540003 7500958651 hp1449 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:similar to egad:23212 percent identity: 38.98;) (le:632) (re:985) (di:direct) HPAE000645 AE000645 g2314625 Helicobacter pylori 210 -11540003 7502853890 hp1449 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:similar to egad:23212 percent identity: 38.98;) (le:632) (re:985) (di:direct) HPAE000645 AE000645 g2314625 Helicobacter pylori 26695 85962 -11540003

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916926	18957	41113	486	162

Description

6500736146 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1453 HP1453 Helicobacter pylori 210 -11540004 7000689850 conserved hypothetical protein hp1453 (db:pir2.dat) E64701 E64701 Helicobacter pylori 210 -11540004 7500958652 hp1453 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 123 of 134 of the complete genome.) (nt:similar to gp:1800185 percent identity: 26.80;) (le:4977) (re:7217) (di:direct) HPAE000645 AE000645 g2314628 Helicobacter pylori 210 -11540004 7502853891 hp1453 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 123 of 134 of the completegenome.) (nt:similar to gp:1800185 percent identity: 26.80;) (le:4977) (re:7217) (di:direct) HPAE000645 AE000645 g2314628 Helicobacter pylori 26695 85962 -11540004

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916933	18958	41114	441	146

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916938	18959	41115	1425	474

Description

6500736147 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1459 HP1459 Helicobacter pylori 210 -11540005 5500686559 hp1459 (sr:,campylobacter pylori) (de:hypothetical protein hp1459) (db:swissprot) YE59_HELPY P55986 HELICOBACTER PYLORI 210 -11540005 7000687579 conserved hypothetical protein hp1459 (db:pir2.dat) C64702 C64702 Helicobacter pylori 210 -11540005 7500922716 hp1459 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:similar to egad:14622 percent identity: 30.09;) (le:584) (re:1372) (di:complement) HPAE000646 AE000646 g2314637 Helicobacter pylori 210 -11540005 7502853892 hp1459 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:similar to egad:14622 percent identity: 30.09;) (le:584) (re:1372) (di:complement) HPAE000646 AE000646 g2314637 Helicobacter pylori 26695 85962 -11540005

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916951	18960	41116	1740	580

Description

GTC ORF with score 782 to: (or:Cochliobolus carbonum) (db:genpept-pln2) (de:cochliobolus carbonum mixed-linked glucanase precursor (mlg1) gene,complete cds.) (nt:family 16 glycosyl hydrolases;) (le:250:518:808:1404) (re:460:743:1348:1445) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916958	18961	41117	486	161

Description

6500736148 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1464 HP1464 Helicobacter pylori 210 -11540006 7000689873 conserved hypothetical secreted protein hp1464 (db:pir2.dat) H64702 H64702 Helicobacter pylori 210 -11540006 7500958674 hp1464 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:similar to gp:1001514 percent identity: 27.38;) (le:7652) (re:8467) (di:complement) HPAE000646 AE000646 g2314641 Helicobacter pylori 210 -11540006 7502853893 hp1464 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:similar to gp:1001514 percent identity: 27.38;) (le:7652) (re:8467) (di:complement) HPAE000646 AE000646 g2314641 Helicobacter pylori 26695 85962 -11540006

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916962	18962	41118	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916968	18963	41119	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916972	18964	41120	204	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916973	18965	41121	435	144

Description

GTC ORF with score 351 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c1a4 left hand region 1-26184 bporiginates from chimeric cosmid.) (nt:spbc1a4.07c, len:436aa; similarity: to sof1_yeast,) (le:16860:17965) (re:17908:18226)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916974	18966	41122	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916987	18967	41123	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916992	18968	41124	1485	494

Description

6500736149 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1466 HP1466 Helicobacter pylori 210 -11540007 7000689762 conserved hypothetical integral membrane protein hp1466 (db:pir2.dat) B64703 B64703 Helicobacter pylori 210 -11540007 7500958568 hp1466 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 124 of 134 of the complete genome.) (nt:similar to egad:28097 percent identity: 30.88;) (le:9237) (re:10370) (di:complement) HPAE000646 AE000646 g2314643 Helicobacter pylori 210 -11540007 7502853894 hp1466 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 124 of 134 of the completegenome.) (nt:similar to egad:28097 percent identity: 30.88;) (le:9237) (re:10370) (di:complement) HPAE000646 AE000646 g2314643 Helicobacter pylori 26695 85962 -11540007

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501916998	18969	41125	1947	648

Description

6500736150 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1484 HP1484 Helicobacter pylori 210 -11540008 7000689471 conserved hypothetical integral membrane protein hp1484 (cl:conserved hypothetical integral membrane protein hp1484) (db:pir2.dat) D64705 D64705 Helicobacter pylori 210 -11540008 7500955767 hp1484 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:35767 percent identity: 41.22;) (le:19322) (re:19768) (di:complement) HPAE000647 AE000647 g2314656 Helicobacter pylori 210 -11540008 7502853895 hp1484 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:35767 percent identity: 41.22;) (le:19322) (re:19768) (di:complement) HPAE000647 AE000647 g2314656 Helicobacter pylori 26695 85962 -11540008

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917006	18970	41126	654	217

Description

6500736151 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1486 HP1486 Helicobacter pylori 210 -11540009 7000689763 conserved hypothetical integral membrane protein hp1486 (db:pir2.dat) F64705 F64705 Helicobacter pylori 210 -11540009 7500958569 hp1486 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:18138 percent identity: 23.82;) (le:20338) (re:21468) (di:complement) HPAE000647 AE000647 g2314658 Helicobacter pylori 210 -11540009 7502853896 hp1486 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:18138 percent identity: 23.82;) (le:20338) (re:21468) (di:complement) HPAE000647 AE000647 g2314658 Helicobacter pylori 26695 85962 -11540009

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917009	18971	41127	327	108

Description

6500736152 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1487 HP1487 Helicobacter pylori 210 -11540010 7000689764 conserved hypothetical integral membrane protein hp1487 (db:pir2.dat) G64705 G64705 Helicobacter pylori 210 -11540010 7500958570 hp1487 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:18897 percent identity: 30.68;) (le:21465) (re:22562) (di:complement) HPAE000647 AE000647 g2314659 Helicobacter pylori 210 -11540010 7502853897 hp1487 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:18897 percent identity: 30.68;) (le:21465) (re:22562) (di:complement) HPAE000647 AE000647 g2314659 Helicobacter pylori 26695 85962 -11540010

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917010	18972	41128	231	76

Description

6500736153 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1488 HP1488 Helicobacter pylori 210 -11540011 5500684868 hp1488 (sr:,campylobacter pylori) (de:36 kd antigen) (db:swissprot) AN36_HELPY P94851 HELICOBACTER PYLORI 210 -11540011 7000684579 conserved hypothetical secreted protein hp1488 (db:pir2.dat) H64705 H64705 Helicobacter pylori 210 -11540011 7500876905 hp1488 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to egad:6141 percent identity: 29.77;) (le:22574) (re:23563) (di:complement) HPAE000647 AE000647 g2314660 Helicobacter pylori 210 -11540011 7502853898 hp1488 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to egad:6141 percent identity: 29.77;) (le:22574) (re:23563) (di:complement) HPAE000647 AE000647 g2314660 Helicobacter pylori 26695 85962 -11540011

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917011	18973	41129	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917018	18974	41130	807	268

Description

6500736154 hemolysin (gtcfc:12.10:12.11) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1490 HP1490 Helicobacter pylori 210 -11540012 7000689490 hemolysin (cl:hypothetical protein hi0107) (db:pir2.dat) B64706 B64706 Helicobacter pylori 210 -11540012 7500955793 hp1490 hemolysin (db:genpept-bct1) (de:helicobacter pylori section 125 of 134 of the complete genome.) (nt:similar to gp:1653594 percent identity: 39.16;) (le:25104) (re:26453) (di:complement) HPAE000647 AE000647 g2314662 Helicobacter pylori 210 -11540012 7502853899 hp1490 hemolysin (db:genpept) (de:helicobacter pylori 26695 section 125 of 134 of the completegenome.) (nt:similar to gp:1653594 percent identity: 39.16;) (le:25104) (re:26453) (di:complement) HPAE000647 AE000647 g2314662 Helicobacter pylori 26695 85962 -11540012

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917060	18975	41131	594	197

Description

7500955770 conserved hypothetical nifu-like protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1492 HP1492 Helicobacter pylori 210 -11540013 7000689473 conserved hypothetical nifu-like protein hp1492 (cl:conserved hypothetical nifu-like protein hp1492) (db:pir2.dat) D64706 D64706 Helicobacter pylori 210 -11540013 7500955769 hp1492 conserved hypothetical nifu-like protein (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to gp:1653754 percent identity: 48.21;) (le:1822) (re:2091) (di:direct) HPAE000648 AE000648 g2314672 Helicobacter pylori 210 -11540013 7502853900 jhp1385 putative (db:genpept) (de:helicobacter pylori, strain j99 section 122 of 132 of the completegenome.) (nt:similar to h. pylori 26695 gene hp1492) (le:1838) (re:2107) (di:direct) AE001561 AE001561 g4156005 Helicobacter pylori J99 85963 -11540013 6500736155 hp1492 conserved hypothetical nifu-like protein (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to gp:1653754 percent identity: 48.21;) (le:1822) (re:2091) (di:direct) HPAE000648 AE000648 g2314672 Helicobacter pylori 26695 85962 -11540013

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917064	18976	41132	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917067	18977	41133	183	60

Description

6500736156 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1504 HP1504 Helicobacter pylori 210 -11540014 7000689851 conserved hypothetical protein hp1504 (db:pir2.dat) H64707 H64707 Helicobacter pylori 210 -11540014 7500958653 hp1504 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 126 of 134 of the complete genome.) (nt:similar to egad:23049 percent identity: 23.87;) (le:12800) (re:13516) (di:complement) HPAE000648 AE000648 g2314678 Helicobacter pylori 210 -11540014 7502853901 hp1504 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 126 of 134 of the completegenome.) (nt:similar to egad:23049 percent identity: 23.87;) (le:12800) (re:13516) (di:complement) HPAE000648 AE000648 g2314678 Helicobacter pylori 26695 85962 -11540014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917069	18978	41134	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917070	18979	41135	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917076	18980	41136	1281	426

Description

6500736157 conserved hypothetical atp-binding protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1507 HP1507 Helicobacter pylori 210 -11540015 7000689727 conserved hypothetical atp-binding protein hp1507 (db:pir2.dat) C64708 C64708 Helicobacter pylori 210 -11540015 7500958534 hp1507 conserved hypothetical atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:similar to egad:48771 percent identity: 51.60;) (le:94) (re:1251) (di:direct) HPAE000649 AE000649 g2314688 Helicobacter pylori 210 -11540015 7502853902 hp1507 conserved hypothetical atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:similar to egad:48771 percent identity: 51.60;) (le:94) (re:1251) (di:direct) HPAE000649 AE000649 g2314688 Helicobacter pylori 26695 85962 -11540015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917093	18981	41137	426	141

Description

6500736158 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1509 HP1509 Helicobacter pylori 210 -11540016 7000689765 conserved hypothetical integral membrane protein hp1509 (cl:escherichia coli ygih protein) (db:pir2.dat) E64708 E64708 Helicobacter pylori 210 -11540016 7500955830 hp1509 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:similar to egad:31455 percent identity: 34.30;) (le:2617) (re:3405) (di:direct) HPAE000649 AE000649 g2314690 Helicobacter pylori 210 -11540016 7502853903 hp1509 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:similar to egad:31455 percent identity: 34.30;) (le:2617) (re:3405) (di:direct) HPAE000649 AE000649 g2314690 Helicobacter pylori 26695 85962 -11540016

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917099	18982	41138	597	198

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917101	18983	41139	252	83

Description

6500736159 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1510 HP1510 Helicobacter pylori 210 -11540017 7000689852 conserved hypothetical protein hp1510 (db:pir2.dat) F64708 F64708 Helicobacter pylori 210 -11540017 7500958654 hp1510 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 127 of 134 of the complete genome.) (nt:similar to egad:36072 percent identity: 30.65;) (le:3402) (re:3755) (di:direct) HPAE000649 AE000649 g2314691 Helicobacter pylori 210 -11540017 7502853904 hp1510 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 127 of 134 of the completegenome.) (nt:similar to egad:36072 percent identity: 30.65;) (le:3402) (re:3755) (di:direct) HPAE000649 AE000649 g2314691 Helicobacter pylori 26695 85962 -11540017

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917102	18984	41140	240	79

Description

6500736160 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1533 HP1533 Helicobacter pylori 210 -11540018 7000689853 conserved hypothetical protein hp1533 (db:pir2.dat) E64711 E64711 Helicobacter pylori 210 -11540018 7500958655 hp1533 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 129 of 134 of the complete genome.) (nt:similar to egad:23693 percent identity: 25.40;) (le:5925) (re:6620) (di:direct) HPAE000651 AE000651 g2314712 Helicobacter pylori 210 -11540018 7502853905 hp1533 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 129 of 134 of the completegenome.) (nt:similar to egad:23693 percent identity: 25.40;) (le:5925) (re:6620) (di:direct) HPAE000651 AE000651 g2314712 Helicobacter pylori 26695 85962 -11540018

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917103	18985	41141	192	63

Description

6500736161 conserved hypothetical integral membrane protein:conserved hypothetical integral membraneprotein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1548 HP1548 Helicobacter pylori 210 -11540019 7000689766 conserved hypothetical integral membrane protein hp1548 (db:pir2.dat) D64713 D64713 Helicobacter pylori 210 -11540019 7500958571 hp1548 conserved hypothetical integral membrane (db:genpept-bct1) (de:helicobacter pylori section 130 of 134 of the complete genome.) (nt:similar to egad:34218 percent identity: 30.59;) (le:12160) (re:12498) (di:complement) HPAE000652 AE000652 g2314728 Helicobacter pylori 210 -11540019 7502853906 hp1548 conserved hypothetical integral membrane (db:genpept) (de:helicobacter pylori 26695 section 130 of 134 of the completegenome.) (nt:similar to egad:34218 percent identity: 30.59;) (le:12160) (re:12498) (di:complement) HPAE000652 AE000652 g2314728 Helicobacter pylori 26695 85962 -11540019

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917110	18986	41142	528	175

Description

6500736162 conserved hypothetical secreted protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1551 HP1551 Helicobacter pylori 210 -11540020 7000689462 conserved hypothetical secreted protein hp1551 (cl:yajc protein) (db:pir2.dat) G64713 G64713 Helicobacter pylori 210 -11540020 7500955735 hp1551 conserved hypothetical secreted protein (db:genpept-bct1) (de:helicobacter pylori section 131 of 134 of the complete genome.) (nt:similar to egad:20690 percent identity: 42.68;) (le:62) (re:445) (di:complement) HPAE000653 AE000653 g2314734 Helicobacter pylori 210 -11540020 7502853907 hp1551 conserved hypothetical secreted protein (db:genpept) (de:helicobacter pylori 26695 section 131 of 134 of the completegenome.) (nt:similar to egad:20690 percent identity: 42.68;) (le:62) (re:445) (di:complement) HPAE000653 AE000653 g2314734 Helicobacter pylori 26695 85962 -11540020

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917112	18987	41143	219	72

Description

6500736163 conserved hypothetical atp-binding protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1567 HP1567 Helicobacter pylori 210 -11540021 7000689728 conserved hypothetical atp-binding protein hp1567 (cl:translation elongation factor tu homology) (db:pir2.dat) G64715 G64715 Helicobacter pylori 210 -11540021 7500958535 hp1567 conserved hypothetical atp-binding protein (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:31550 percent identity: 40.94;) (le:8021) (re:8647) (di:complement) HPAE000654 AE000654 g2314750 Helicobacter pylori 210 -11540021 7502853908 hp1567 conserved hypothetical atp-binding protein (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:31550 percent identity: 40.94;) (le:8021) (re:8647) (di:complement) HPAE000654 AE000654 g2314750 Helicobacter pylori 26695 85962 -11540021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917114	18988	41144	486	161

Description

6500736164 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1570 HP1570 Helicobacter pylori 210 -11540022 7000689854 conserved hypothetical protein hp1570 (cl:hypothetical protein hi1679) (db:pir2.dat) B64716 B64716 Helicobacter pylori 210 -11540022 7500958656 hp1570 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 132 of 134 of the complete genome.) (nt:similar to egad:28667 percent identity: 40.52;) (le:9763) (re:10257) (di:complement) HPAE000654 AE000654 g2314751 Helicobacter pylori 210 -11540022 7502853909 hp1570 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 132 of 134 of the completegenome.) (nt:similar to egad:28667 percent identity: 40.52;) (le:9763) (re:10257) (di:complement) HPAE000654 AE000654 g2314751 Helicobacter pylori 26695 85962 -11540022

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917127	18989	41145	267	88

Description

6500736165 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1573 HP1573 Helicobacter pylori 210 -11540023 7000689855 conserved hypothetical protein hp1573 (cl:hypothetical protein hi0454) (db:pir2.dat) E64716 E64716 Helicobacter pylori 210 -11540023 7500958657 hp1573 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 133 of 134 of the complete genome.) (nt:similar to egad:17549 percent identity: 42.23;) (le:74) (re:838) (di:complement) HPAE000655 AE000655 g2314758 Helicobacter pylori 210 -11540023 7502853910 hp1573 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 133 of 134 of the completegenome.) (nt:similar to egad:17549 percent identity: 42.23;) (le:74) (re:838) (di:complement) HPAE000655 AE000655 g2314758 Helicobacter pylori 26695 85962 -11540023

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917128	18990	41146	306	102

Description

6500736166 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1587 HP1587 Helicobacter pylori 210 -11540024 7000689856 conserved hypothetical protein hp1587 (db:pir2.dat) C64718 C64718 Helicobacter pylori 210 -11540024 7500958658 hp1587 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 134 of 134 of the complete genome.) (nt:similar to egad:18951 percent identity: 39.00;) (le:493) (re:960) (di:complement) HPAE000656 AE000656 g2314772 Helicobacter pylori 210 -11540024 7502853911 hp1587 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 134 of 134 of the completegenome.) (nt:similar to egad:18951 percent identity: 39.00;) (le:493) (re:960) (di:complement) HPAE000656 AE000656 g2314772 Helicobacter pylori 26695 85962 -11540024

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917130	18991	41147	396	131

Description

6500736167 conserved hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-helicobacter pylori) HP1588 HP1588 Helicobacter pylori 210 -11540025 7000689857 conserved hypothetical protein hp1588 (db:pir2.dat) D64718 D64718 Helicobacter pylori 210 -11540025 7500958659 hp1588 conserved hypothetical protein (db:genpept-bct1) (de:helicobacter pylori section 134 of 134 of the complete genome.) (nt:similar to egad:18951 percent identity: 32.00;) (le:1645) (re:2406) (di:complement) HPAE000656 AE000656 g2314773 Helicobacter pylori 210 -11540025 7502853912 hp1588 conserved hypothetical protein (db:genpept) (de:helicobacter pylori 26695 section 134 of 134 of the completegenome.) (nt:similar to egad:18951 percent identity: 32.00;) (le:1645) (re:2406) (di:complement) HPAE000656 AE000656 g2314773 Helicobacter pylori 26695 85962 -11540025

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917139	18992	41148	414	137

Description

6500736168 ss-dna binding protein 12rnp2 precursor (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.1) (db:gtc-helicobacter pylori) HP0827 HP0827 Helicobacter pylori 210 -11540026 7000690718 ss-dna binding protein 12rnp2 precursor (cl:ribonucleoprotein repeat homology) (db:pir2.dat) C64623 C64623 Helicobacter pylori 210 -11540026 7500959484 hp0827 ss-dna binding protein 12rnp2 precursor (db:genpept-bct1) (de:helicobacter pylori section 72 of 134 of the complete genome.) (nt:similar to egad:43257 percent identity: 46.84;) (le:2578) (re:2826) (di:complement) HPAE000594 AE000594 g2313961 Helicobacter pylori 210 -11540026 7502853913 hp0827 ss-dna binding protein 12rnp2 precursor (db:genpept) (de:helicobacter pylori 26695 section 72 of 134 of the complete genome.) (nt:similar to egad:43257 percent identity: 46.84;) (le:2578) (re:2826) (di:complement) HPAE000594 AE000594 g2313961 Helicobacter pylori 26695 85962 -11540026

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917140	18993	41149	426	141

Description

6500736169 dmpi:hp0924 4-oxalocrotonate tautomerase (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.1) (db:gtc-helicobacter pylori) HP0924 HP0924 Helicobacter pylori 210 -11540027 7000689594 4-oxalocrotonate tautomerase (cl:4-oxalocrotonate tautomerase) (db:pir2.dat) D64635 D64635 Helicobacter pylori 210 -11540027 7500958415 hp0924 4-oxalocrotonate tautomerase dmpi (db:genpept-bct1) (de:helicobacter pylori section 80 of 134 of the complete genome.) (nt:similar to egad:19098 percent identity: 37.74;) (le:8881) (re:9087) (di:complement) HPAE000602 AE000602 g2314069 Helicobacter pylori 210 -11540027 7502853914 hp0924 4-oxalocrotonate tautomerase dmpi (db:genpept) (de:helicobacter pylori 26695 section 80 of 134 of the complete genome.) (nt:similar to egad:19098 percent identity: 37.74;) (le:8881) (re:9087) (di:complement) HPAE000602 AE000602 g2314069 Helicobacter pylori 26695 85962 -11540027

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917150	18994	41150	750	249

Description

6500736170 para protein (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.1) (db:gtc-helicobacter pylori) HP1000 HP1000 Helicobacter pylori 210 -11540028 7000690605 para protein (db:pir2.dat) H64644 H64644 Helicobacter pylori 210 -11540028 7500959385 hp1000 para protein (db:genpept-bct1) (de:helicobacter pylori section 86 of 134 of the complete genome.) (nt:similar to egad:9023 percent identity: 29.73;) (le:6718) (re:7374) (di:direct) HPAE000608 AE000608 g2314143 Helicobacter pylori 210 -11540028 7502853915 hp1000 para protein (db:genpept) (de:helicobacter pylori 26695 section 86 of 134 of the complete genome.) (nt:similar to egad:9023 percent identity: 29.73;) (le:6718) (re:7374) (di:direct) HPAE000608 AE000608 g2314143 Helicobacter pylori 26695 85962 -11540028

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917151	18995	41151	594	197

Description

6500736171 ylxh:hp1034 atp-binding protein (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.1) (db:gtc-helicobacter pylori) HP1034 HP1034 Helicobacter pylori 210 -11540029 7000689650 atp-binding protein (db:pir2.dat) B64649 B64649 Helicobacter pylori 210 -11540029 7500958466 hp1034 atp-binding protein ylxh (db:genpept-bct1) (de:helicobacter pylori section 89 of 134 of the complete genome.) (nt:similar to egad:38115 percent identity: 36.33;) (le:4631) (re:5515) (di:complement) HPAE000611 AE000611 g2314178 Helicobacter pylori 210 -11540029 7502853916 hp1034 atp-binding protein ylxh (db:genpept) (de:helicobacter pylori 26695 section 89 of 134 of the complete genome.) (nt:similar to egad:38115 percent identity: 36.33;) (le:4631) (re:5515) (di:complement) HPAE000611 AE000611 g2314178 Helicobacter pylori 26695 85962 -11540029

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917161	18996	41152	426	141

Description

6500736172 spooj regulator soj:spooj regulator:soj (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.1) (db:gtc-helicobacter pylori) HP1139 HP1139 Helicobacter pylori 210 -11540030 7000689445 regulatory protein spo0j (cl:regulatory protein spo0j) (db:pir2.dat) C64662 C64662 Helicobacter pylori 210 -11540030 7500955520 hp1139 spooj regulator soj (db:genpept-bct1) (de:helicobacter pylori section 98 of 134 of the complete genome.) (nt:similar to egad:23975 percent identity: 47.41;) (le:961) (re:1755) (di:complement) HPAE000620 AE000620 g2314295 Helicobacter pylori 210 -11540030 7502853917 hp1139 spooj regulator soj (db:genpept) (de:helicobacter pylori 26695 section 98 of 134 of the complete genome.) (nt:similar to egad:23975 percent identity: 47.41;) (le:961) (re:1755) (di:complement) HPAE000620 AE000620 g2314295 Helicobacter pylori 26695 85962 -11540030

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917178	18997	41153	468	155

Description

6500736173 phage/colicin/tellurite resistance cluster:tery protein (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.3) (db:gtc-helicobacter pylori) HP0428 HP0428 Helicobacter pylori 210 -11540031 7000690617 phage/colicin/tellurite resistance cluster tery protein (db:pir2.dat) D64573 D64573 Helicobacter pylori 210 -11540031 7500959395 hp0428 phage/colicin/tellurite resistance cluster tery (db:genpept-bct1) (de:helicobacter pylori section 37 of 134 of the complete genome.) (nt:similar to gp:1354148 percent identity: 25.58;) (le:843) (re:1400) (di:direct) HPAE000559 AE000559 g2313537 Helicobacter pylori 210 -11540031 7502853918 hp0428 phage/colicin/tellurite resistance cluster tery (db:genpept) (de:helicobacter pylori 26695 section 37 of 134 of the complete genome.) (nt:similar to gp:1354148 percent identity: 25.58;) (le:843) (re:1400) (di:direct) HPAE000559 AE000559 g2313537 Helicobacter pylori 26695 85962 -11540031

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917189	18998	41154	543	180

Description

6500736174 tolb:hp1126 colicin tolerance-like protein (gtcfc:11.1) (keggfc:14.2) (tigrfc:14.3) (db:gtc-helicobacter pylori) HP1126 HP1126 Helicobacter pylori 210 -11540032 7000689718 colicin tolerance-like protein (db:pir2.dat) F64660 F64660 Helicobacter pylori 210 -11540032 7500958525 hp1126 colicin tolerance-like protein tolb (db:genpept-bct1) (de:helicobacter pylori section 97 of 134 of the complete genome.) (nt:similar to egad:29018 percent identity: 25.71;) (le:2769) (re:4022) (di:complement) HPAE000619 AE000619 g2314279 Helicobacter pylori 210 -11540032 7502853919 hp1126 colicin tolerance-like protein tolb (db:genpept) (de:helicobacter pylori 26695 section 97 of 134 of the complete genome.) (nt:similar to egad:29018 percent identity: 25.71;) (le:2769) (re:4022) (di:complement) HPAE000619 AE000619 g2314279 Helicobacter pylori 26695 85962 -11540032

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917190	18999	41155	516	171

Description

6500736175 2-hydroxy-6-oxohepta-2:4-dienoa hydrolase:2-hydroxy-6-oxohepta-2:4-dienoate hydrolase (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.6) (db:gtc-helicobacter pylori) HP0739 HP0739 Helicobacter pylori 210 -11540033 7000689588 2-hydroxy-6-oxohepta-2:4-dienoate hydrolase (db:pir2.dat) C64612 C64612 Helicobacter pylori 210 -11540033 7500958408 hp0739 2-hydroxy-6-oxohepta-2:4-dienoate hydrolase (db:genpept-bct1) (de:helicobacter pylori section 64 of 134 of the complete genome.) (nt:similar to egad:48093 percent identity: 30.11;) (le:10947) (re:11672) (di:direct) HPAE000586 AE000586 g2313861 Helicobacter pylori 210 -11540033 7502853920 hp0739 2-hydroxy-6-oxohepta-2:4-dienoate hydrolase (db:genpept) (de:helicobacter pylori 26695 section 64 of 134 of the complete genome.) (nt:similar to egad:48093 percent identity: 30.11;) (le:10947) (re:11672) (di:direct) HPAE000586 AE000586 g2313861 Helicobacter pylori 26695 85962 -11540033

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917194	19000	41156	1524	507

Description

6500736176 acka:mg357 acetate kinase:acetokinase (gtcfc:1.10:1.8:8.1) (ec:2.7.2.1) (keggfc:1.8:1.10) (tigrfc:5.4) (db:gtc-mycoplasma genitalium) MG357 MG357 Mycoplasma genitalium 2097 -11540034 58188 acka:mg357 (ec:2.7.2.1) (de:acetate kinase, (acetokinase)) (db:swissprot) ACKA_MYCGE P47599 MYCOPLASMA GENITALIUM 2097 -11540034 172285 acetate kinase (cl:acetate kinase) (ec:2.7.2.1) (db:pir2.dat) E64239 E64239 Mycoplasma genitalium 2097 -11540034 7500876319 mg357 acetate kinase acka (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75245 pid:1673981 percent) (le:5895) (re:7076) (di:complement) U39717 U39717 g3844941 Mycoplasma genitalium 2097 -11540034 5000697343 (de:(mg357) (pn:acetokinase:acetate kinase:acka) (gn:acka) (gtcfc:1.10:1.8) (ec:2.7.2.1) (acka_mycge) (keggfc:1.8:1.10) (tigrfc:5.4) (db:gtc-mycoplasma genitalium)) MG357 MG357 Mycoplasma genitalium 2097 10000968

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917202	19001	41157	870	289

Description

6500736177 ldh:mg460 l-lactate dehydrogenase (gtcfc:1.1:1.8:2.8) (ec:1.1.1.27) (keggfc:1.1:1.8:1.10:5.5:5.12:5.13) (tigrfc:6.1) (db:gtc-mycoplasma genitalium) MG460 MG460 Mycoplasma genitalium 2097 -11540035 81688 ldh:mg460 (ec:1.1.1.27) (de:l-lactate dehydrogenase,) (db:swissprot) LDH_MYCGE P47698 MYCOPLASMA GENITALIUM 2097 -11540035 172544 l-lactate dehydrogenase (ec:1.1.1.27) (db:pir2.dat) H64250 H64250 Mycoplasma genitalium 2097 -11540035 7500884849 mg460 l-lactate dehydrogenase ldh (db:genpept-bct2) (de:mycoplasma genitalium section 50 of 51 of the complete genome.) (nt:similar to sp:p33572 pid:49110 percent identity:) (le:117) (re:1055) (di:direct) U39728 U39728 g3845055 Mycoplasma genitalium 2097 -11540035 5000697340 (de:(mg460) (pn:l-lactate dehydrogenase:ldh) (gn:ldh) (gtcfc:1.1:1.10:1.8:5.12:5.13) (ec:1.1.1.27) (ldh_mycge) (keggfc:1.1:1.8:1.10:5.12:5.13) (tigrfc:6.1) (db:gtc-mycoplasma genitalium)) MG460 MG460 Mycoplasma genitalium 2097 10023922

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917203	19002	41158	1158	385

Description

GTC ORF with score 661 to: (fn:putative mismatch repair/binding protein) (sr:human) (db:genpept-pri1) (de:human putative mismatch repair/binding protein hmsh3 (hmsh3) mrna,complete cds.) (nt:humdug; human divergent upstream protein gene dug,) (le:17) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917211	19003	41159	303	100

Description

5000697325 fba:tsr:mg023 tsr:fructose-bisphosphate aldolase (gtcfc:1.1:1.3:1.5:2.4) (ec:4.1.2.13) (keggfc:1.1:1.3:1.5:2.3) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG023 MG023 Mycoplasma genitalium 2097 -11540036 59157 fbaa:fba:tsr:mg023 (ec:4.1.2.13) (de:fructose-bisphosphate aldolase,) (db:swissprot) ALF_MYCGE P47269 MYCOPLASMA GENITALIUM 2097 -11540036 172352 fructose-bisphosphate aldolase (cl:fructose-bisphosphate aldolase ii) (ec:4.1.2.13) (db:pir2.dat) E64202 E64202 Mycoplasma genitalium 2097 -11540036 7500876748 mg023 fructose-bisphosphate aldolase fba (db:genpept-bct2) (de:mycoplasma genitalium section 3 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75089 pid:1673788 percent) (le:6059) (re:6925) (di:direct) U39681 U39681 g3844632 Mycoplasma genitalium 2097 -11540036 6500736178 fba:tsr tsr:fructose-bisphosphate aldolase (gtcfc:1.1:1.3:1.5:2.4) (ec:4.1.2.13) (keggfc:1.1:1.3:1.5:2.3) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG023 MG023 Mycoplasma genitalium 2097 -11540036

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917212	19004	41160	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917261	19005	41161	624	207

Description

6500736179 frua:mg062 pts system:fructose-specific iibc component:eiibc-fru:fructose-permease iibc component:phosphotransferase enzyme ii:bc component:eii-fru (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG062 MG062 Mycoplasma genitalium 2097 -11540037 92155 frua:mg062 (ec:2.7.1.69) (de:component), (eii-fru / eiii-fru)) (db:swissprot) PTFA_MYCGE P47308 MYCOPLASMA GENITALIUM 2097 -11540037 172353 fructose-permease iibc component frua homolog (db:pir2.dat) H64206 H64206 Mycoplasma genitalium 2097 -11540037 7500888939 mg062 pts system:fructose-specific iiabc component (db:genpept-bct2) (de:mycoplasma genitalium section 7 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75039 pid:1673731 percent) (le:6016) (re:8058) (di:direct) U39685 U39685 g1045736 Mycoplasma genitalium 2097 -11540037 5000697326 (de:(mg062) (pn:pts system, fructose-specific iibc component:eiibc-fru:phosphotransferase enzyme ii, bc component:eii-fru:fructose-permease iibc component:frua) (gn:frua) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptfb_mycge) (ke) MG062 MG062 Mycoplasma genitalium 2097 10034189

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917271	19006	41162	312	103

Description

6500736180 ptsg:mg069 pts system:glucose-specific iiabc component:eiiabc-glc:glucose-permease iiabc component:phosphotransferase enzyme ii:abc component:eii-glc / eiii-glc (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG069 MG069 Mycoplasma genitalium 2097 -11540038 92165 ptsg:mg069 (ec:2.7.1.69) (de:component), (eii-glc / eiii-glc)) (db:swissprot) PTGA_MYCGE P47315 MYCOPLASMA GENITALIUM 2097 -11540038 172593 phosphotransferase enzyme ii abc component ptsg homolog (cl:phosphotransferase system glucose-specific enzyme ii, factor iii homology) (db:pir2.dat) F64207 F64207 Mycoplasma genitalium 2097 -11540038 7500888950 mg069 pts system:glucose-specific iiabc component (db:genpept-bct2) (de:mycoplasma genitalium section 9 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75569 pid:1674328 percent) (le:2122) (re:4848) (di:direct) U39687 U39687 g1045745 Mycoplasma genitalium 2097 -11540038 5000697327 (de:(mg069) (pn:pts system, glucose-specific iiabc component:eiiabc-glc:glucose-permease iiabc component:eii-glc :phosphotransferase enzyme ii, abc component:ptsg) (gn:ptsg) (gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptga_mycge)) MG069 MG069 Mycoplasma genitalium 2097 10034199

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917274	19007	41163	225	74

Description

5000697328 pgi:mg111 phosphoglucose isomerase b:pgib:glucose-6-phosphate isomerase:gpi:phosphoglucose isomerase:pgi:phosphohexose isomerase:phi (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (keggfc:1.1:1.3:7.1) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG111 MG111 Mycoplasma genitalium 2097 -11540039 72810 pgi:mg111 (ec:5.3.1.9) (de:isomerase) (pgi) (phosphohexose isomerase) (phi)) (db:swissprot) G6PI_MYCGE P47357 MYCOPLASMA GENITALIUM 2097 -11540039 172589 glucose-6-phosphate isomerase:b (ec:5.3.1.9) (db:pir2.dat) C64212 C64212 Mycoplasma genitalium 2097 -11540039 7500882024 mg111 glucose-6-phosphate isomerase pgi (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78033 pid:1674283 percent) (le:6881) (re:8182) (di:direct) U39691 U39691 g3844700 Mycoplasma genitalium 2097 -11540039 6500736181 pgi phosphoglucose isomerase b:pgib:glucose-6-phosphate isomerase:gpi:phosphoglucose isomerase:pgi:phosphohexose isomerase:phi (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (keggfc:1.1:1.3:7.1) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG111 MG111 Mycoplasma genitalium 2097 -11540039

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917285	19008	41164	477	158

Description

5000697329 pfka:pfk:mg215 pfk:6-phosphofructokinase:phosphofructokinase:phosphohexokinase (gtcfc:1.1:1.3:1.5:1.6) (ec:2.7.1.11) (keggfc:1.1:1.3:1.5:1.6) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG215 MG215 Mycoplasma genitalium 2097 -11540040 80274 pfka:pfk:mg215 (ec:2.7.1.11) (de:(phosphohexokinase)) (db:swissprot) K6PF_MYCGE P47457 MYCOPLASMA GENITALIUM 2097 -11540040 172283 6-phosphofructokinase (cl:6-phosphofructokinase:6-phosphofructokinase 1 homology) (ec:2.7.1.11) (db:pir2.dat) G64223 G64223 Mycoplasma genitalium 2097 -11540040 7500884439 mg215 6-phosphofructokinase pfk (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75476 pid:1674230 percent) (le:3749) (re:4720) (di:direct) U39701 U39701 g3844815 Mycoplasma genitalium 2097 -11540040 6500736182 pfka:pfk pfk:6-phosphofructokinase:phosphofructokinase:phosphohexokinase (gtcfc:1.1:1.3:1.5:1.6) (ec:2.7.1.11) (keggfc:1.1:1.3:1.5:1.6) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG215 MG215 Mycoplasma genitalium 2097 -11540040

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917307	19009	41165	1407	468

Description

6500736183 pyk:mg216 pyruvate kinase (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (keggfc:1.1:1.8:2.3) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG216 MG216 Mycoplasma genitalium 2097 -11540041 81050 pyk:mg216 (ec:2.7.1.40) (de:pyruvate kinase, (pk)) (db:swissprot) KPYK_MYCGE P47458 MYCOPLASMA GENITALIUM 2097 -11540041 172617 pyruvate kinase (ec:2.7.1.40) (db:pir2.dat) H64223 H64223 Mycoplasma genitalium 2097 -11540041 7500884728 mg216 pyruvate kinase pyk (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78031 pid:1674229 percent) (le:4723) (re:6249) (di:direct) U39701 U39701 g3844816 Mycoplasma genitalium 2097 -11540041 5000697330 (de:(mg216) (pn:pyruvate kinase) (gn:pyk) (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (kpyk_mycge) (keggfc:1.1:1.8:2.3) (tigrfc:6.4) (db:gtc-mycoplasma genitalium)) MG216 MG216 Mycoplasma genitalium 2097 10023287

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917312	19010	41166	537	178

Description

6500736184 pdhd:mg271 lipoamide dehydrogenase component:e3 of pyruvate dehydrogenase complex:dihydrolipoamide dehydrogenase (gtcfc:1.1:1.8) (ec:1.8.1.4) (keggfc:1.1:1.2:1.8:5.3) (tigrfc:6.6) (db:gtc-mycoplasma genitalium) MG271 MG271 Mycoplasma genitalium 2097 -11540042 68742 pdhd:mg271 (ec:1.8.1.4) (de:(ec 1.8.1.4) (e3) (dihydrolipoamide dehydrogenase)) (db:swissprot) DLDH_MYCGE P47513 MYCOPLASMA GENITALIUM 2097 -11540042 172327 dihydrolipoamide dehydrogenase:pdhd (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (ec:1.8.1.4) (db:pir2.dat) I64229 I64229 Mycoplasma genitalium 2097 -11540042 7500880356 mg271 dihydrolipoamide dehydrogenase pdhd (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75393 pid:1674136 percent) (le:8367) (re:9740) (di:complement) U39706 U39706 g1045965 Mycoplasma genitalium 2097 -11540042 5000697331 (de:(mg271) (pn:lipoamide dehydrogenase component:e3 of pyruvate dehydrogenase complex:dihydrolipoamide dehydrogenase:pdhd) (gn:pdhd) (gtcfc:1.1:1.2:5.3) (ec:1.8.1.4) (dldh_mycge) (keggfc:1.1:1.2:5.3) (tigrfc:6.6) (db:gtc-mycopl) MG271 MG271 Mycoplasma genitalium 2097 10011327

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917315	19011	41167	2088	695

Description

6500736185 pdhc:mg272 dihydrolipoamide acetyltransferase:dihydrolipoamide acetyltransferase component:e2 of pyruvate dehydrogenase complex (gtcfc:1.1:1.8) (ec:2.3.1.12) (keggfc:1.1:1.8) (tigrfc:6.6) (db:gtc-mycoplasma genitalium) MG272 MG272 Mycoplasma genitalium 2097 -11540043 87488 pdhc:mg272 (ec:2.3.1.12) (de:complex, (e2)) (db:swissprot) ODP2_MYCGE P47514 MYCOPLASMA GENITALIUM 2097 -11540043 172326 dihydrolipoamide acetyltransferase pdhc (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (db:pir2.dat) A64230 A64230 Mycoplasma genitalium 2097 -11540043 7500887104 mg272 dihydrolipoamide acetyltransferase pdhc (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75392 pid:1674135 percent) (le:9744) (re:10898) (di:complement) U39706 U39706 g1045966 Mycoplasma genitalium 2097 -11540043 5000697332 (de:(mg272) (pn:dihydrolipoamide acetyltransferase component:e2 of pyruvate dehydrogenase complex:dihydrolipoamide acetyltransferase:pdhc) (gn:pdhc) (gtcfc:1.1) (ec:2.3.1.12) (odp2_mycge) (keggfc:1.1) (tigrfc:6.6) (db:gtc-mycopl) MG272 MG272 Mycoplasma genitalium 2097 10029631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917331	19012	41168	1497	498

Description

6500736186 pdhb:mg273 pyruvate dehydrogenase e1-beta subunit:pyruvate dehydrogenase e1 component:beta subunit (gtcfc:1.1:1.11:1.8:5.7) (ec:1.2.4.1) (keggfc:1.1:1.8:1.11:5.7) (tigrfc:6.6) (db:gtc-mycoplasma genitalium) MG273 MG273 Mycoplasma genitalium 2097 -11540044 87516 pdhb:mg273 (ec:1.2.4.1) (de:pyruvate dehydrogenase e1 component, beta subunit,) (db:swissprot) ODPB_MYCGE P47515 MYCOPLASMA GENITALIUM 2097 -11540044 172616 pyruvate dehydrogenase lipoamide:e1-beta chain pdhb (cl:pyruvate dehydrogenase (lipoamide) beta chain) (ec:1.2.4.1) (db:pir2.dat) B64230 B64230 Mycoplasma genitalium 2097 -11540044 7500887112 mg273 pyruvate dehydrogenase component e1:subunit (db:genpept-bct2) (de:mycoplasma genitalium section 29 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75391 pid:1674134 percent) (le:156) (re:1136) (di:complement) U39707 U39707 g3844866 Mycoplasma genitalium 2097 -11540044 5000697333 (de:(mg273) (pn:pyruvate dehydrogenase e1 component, beta subunit:pyruvate dehydrogenase e1-beta subunit:pdhb) (gn:pdhb) (gtcfc:1.1:5.7) (ec:1.2.4.1) (odpb_mycge) (keggfc:1.1:5.7) (tigrfc:6.6) (db:gtc-mycoplasma genitalium)) MG273 MG273 Mycoplasma genitalium 2097 10029659

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917336	19013	41169	1164	387

Description

6500736187 pdha:mg274 pyruvate dehydrogenase e1-alpha subunit:pyruvate dehydrogenase e1 component:alpha subunit (gtcfc:1.1:1.11:1.8:5.7) (ec:1.2.4.1) (keggfc:1.1:1.8:1.11:5.7) (tigrfc:6.6) (db:gtc-mycoplasma genitalium) MG274 MG274 Mycoplasma genitalium 2097 -11540045 87501 pdha:mg274 (ec:1.2.4.1) (de:pyruvate dehydrogenase e1 component, alpha subunit,) (db:swissprot) ODPA_MYCGE P47516 MYCOPLASMA GENITALIUM 2097 -11540045 172615 pyruvate dehydrogenase lipoamide:e1-alpha chain pdha (cl:pyruvate dehydrogenase (lipoamide) alpha chain:thiamine pyrophosphate-binding domain homology) (ec:1.2.4.1) (db:pir2.dat) C64230 C64230 Mycoplasma genitalium 2097 -11540045 7500887109 mg274 pyruvate dehydrogenase component e1:subunit (db:genpept-bct2) (de:mycoplasma genitalium section 29 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75390 pid:1674133 percent) (le:1154) (re:2230) (di:complement) U39707 U39707 g3844867 Mycoplasma genitalium 2097 -11540045 5000697334 (de:(mg274) (pn:pyruvate dehydrogenase e1 component, alpha subunit:pyruvate dehydrogenase e1-alpha subunit:pdha) (gn:pdha) (gtcfc:1.1:5.7) (ec:1.2.4.1) (odpa_mycge) (keggfc:1.1:5.7) (tigrfc:6.6) (db:gtc-mycoplasma genitalium)) MG274 MG274 Mycoplasma genitalium 2097 10029644

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917339	19014	41170	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917346	19015	41171	843	280

Description

6500736188 pgk:mg300 phosphoglycerate kinase (gtcfc:1.1:2.4) (ec:2.7.2.3) (keggfc:1.1:2.3) (tigrfc:6.3) (db:gtc-mycoplasma genitalium) MG300 MG300 Mycoplasma genitalium 2097 -11540046 89297 pgk:mg300 (ec:2.7.2.3) (de:phosphoglycerate kinase,) (db:swissprot) PGK_MYCGE P47542 MYCOPLASMA GENITALIUM 2097 -11540046 123863 phosphoglycerate kinase (cl:phosphoglycerate kinase) (ec:2.7.2.3) (db:pir1.dat) B64233 B64233 Mycoplasma genitalium 2097 -11540046 7500887939 mg300 phosphoglycerate kinase pgk (db:genpept-bct2) (de:mycoplasma genitalium section 32 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78018 pid:1674096 percent) (le:5269) (re:6519) (di:complement) U39710 U39710 g3844879 Mycoplasma genitalium 2097 -11540046 5000697335 (de:(mg300) (pn:phosphoglycerate kinase:pgk) (gn:pgk) (gtcfc:1.1:2.4) (ec:2.7.2.3) (pgk_mycge) (keggfc:1.1:2.3) (tigrfc:6.3) (db:gtc-mycoplasma genitalium)) MG300 MG300 Mycoplasma genitalium 2097 10031420

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917347	19016	41172	1644	547

Description

5000697336 gapa:gap:mg301 glyceraldehyde-3-phosphate dehydrogenase:gap:glyceraldehyde 3-phosphate dehydrogenase:gapdh (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG301 MG301 Mycoplasma genitalium 2097 -11540047 72730 gapa:gap:mg301 (ec:1.2.1.12) (de:glyceraldehyde 3-phosphate dehydrogenase, (gapdh)) (db:swissprot) G3P_MYCGE P47543 MYCOPLASMA GENITALIUM 2097 -11540047 136510 glyceraldehyde-3-phosphate dehydrogenase (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir2.dat) C64233 C64233 Mycoplasma genitalium 2097 -11540047 7500881980 mg301 glyceraldehyde-3-phosphate dehydrogenase gap (db:genpept-bct2) (de:mycoplasma genitalium section 32 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75358 pid:1674095 percent) (le:6506) (re:7519) (di:complement) U39710 U39710 g3844880 Mycoplasma genitalium 2097 -11540047 6500736189 gapa:gap glyceraldehyde-3-phosphate dehydrogenase:gap:glyceraldehyde 3-phosphate dehydrogenase:gapdh (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG301 MG301 Mycoplasma genitalium 2097 -11540047

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917372	19017	41173	1056	351

Description

6500736190 eno:mg407 enolase:lase:2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase (gtcfc:1.1) (ec:4.2.1.11) (keggfc:1.1) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG407 MG407 Mycoplasma genitalium 2097 -11540048 70203 eno:mg407 (ec:4.2.1.11) (de:glycerate hydro-lyase)) (db:swissprot) ENO_MYCGE P47647 MYCOPLASMA GENITALIUM 2097 -11540048 141850 phosphopyruvate hydratase::enolase (cl:enolase) (ec:4.2.1.11) (db:pir2.dat) A64245 A64245 Mycoplasma genitalium 2097 -11540048 7500881044 mg407 enolase eno (db:genpept-bct2) (de:mycoplasma genitalium section 45 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75189 pid:1673903 percent) (le:101) (re:1477) (di:complement) U39723 U39723 g3845000 Mycoplasma genitalium 2097 -11540048 5000697337 (de:(mg407) (pn:lase:2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase:enolase:eno) (gn:eno) (gtcfc:1.1) (ec:4.2.1.11) (eno_mycge) (keggfc:1.1) (tigrfc:6.4) (db:gtc-mycoplasma genitalium)) MG407 MG407 Mycoplasma genitalium 2097 10012781

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917390	19018	41174	429	142

Description

6500736191 pgm:mg430 phosphoglycerate mutase:2:3-bisphosphoglycerate-independent phosphoglycerate mutase:phosphoglyceromutase:bpg-independent pgam (gtcfc:1.1) (ec:5.4.2.1) (keggfc:1.1) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG430 MG430 Mycoplasma genitalium 2097 -11540049 90089 pgm:mg430 (ec:5.4.2.1) (de:(ec 5.4.2.1) (phosphoglyceromutase) (bpg-independent pgam)) (db:swissprot) PMGI_MYCGE P47669 MYCOPLASMA GENITALIUM 2097 -11540049 172590 phosphoglycerate mutase::2:3-diphosphoglycerate-independent (cl:phosphoglycerate mutase, 2, 3-bisphosphoglycerate-independent) (ec:5.4.2.1) (db:pir2.dat) E64247 E64247 Mycoplasma genitalium 2097 -11540049 7500888193 mg430 phosphoglycerate mutase pgm (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75167 pid:1673879 percent) (le:4497) (re:6020) (di:complement) U39725 U39725 g3845023 Mycoplasma genitalium 2097 -11540049 5000697338 (de:(mg430) (pn:2,3-bisphosphoglycerate-independent phosphoglycerate mutase:phosphoglyceromutase:bpg-independent pgam:phosphoglycerate mutase:pgm) (gn:pgm) (gtcfc:1.1) (ec:5.4.2.1) (pmgi_mycge) (keggfc:1.1) (tigrfc:6.4) (db:gtc-) MG430 MG430 Mycoplasma genitalium 2097 10032209

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917391	19019	41175	306	101

Description

5000697339 tpia:tim:mg431 triosephosphate isomerase:tim (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (keggfc:1.1:1.5:2.3:8.1) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG431 MG431 Mycoplasma genitalium 2097 -11540050 101925 tpia:tpi:tim:mg431 (ec:5.3.1.1) (de:triosephosphate isomerase, (tim)) (db:swissprot) TPIS_MYCGE P47670 MYCOPLASMA GENITALIUM 2097 -11540050 172697 triose-phosphate isomerase (cl:triose-phosphate isomerase) (ec:5.3.1.1) (db:pir2.dat) F64247 F64247 Mycoplasma genitalium 2097 -11540050 7500893316 mg431 triosephosphate isomerase tpia (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78010 pid:1673878 percent) (le:6013) (re:6747) (di:complement) U39725 U39725 g3845024 Mycoplasma genitalium 2097 -11540050 6500736192 tpia:tim triosephosphate isomerase:tim (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (keggfc:1.1:1.5:2.3:8.1) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG431 MG431 Mycoplasma genitalium 2097 -11540050

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917401	19020	41176	510	169

Description

6500736193 fruk:mg063 1-phosphofructokinase (gtcfc:1.1:1.5:1.6) (ec:2.7.1.56) (keggfc:1.5:1.6) (tigrfc:6.4) (db:gtc-mycoplasma genitalium) MG063 MG063 Mycoplasma genitalium 2097 -11540051 172281 1-phosphofructokinase:homolog (ec:2.7.1.56) (db:pir2.dat) I64206 I64206 Mycoplasma genitalium 2097 -11540051 7500965548 mg063 1-phosphofructokinase fruk (db:genpept-bct2) (de:mycoplasma genitalium section 7 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75038 pid:1673730 percent) (le:8153) (re:8920) (di:direct) U39685 U39685 g3844659 Mycoplasma genitalium 2097 -11540051 5000697349 (de:(mg063) (pn:1-phosphofructokinase:fruk) (gn:fruk) (gtcfc:1.5:1.6) (ec:2.7.1.56) (keggfc:1.5:1.6) (tigrfc:6.4) (db:gtc-mycoplasma genitalium)) MG063 MG063 Mycoplasma genitalium 2097 10091233

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917406	19021	41177	534	177

Description

6500736194 deoc:mg050 deoxyribose-phosphate aldolase:phosphodeoxyriboaldolase:deoxyriboaldolase (gtcfc:1.3:7.1) (ec:4.1.2.4) (keggfc:1.3) (tigrfc:6.7) (db:gtc-mycoplasma genitalium) MG050 MG050 Mycoplasma genitalium 2097 -11540052 68254 deoc:mg050 (ec:4.1.2.4) (de:(deoxyriboaldolase)) (db:swissprot) DEOC_MYCGE P47296 MYCOPLASMA GENITALIUM 2097 -11540052 141633 deoxyribose-phosphate aldolase (cl:deoxyribose-phosphate aldolase) (ec:4.1.2.4) (db:pir2.dat) E64205 E64205 Mycoplasma genitalium 2097 -11540052 7500880166 mg050 deoxyribose-phosphate aldolase (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to sp:p09924 gb:l38997 pid:44481) (le:9372) (re:10043) (di:direct) U39684 U39684 g1045723 Mycoplasma genitalium 2097 -11540052 5000697344 (de:(mg050) (pn:deoxyriboaldolase:deoxyribose-phosphate aldolase:phosphodeoxyriboaldolase:deoxyriboaldolase) (gn:deoc) (gtcfc:1.3) (ec:4.1.2.4) (deoc_mycge) (keggfc:1.3) (tigrfc:6.7) (db:gtc-mycoplasma genitalium)) MG050 MG050 Mycoplasma genitalium 2097 10010847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917407	19022	41178	330	109

Description

5000697345 prsa:prs:mg058 phosphoribosylpyrophosphate synthetase:prs:ribose-phosphate pyrophosphokinase:phosphoribosyl pyrophosphate synthetase (gtcfc:1.3:4.1) (ec:2.7.6.1) (keggfc:1.3:4.1) (tigrfc:8.3) (db:gtc-mycoplasma genitalium) MG058 MG058 Mycoplasma genitalium 2097 -11540053 81016 prsa:prs:mg058 (ec:2.7.6.1) (de:pyrophosphate synthetase)) (db:swissprot) KPRS_MYCGE P47304 MYCOPLASMA GENITALIUM 2097 -11540053 139043 ribose-phosphate pyrophosphokinase::phosphoribosylpyrophosphate synthetase (cl:ribose-phosphate pyrophosphokinase catalytic chain) (ec:2.7.6.1) (db:pir2.dat) D64206 D64206 Mycoplasma genitalium 2097 -11540053 7500884708 mg058 ribose-phosphate pyrophosphokinase prs (db:genpept-bct2) (de:mycoplasma genitalium section 7 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75044 pid:1673736 percent) (le:1713) (re:2606) (di:complement) U39685 U39685 g1045732 Mycoplasma genitalium 2097 -11540053 6500736195 prsa:prs phosphoribosylpyrophosphate synthetase:prs:ribose-phosphate pyrophosphokinase:phosphoribosyl pyrophosphate synthetase (gtcfc:1.3:4.1) (ec:2.7.6.1) (keggfc:1.3:4.1) (tigrfc:8.3) (db:gtc-mycoplasma genitalium) MG058 MG058 Mycoplasma genitalium 2097 -11540053

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917408	19023	41179	258	85

Description

6500736196 tkta:mg066 transketolase 1:tk 1:transketolase:tk (gtcfc:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (tigrfc:6.5) (db:gtc-mycoplasma genitalium) MG066 MG066 Mycoplasma genitalium 2097 -11540054 101625 tkta:mg066 (ec:2.2.1.1) (de:transketolase, (tk)) (db:swissprot) TKT_MYCGE P47312 MYCOPLASMA GENITALIUM 2097 -11540054 172686 transketolase (cl:transketolase:thiamine pyrophosphate-binding domain homology) (ec:2.2.1.1) (db:pir2.dat) C64207 C64207 Mycoplasma genitalium 2097 -11540054 7500893210 mg066 transketolase tkta (db:genpept-bct2) (de:mycoplasma genitalium section 8 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75611 pid:1673726 percent) (le:5558) (re:7504) (di:direct) U39686 U39686 g1045741 Mycoplasma genitalium 2097 -11540054 5000697346 (de:(mg066) (pn:transketolase:tk:transketolase 1:tk 1) (gn:tkta) (gtcfc:1.3:2.4) (ec:2.2.1.1) (tkt_mycge) (keggfc:1.3:2.3) (tigrfc:6.5) (db:gtc-mycoplasma genitalium)) MG066 MG066 Mycoplasma genitalium 2097 10043457

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917424	19024	41180	1014	337

Description

5000697364 6-phosphogluconate dehydrogenase:gnd:hypothetical protein mg264 (gtcfc:1.3) (keggfc:14.2) (tigrfc:6.5) (db:gtc-mycoplasma genitalium) MG264 MG264 Mycoplasma genitalium 2097 -11540055 109036 mg264 (de:hypothetical protein mg264) (db:swissprot) Y264_MYCGE P47506 MYCOPLASMA GENITALIUM 2097 -11540055 172284 phosphogluconate dehydrogenase decarboxylating:gnd (cl:phosphogluconate dehydrogenase (decarboxylating) gnd) (ec:1.1.1.44) (db:pir2.dat) B64229 B64229 Mycoplasma genitalium 2097 -11540055 7500894998 mg264 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75400 pid:1674143 percent) (le:958) (re:1554) (di:direct) U39706 U39706 g3844860 Mycoplasma genitalium 2097 -11540055 6500736197 6-phosphogluconate dehydrogenase:gnd:hypothetical protein mg264 (gtcfc:1.3) (keggfc:14.2) (tigrfc:6.5) (db:gtc-mycoplasma genitalium) MG264 MG264 Mycoplasma genitalium 2097 -11540055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917447	19025	41181	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917472	19026	41182	483	160

Description

5000697347 galu:gtab:mg453 gtab:utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp:alpha-d-glucosyl-1-phosphate uridylyltransferase:uridine diphosphoglucose pyrophosphorylase (gtcfc:1.4:1.6:4.3:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (tigrfc:8.5) (db:gtc-mycoplasma genitalium) MG453 MG453 Mycoplasma genitalium 2097 -11540056 73095 galu:gtab:mg453 (ec:2.7.7.9) (de:uridylyltransferase) (uridine diphosphoglucose pyrophosphorylase)) (db:swissprot) GALU_MYCGE P47691 MYCOPLASMA GENITALIUM 2097 -11540056 172704 utp--glucose-1-phosphate uridylyltransferase::udp-glucose pyrophosphorylase (cl:escherichia coli utp--glucose-1-phosphate uridylyltransferase) (ec:2.7.7.9) (db:pir1.dat) A64250 A64250 Mycoplasma genitalium 2097 -11540056 7500882104 mg453 utp--glucose-1-phosphate uridylyltransferase (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75124 pid:1673837 percent) (le:2117) (re:2995) (di:direct) U39727 U39727 g3845047 Mycoplasma genitalium 2097 -11540056 6500736198 galu:gtab gtab:utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp:alpha-d-glucosyl-1-phosphate uridylyltransferase:uridine diphosphoglucose pyrophosphorylase (gtcfc:1.4:1.6:4.3:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (tigrfc:8.5) (db:gtc-mycoplasma genitalium) MG453 MG453 Mycoplasma genitalium 2097 -11540056

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917475	19027	41183	960	319

Description

GTC ORF with score 307 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917479	19028	41184	543	180

Description

6500736199 cpsg:mg053 phosphomannomutase:pmm (gtcfc:1.5:7.1) (ec:5.4.2.8) (keggfc:1.5) (tigrfc:6.7) (db:gtc-mycoplasma genitalium) MG053 MG053 Mycoplasma genitalium 2097 -11540057 66186 manb:cpsg:mg053 (ec:5.4.2.8) (de:phosphomannomutase, (pmm)) (db:swissprot) MANB_MYCGE P47299 MYCOPLASMA GENITALIUM 2097 -11540057 172592 phosphomannomutase (ec:5.4.2.8) (db:pir2.dat) H64205 H64205 Mycoplasma genitalium 2097 -11540057 7500885307 mg053 phosphomannomutase manb (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75050 pid:1673743 percent) (le:11696) (re:13348) (di:direct) U39684 U39684 g1045726 Mycoplasma genitalium 2097 -11540057 5000697348 (de:(mg053) (pn:pmm:phosphomannomutase) (gn:cpsg) (gtcfc:1.5) (ec:5.4.2.8) (cpsg_mycge) (keggfc:1.5) (tigrfc:6.7) (db:gtc-mycoplasma genitalium)) MG053 MG053 Mycoplasma genitalium 2097 10008817

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917482	19029	41185	219	72

Description

6500736200 gale:mg118 udp-glucose 4-epimerase:galactowaldenase:udp-galactose 4-epimerase (gtcfc:1.6:4.3) (ec:5.1.3.2) (keggfc:1.6:4.3) (tigrfc:8.5) (db:gtc-mycoplasma genitalium) MG118 MG118 Mycoplasma genitalium 2097 -11540058 73074 gale:mg118 (ec:5.1.3.2) (de:galactose 4-epimerase)) (db:swissprot) GALE_MYCGE P47364 MYCOPLASMA GENITALIUM 2097 -11540058 172703 udp-glucose 4-epimerase gale (cl:udpglucose 4-epimerase homology) (db:pir2.dat) A64213 A64213 Mycoplasma genitalium 2097 -11540058 7500882083 mg118 udp-glucose 4-epimerase gale (db:genpept-bct2) (de:mycoplasma genitalium section 14 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75517 pid:1674276 percent) (le:1873) (re:2895) (di:direct) U39692 U39692 g3844708 Mycoplasma genitalium 2097 -11540058 5000697350 (de:(mg118) (pn:galactowaldenase:udp-galactose 4- epimerase:udp-glucose 4-epimerase:gale) (gn:gale) (gtcfc:1.6:4.3) (ec:5.1.3.2) (gale_mycge) (keggfc:1.6:4.3) (tigrfc:8.5) (db:gtc-mycoplasma genitalium)) MG118 MG118 Mycoplasma genitalium 2097 10015621

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917483	19030	41186	258	85

Description

6500736201 pta:mg299 probable phosphate acetyltransferase:phosphotransacetylase (gtcfc:1.8:8.1) (ec:2.3.1.8) (keggfc:1.8) (tigrfc:5.4) (db:gtc-mycoplasma genitalium) MG299 MG299 Mycoplasma genitalium 2097 -11540059 92124 pta:mg299 (ec:2.3.1.8) (de:(phosphotransacetylase)) (db:swissprot) PTA_MYCGE P47541 MYCOPLASMA GENITALIUM 2097 -11540059 172586 phosphate acetyltransferase::phosphotransacetylase (ec:2.3.1.8) (db:pir2.dat) A64233 A64233 Mycoplasma genitalium 2097 -11540059 7500888924 mg299 phosphotransacetylase pta (db:genpept-bct2) (de:mycoplasma genitalium section 32 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75359 pid:1674097 percent) (le:4289) (re:5251) (di:complement) U39710 U39710 g3844878 Mycoplasma genitalium 2097 -11540059 5000697351 (de:(mg299) (pn:probable phosphate acetyltransferase:phosphotransacetylase:pta) (gn:pta) (gtcfc:1.8) (ec:2.3.1.8) (pta_mycge) (keggfc:1.8) (tigrfc:5.4) (db:gtc-mycoplasma genitalium)) MG299 MG299 Mycoplasma genitalium 2097 10034158

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917486	19031	41187	1155	384

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917488	19032	41188	741	246

Description

6500736202 fold:mg013 5:10-methylene-tetrahydrofolate dehydrogenase:methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase (gtcfc:1.9:9.6) (keggfc:1.9:9.8) (tigrfc:2.1) (db:gtc-mycoplasma genitalium) (gtcfc:carbohydrate metabolism-glyoxylate and dicarboxylate metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MG013 MG013 Mycoplasma genitalium 2097 -11540060 72240 fold:mg013 (ec:1.5.1.5:3.5.4.9) (de:methenyltetrahydrofolate cyclohydrolase,) (db:swissprot) FOLD_MYCGE P47259 MYCOPLASMA GENITALIUM 2097 -11540060 172282 methylenetetrahydrofolate dehydrogenase nadp+:methenyltetrahydrofolate cyclohydrolase::fold bifunctional enzyme (cl:methylenetetrahydrofolate dehydrogenase (nad+) homology) (ec:1.5.1.5:3.5.4.9) (db:pir2.dat) D64201 D64201 Mycoplasma genitalium 2097 -11540060 7500881713 fold 5:10-methylene-tetrahydrofolate dehydrogenase (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium dnaj_2, fold, gtp1, mets, mot1, msba, pip_1,rpoe, trna-ala, trna-ile_1, tsr genes from bases 14296 to 28573(section 2 of 56) of the complete genome.) (n... U39680 U39680 g1045682 Mycoplasma genitalium 2097 -11540060 5000697352 (de:(mg013) (pn:methylenetetrahydrofolate dehydrogenase :5,10-methylene-tetrahydrofolate dehydrogenase:fold) (gn:fold) (gtcfc:1.9) (ec:1.5.1.5) (fold_mycge) (keggfc:1.9:9.8) (tigrfc:2.1) (db:gtc-mycoplasma genitalium)) MG013 MG013 Mycoplasma genitalium 2097 10014791

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917489	19033	41189	492	163

Description

6500736203 def:mg106 polypeptide deformylase:formylmethionine deformylase:polypeptide ormylase:pdf:formylmethionine ormylase (gtcfc:1.9:5.4:10.6:10.7) (ec:3.5.1.31) (keggfc:1.9:5.4:10.1) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG106 MG106 Mycoplasma genitalium 2097 -11540061 172351 formylmethionine deformylase homolog (cl:polypeptide deformylase) (db:pir2.dat) G64211 G64211 Mycoplasma genitalium 2097 -11540061 7500955892 mg106 polypeptide deformylase def (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75527 pid:1674288 percent) (le:2922) (re:3602) (di:complement) U39691 U39691 g3844695 Mycoplasma genitalium 2097 -11540061 5000697353 (de:(mg106) (pn:polypeptide ormylase:pdf:formylmethionine ormylase:polypeptide deformylase:formylmethionine deformylase:def) (gn:def) (gtcfc:1.9:5.4:10.5) (ec:3.5.1.31) (def_mycge) (keggfc:1.9:5.4:10.1) (tigrfc:12.4) (db:gtc-myc) MG106 MG106 Mycoplasma genitalium 2097 10010818

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917491	19034	41190	489	162

Description

6500736204 ppa:mg351 inorganic pyrophosphatase:pyrophosphate phospho-hydrolase:ppase (gtcfc:2.1:13.10) (ec:3.6.1.1) (keggfc:2.1) (tigrfc:5.3) (db:gtc-mycoplasma genitalium) MG351 MG351 Mycoplasma genitalium 2097 -11540062 79866 ppa:mg351 (ec:3.6.1.1) (de:hydrolase) (ppase)) (db:swissprot) IPYR_MYCGE P47593 MYCOPLASMA GENITALIUM 2097 -11540062 172542 inorganic pyrophosphatase (cl:inorganic pyrophosphatase) (ec:3.6.1.1) (db:pir2.dat) H64238 H64238 Mycoplasma genitalium 2097 -11540062 7500884234 mg351 inorganic pyrophosphatase ppa (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75250 pid:1673987 percent) (le:794) (re:1348) (di:direct) U39717 U39717 g3844935 Mycoplasma genitalium 2097 -11540062 5000697354 (de:(mg351) (pn:pyrophosphate phospho-hydrolase:ppase:inorganic pyrophosphatase:ppa) (gn:ppa) (gtcfc:2.1) (ec:3.6.1.1) (ipyr_mycge) (keggfc:2.1) (tigrfc:5.3) (db:gtc-mycoplasma genitalium)) MG351 MG351 Mycoplasma genitalium 2097 10022120

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917493	19035	41191	603	200

Description

GTC ORF with score 443 to: (db:genpept-bct1) (de:methanobacterium thermoautotrophicum from bases 161632 to 172569(section 15 of 148) of the complete genome.) (nt:function code:5.01 - l-amino acid metabolism,) (le:5667) (re:6947) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917499	19036	41192	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917501	19037	41193	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917505	19038	41194	261	86

Description

6500736205 atpc:mg398 atp synthase epsilon chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG398 MG398 Mycoplasma genitalium 2097 -11540063 60987 atpc:mg398 (ec:3.6.1.34) (de:atp synthase epsilon chain,) (db:swissprot) ATPE_MYCGE P47638 MYCOPLASMA GENITALIUM 2097 -11540063 172298 atp synthase epsilon chain atpc (cl:atp synthase epsilon chain) (db:pir2.dat) A64244 A64244 Mycoplasma genitalium 2097 -11540063 7500877528 mg398 atp synthase f1:subunit epsilon atpc (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to pid:1209767 gb:u00089 sp:q50332) (le:2377) (re:2778) (di:complement) U39722 U39722 g3844990 Mycoplasma genitalium 2097 -11540063 5000697355 (de:(mg398) (pn:atp synthase epsilon chain:atpc) (gn:atpc) (gtcfc:2.1) (ec:3.6.1.34) (atpe_mycge) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium)) MG398 MG398 Mycoplasma genitalium 2097 10003705

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917509	19039	41195	522	174

Description

6500736206 atpd:mg399 atp synthase beta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG399 MG399 Mycoplasma genitalium 2097 -11540064 141039 h+-transporting atp synthase:beta chain (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir2.dat) B64244 B64244 Mycoplasma genitalium 2097 -11540064 7500954335 atpd atp synthase beta chain (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium atpc, atpd, glya, laca genes from bases496998 to 504142 (section 47 of 56) of the complete genome.) (nt:identified by sequence similarity; similar to) (... U39725 U39725 g1046112 Mycoplasma genitalium 2097 -11540064 5000697356 (de:(mg399) (pn:atp synthase beta chain:atpd) (gn:atpd) (gtcfc:2.1) (ec:3.6.1.34) (atpb_mycge) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium)) MG399 MG399 Mycoplasma genitalium 2097 10003603

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917514	19040	41196	1230	409

Description

6500736207 atpg:mg400 atp synthase:gamma subunit:atp synthase gamma chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG400 MG400 Mycoplasma genitalium 2097 -11540065 61067 atpg:mg400 (ec:3.6.1.34) (de:atp synthase gamma chain,) (db:swissprot) ATPG_MYCGE P47640 MYCOPLASMA GENITALIUM 2097 -11540065 172299 h+-transporting atp synthase:gamma chain (cl:h+-transporting atp synthase gamma chain) (ec:3.6.1.34) (db:pir2.dat) C64244 C64244 Mycoplasma genitalium 2097 -11540065 7500877553 mg400 atp synthase f1:subunit gamma atpg (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to pid:1209765 gb:u00089 sp:q50330) (le:4215) (re:5054) (di:complement) U39722 U39722 g3844992 Mycoplasma genitalium 2097 -11540065 5000697357 (de:(mg400) (pn:atp synthase gamma chain:atp synthase, gamma subunit) (gn:atpg) (gtcfc:2.1) (ec:3.6.1.34) (atpg_mycge) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium)) MG400 MG400 Mycoplasma genitalium 2097 10003782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917518	19041	41197	729	242

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917531	19042	41198	321	106

Description

6500736208 atpa:mg401 atp synthase alpha chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG401 MG401 Mycoplasma genitalium 2097 -11540066 60813 atpa:mg401 (ec:3.6.1.34) (de:atp synthase alpha chain,) (db:swissprot) ATPA_MYCGE P47641 MYCOPLASMA GENITALIUM 2097 -11540066 141115 h+-transporting atp synthase:alpha chain (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir2.dat) D64244 D64244 Mycoplasma genitalium 2097 -11540066 7500877462 mg401 atp synthase f1:subunit alpha atpa (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to gb:z32649 pid:1209764 pid:474066) (le:5054) (re:6610) (di:complement) U39722 U39722 g3844993 Mycoplasma genitalium 2097 -11540066 5000697358 (de:(mg401) (pn:atp synthase alpha chain:atpa) (gn:atpa) (gtcfc:2.1) (ec:3.6.1.34) (atpa_mycge) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium)) MG401 MG401 Mycoplasma genitalium 2097 10003533

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917537	19043	41199	471	156

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917540	19044	41200	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917559	19045	41201	720	240

Description

6500736209 atph:mg402 atp synthase delta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG402 MG402 Mycoplasma genitalium 2097 -11540067 60940 atph:mg402 (ec:3.6.1.34) (de:atp synthase delta chain,) (db:swissprot) ATPD_MYCGE P47642 MYCOPLASMA GENITALIUM 2097 -11540067 172297 atp synthase delta chain atph (db:pir2.dat) E64244 E64244 Mycoplasma genitalium 2097 -11540067 7500877515 mg402 atp synthase f1:subunit delta atph (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to pid:1209763 gb:u00089 sp:q50328) (le:6626) (re:7156) (di:complement) U39722 U39722 g3844994 Mycoplasma genitalium 2097 -11540067 5000697359 (de:(mg402) (pn:atp synthase delta chain:atph) (gn:atph) (gtcfc:2.1) (ec:3.6.1.34) (atpd_mycge) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium)) MG402 MG402 Mycoplasma genitalium 2097 10003658

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917561	19046	41202	432	143

Description

6500736210 atpf:mg403 atp synthase b chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG403 MG403 Mycoplasma genitalium 2097 -11540068 61032 atpf:mg403 (ec:3.6.1.34) (de:atp synthase b chain,) (db:swissprot) ATPF_MYCGE P47643 MYCOPLASMA GENITALIUM 2097 -11540068 172295 atp synthase b chain atpf (cl:h+-transporting atp synthase chain b) (db:pir2.dat) F64244 F64244 Mycoplasma genitalium 2097 -11540068 7500877545 mg403 atp synthase f0:subunit b atpf (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to pid:1209762 gb:u00089 sp:q50327) (le:7149) (re:7775) (di:complement) U39722 U39722 g3844995 Mycoplasma genitalium 2097 -11540068 5000697360 (de:(mg403) (pn:atp synthase b chain:atpf) (gn:atpf) (gtcfc:2.1) (ec:3.6.1.34) (atpf_mycge) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium)) MG403 MG403 Mycoplasma genitalium 2097 10003747

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917565	19047	41203	2217	738

Description

6500736211 atpe:mg404 atp synthase c chain:lipid-binding protein:dicyclohexylcarbodiimide-binding protein (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG404 MG404 Mycoplasma genitalium 2097 -11540069 61135 atpe:mg404 (ec:3.6.1.34) (de:(dicyclohexylcarbodiimide-binding protein)) (db:swissprot) ATPL_MYCGE P47644 MYCOPLASMA GENITALIUM 2097 -11540069 172296 atp synthase c chain atpe (cl:h+-transporting atp synthase lipid-binding protein) (db:pir2.dat) G64244 G64244 Mycoplasma genitalium 2097 -11540069 7500877576 mg404 atp synthase f0:subunit c atpe (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to pid:1209761 gb:u00089 sp:q59550) (le:7778) (re:8086) (di:complement) U39722 U39722 g3844996 Mycoplasma genitalium 2097 -11540069 5000697361 (de:(mg404) (pn:lipid-binding protein:dicyclohexylcarbodiimide-binding protein:atp synthase c chain:atpe) (gn:atpe) (gtcfc:2.1) (ec:3.6.1.34) (atpl_mycge) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium)) MG404 MG404 Mycoplasma genitalium 2097 10003847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917578	19048	41204	516	171

Description

6500736212 atpb:mg405 atp synthase:a subunit:atp synthase a chain:protein 6 (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG405 MG405 Mycoplasma genitalium 2097 -11540070 60684 atpb:mg405 (ec:3.6.1.34) (de:atp synthase a chain, (protein 6)) (db:swissprot) ATP6_MYCGE P47645 MYCOPLASMA GENITALIUM 2097 -11540070 172287 h+-transporting atp synthase:chain a:atpase atpb (cl:h+-transporting atp synthase protein 6) (ec:3.6.1.34) (db:pir2.dat) H64244 H64244 Mycoplasma genitalium 2097 -11540070 7500877370 mg405 atp synthase f0:subunit a atpb (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to pid:1209760 gb:u00089 sp:q50326) (le:8089) (re:8967) (di:complement) U39722 U39722 g3844997 Mycoplasma genitalium 2097 -11540070 5000697362 (de:(mg405) (pn:atp synthase a chain:protein 6:atp synthase, a subunit) (gn:atpb) (gtcfc:2.1) (ec:3.6.1.34) (atp6_mycge) (keggfc:2.1) (tigrfc:6.2) (db:gtc-mycoplasma genitalium)) MG405 MG405 Mycoplasma genitalium 2097 10003410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917579	19049	41205	1131	376

Description

5000697341 glycerol-3-phospate dehydrogenase:gut2:hypothetical protein mg039 (gtcfc:2.1) (keggfc:14.2) (tigrfc:6.1) (db:gtc-mycoplasma genitalium) MG039 MG039 Mycoplasma genitalium 2097 -11540071 108459 mg039 (de:hypothetical protein mg039) (db:swissprot) Y039_MYCGE P47285 MYCOPLASMA GENITALIUM 2097 -11540071 172361 glycerol-3-phosphate dehydrogenase gut2 homolog (db:pir2.dat) C64204 C64204 Mycoplasma genitalium 2097 -11540071 7500894569 mg039 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 5 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75063 pid:1673759 percent) (le:7246) (re:8400) (di:complement) U39683 U39683 g3844649 Mycoplasma genitalium 2097 -11540071 6500736213 glycerol-3-phospate dehydrogenase:gut2:hypothetical protein mg039 (gtcfc:2.1) (keggfc:14.2) (tigrfc:6.1) (db:gtc-mycoplasma genitalium) MG039 MG039 Mycoplasma genitalium 2097 -11540071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917587	19050	41206	255	84

Description

6500736214 nox:mg275 nadh oxidase (gtcfc:2.1) (ec:1.6.-.-) (keggfc:14.1) (tigrfc:6.1) (db:gtc-mycoplasma genitalium) MG275 MG275 Mycoplasma genitalium 2097 -11540072 121043 nox:mg275 (ec:1.6.99.3) (de:probable nadh oxidase, (noxase)) (db:swissprot) NAOX_MYCGE Q49408 MYCOPLASMA GENITALIUM 2097 -11540072 172569 nadh oxidase nox homolog (db:pir2.dat) D64230 D64230 Mycoplasma genitalium 2097 -11540072 7500886281 mg275 nadh oxidase nox (db:genpept-bct2) (de:mycoplasma genitalium section 29 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75389 pid:1674132 percent) (le:2258) (re:3694) (di:complement) U39707 U39707 g3844868 Mycoplasma genitalium 2097 -11540072 5000697342 (de:(mg275) (pn:nadh oxidase:nox) (gn:nox) (gtcfc:1.1:13.7) (ec:1.6.-.-) (keggfc:11.1) (tigrfc:6.1) (db:gtc-mycoplasma genitalium)) MG275 MG275 Mycoplasma genitalium 2097 10064296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917593	19051	41207	720	239

Description

6500736215 glya:mg394 serine hydroxymethyltransferase:serine methylase:shmt (gtcfc:2.2:5.3:5.9:6.5:9.3:9.6) (ec:2.1.2.1) (keggfc:2.2:5.3:5.9:6.5:9.3:9.8) (tigrfc:1.1) (db:gtc-mycoplasma genitalium) (gtcfc:energy metabolism-methane metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:l-amino acid metaboli... MG394 MG394 Mycoplasma genitalium 2097 -11540073 74200 glya:mg394 (ec:2.1.2.1) (de:(shmt)) (db:swissprot) GLYA_MYCGE P47634 MYCOPLASMA GENITALIUM 2097 -11540073 137819 glya glycine hydroxymethyltransferase::serine hydroxymethyltransferase (cl:glycine hydroxymethyltransferase) (ec:2.1.2.1) (db:pir2.dat) F64243 F64243 Mycoplasma genitalium 2097 -11540073 7500882601 mg394 serine hydroxymethyltransferase glya (db:genpept-bct2) (de:mycoplasma genitalium section 43 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78011 pid:1673936 percent) (le:6041) (re:7261) (di:complement) U39721 U39721 g3844985 Mycoplasma genitalium 2097 -11540073 5000697363 (de:(mg394) (pn:serine methylase:shmt:serine hydroxymethyltransferase:glya) (gn:glya) (gtcfc:2.2:5.3:5.9:6.5:9.3) (ec:2.1.2.1) (glya_mycge) (keggfc:2.2:5.3:5.9:6.5:9.3:9.8) (tigrfc:1.1) (db:gtc-mycoplasma genitalium)) MG394 MG394 Mycoplasma genitalium 2097 10016722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917594	19052	41208	516	171

Description

5000697365 na+ atpase subunit j:ntpj:hypothetical protein mg322 (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG322 MG322 Mycoplasma genitalium 2097 -11540074 109083 mg322 (de:hypothetical protein mg322) (db:swissprot) Y322_MYCGE P47564 MYCOPLASMA GENITALIUM 2097 -11540074 172568 na+ atpase chain j homolog (cl:na+-atp synthase chain j) (db:pir2.dat) F64235 F64235 Mycoplasma genitalium 2097 -11540074 7500895125 mg322 cation transporter:putative (db:genpept-bct2) (de:mycoplasma genitalium section 35 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75323 pid:1674061 percent) (le:4868) (re:6544) (di:complement) U39713 U39713 g3844899 Mycoplasma genitalium 2097 -11540074 6500736216 na+ atpase subunit j:ntpj:hypothetical protein mg322 (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.2) (db:gtc-mycoplasma genitalium) MG322 MG322 Mycoplasma genitalium 2097 -11540074

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917595	19053	41209	258	85

Description

5000697367 hydroxymethylglutaryl-coa reductase:nadph:hypothetical protein mg085 (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-mycoplasma genitalium) MG085 MG085 Mycoplasma genitalium 2097 -11540075 108685 ptsk:mg085 (ec:2.7.1.-) (de:probable hpr(ser) kinase,) (db:swissprot) HPRK_MYCGE P47331 MYCOPLASMA GENITALIUM 2097 -11540075 172385 hydroxymethylglutaryl-coa reductase nadph homolog (cl:hypothetical protein yvob) (db:pir2.dat) D64209 D64209 Mycoplasma genitalium 2097 -11540075 7500883501 mg085 hpr ser kinase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75548 pid:1674310 percent) (le:2567) (re:3502) (di:direct) U39689 U39689 g3844672 Mycoplasma genitalium 2097 -11540075 6500736217 hydroxymethylglutaryl-coa reductase:nadph:hypothetical protein mg085 (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-mycoplasma genitalium) MG085 MG085 Mycoplasma genitalium 2097 -11540075

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917597	19054	41210	552	183

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917598	19055	41211	717	238

Description

6500736218 pgsa:mg114 cdp-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase:phosphatidylglycerophosphate synthase:pgp synthase (gtcfc:3.1:3.2:8.1) (ec:2.7.8.5) (keggfc:8.1) (tigrfc:7.1) (db:gtc-mycoplasma genitalium) MG114 MG114 Mycoplasma genitalium 2097 -11540076 89371 pgsa:mg114 (ec:2.7.8.5) (de:(ec 2.7.8.5) (phosphatidylglycerophosphate synthase) (pgp synthase)) (db:swissprot) PGSA_MYCGE P47360 MYCOPLASMA GENITALIUM 2097 -11540076 172588 cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (cl:cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase) (ec:2.7.8.5) (db:pir2.dat) F64212 F64212 Mycoplasma genitalium 2097 -11540076 7500887989 mg114 phosphatidylglycerophosphate synthase pgsa (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75520 pid:1674280 percent) (le:10121) (re:10831) (di:direct) U39691 U39691 g3844703 Mycoplasma genitalium 2097 -11540076 5000697426 (de:(mg114) (pn:cdp-diacylglycerol--glycerol-3-phosphate 3- phosphatidyltransferase:pgp synthase:phosphatidylglycerophosphate synthase:pgsa) (gn:pgsa) (gtcfc:8.1) (ec:2.7.8.5) (pgsa_mycge) (keggfc:8.1) (tigrfc:7.1) (db:gtc-mycop) MG114 MG114 Mycoplasma genitalium 2097 10031494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917612	19056	41212	939	312

Description

6500736219 plsc:mg212 1-acyl-sn-glycerol-3-phosphate acetyltransferase (gtcfc:3.1:3.2:8.1) (ec:2.3.1.51) (keggfc:8.1) (tigrfc:7.1) (db:gtc-mycoplasma genitalium) MG212 MG212 Mycoplasma genitalium 2097 -11540077 120374 plsc:mg212 (ec:2.3.1.51) (de:acyltransferase) (lpaat)) (db:swissprot) PLSC_MYCGE Q49402 MYCOPLASMA GENITALIUM 2097 -11540077 172280 1-acyl-sn-glycerol-3-phosphate acetyltransferase homolog (db:pir2.dat) D64223 D64223 Mycoplasma genitalium 2097 -11540077 7500888172 mg212 1-acyl-sn-glycerol-3-phosphate acetyltransferase (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75479 pid:1674233 percent) (le:909) (re:1715) (di:direct) U39701 U39701 g3844812 Mycoplasma genitalium 2097 -11540077 5000697427 (de:(mg212) (pn:1-acyl-sn-glycerol-3-phosphate acetyltransferase:plsc) (gn:plsc) (gtcfc:8.1) (ec:2.3.1.51) (keggfc:8.1) (tigrfc:7.1) (db:gtc-mycoplasma genitalium)) MG212 MG212 Mycoplasma genitalium 2097 10063354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917650	19057	41213	822	273

Description

GTC ORF with score 128 to: (sr:human) (db:genpept-pri1) (de:human dna sequence from cosmid l191f1, huntington's disease region,chromosome 4p16.3 contains huntington disease (hd) gene, cpg islandests and u7 small nuclear rna.) (le:<1735:13662) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917654	19058	41214	1515	504

Description

6500736220 lip1:mg344 lipase-esterase (gtcfc:3.1:3.2:8.1) (ec:3.1.1.3) (keggfc:8.1) (tigrfc:7.1) (db:gtc-mycoplasma genitalium) MG344 MG344 Mycoplasma genitalium 2097 -11540078 500684882 mg344 (ec:3.1.-.-) (de:putative esterase/lipase 3,) (db:swissprot) ESL3_MYCGE Q49421 MYCOPLASMA GENITALIUM 2097 -11540078 172548 lipase-esterase lip1 homolog (cl:triacylglycerol lipase 1) (db:pir2.dat) A64238 A64238 Mycoplasma genitalium 2097 -11540078 7500881169 mg344 lipase/esterase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75268 pid:1673997 percent) (le:1680) (re:2501) (di:complement) U39716 U39716 g3844927 Mycoplasma genitalium 2097 -11540078 5000697428 (de:(mg344) (pn:lipase-esterase:lip1) (gn:lip1) (gtcfc:8.1) (ec:3.1.1.3) (keggfc:8.1) (tigrfc:7.1) (db:gtc-mycoplasma genitalium)) MG344 MG344 Mycoplasma genitalium 2097 10060208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917676	19059	41215	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917682	19060	41216	231	76

Description

6500736221 plsx:mg368 fatty acid/phospholipid synthesis protein (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-mycoplasma genitalium) MG368 MG368 Mycoplasma genitalium 2097 -11540079 500685148 plsx:mg368 (de:fatty acid/phospholipid synthesis protein plsx homolog) (db:swissprot) PLSX_MYCGE Q49427 MYCOPLASMA GENITALIUM 2097 -11540079 172349 fatty acid/phospholipid synthesis protein plsx homolog (cl:phospholipid synthesis protein) (db:pir2.dat) G64240 G64240 Mycoplasma genitalium 2097 -11540079 7500888176 mg368 fatty acid/phospholipid synthesis protein (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75232 pid:1673967 percent) (le:5900) (re:6886) (di:complement) U39718 U39718 g3844955 Mycoplasma genitalium 2097 -11540079 5000697368 (de:(mg368) (pn:fatty acid) (gn:plsx) (gtcfc:3.8:8.2:8.3) (ec:) (keggfc:11.2) (tigrfc:7.1) (db:gtc-mycoplasma genitalium)) MG368 MG368 Mycoplasma genitalium 2097 10063357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917695	19061	41217	1470	489

Description

GTC ORF with score 135 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana dna chromosome 4, bac clone f8b4 (essaiiproject).) (nt:similarity to cdc28/cdc2-like kinase associating) (le:47842:48271:48426) (re:48154:48339:49698) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917696	19062	41218	2685	894

Description

6500736222 cdsa:mg437 cdp-diglyceride synthetase (gtcfc:3.1:3.2:8.1) (ec:2.7.7.41) (keggfc:8.1) (tigrfc:7.1) (db:gtc-mycoplasma genitalium) MG437 MG437 Mycoplasma genitalium 2097 -11540080 120120 cdsa:mg437 (ec:2.7.7.41) (de:cytidylyltransferase) (cdp-dag synthase)) (db:swissprot) CDSA_MYCGE Q49433 MYCOPLASMA GENITALIUM 2097 -11540080 172587 phosphatidate cytidylyltransferase::cdp-diglyceride synthetase (ec:2.7.7.41) (db:pir2.dat) C64248 C64248 Mycoplasma genitalium 2097 -11540080 7500878467 cdsa cdp-diglyceride synthetase (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium cdsa, frr, hsds, smba, tsf genes from bases539564 to 546816 (section 52 of 56) of the complete genome.) (nt:identified by sequence similarity; similar t... U39730 U39730 g1046154 Mycoplasma genitalium 2097 -11540080 5000697429 (de:(mg437) (pn:cdp-diglyceride synthetase:cdsa) (gn:cdsa) (gtcfc:8.1) (ec:2.7.7.41) (keggfc:8.1) (tigrfc:7.1) (db:gtc-mycoplasma genitalium)) MG437 MG437 Mycoplasma genitalium 2097 10062972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917701	19063	41219	636	211

Description

GTC ORF with score 282 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.pombe unknown protein : ddbj acc#) (le:15395) (re:16642)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917707	19064	41220	1209	402

Description

6500736223 ksga:mg463 dimethyladenosine transferase:s-adenosylmethionine-6-n:n-adenosyl:rrna dimethyltransferase:16s rrna dimethylase:high level kasugamycin resistance protein ksga:kasugamycin dimethyltransferase (gtcfc:3.7:5.11:5.14:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (db:gtc-mycoplasma genitalium) MG463 MG463 Mycoplasma genitalium 2097 -11540081 81180 ksga:mg463 (ec:2.1.1.-) (de:dimethyltransferase)) (db:swissprot) KSGA_MYCGE P47701 MYCOPLASMA GENITALIUM 2097 -11540081 172380 high level kasgamycin resistance ksga homolog (cl:rrna (adenine-n6-)-methyltransferase) (db:pir2.dat) B64251 B64251 Mycoplasma genitalium 2097 -11540081 7500884749 mg463 dimethyladenosine transferase (db:genpept-bct2) (de:mycoplasma genitalium section 50 of 51 of the complete genome.) (nt:similar to sp:p43038 pid:416234 percent identity:) (le:3751) (re:4530) (di:complement) U39728 U39728 g3845058 Mycoplasma genitalium 2097 -11540081 5000697366 (de:(mg463) (pn:dimethyladenosine transferase:s-adenosylmethionine-6-n", n"-adenosyl:rrna dimethyltransferase:16s rrna dimethylase:high level kasugamycin resistance protein ksga:kasugamycin dimethyltransferase) (gn:ksga) (gtcfc:3.7:5.1) MG463 MG463 Mycoplasma genitalium 2097 10023416

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917725	19065	41221	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917750	19066	41222	408	135

Description

GTC ORF with score 197 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri3) (de:homo sapiens mrna for kiaa0017 protein, complete cds.) (nt:similar to human xeroderma pigmentosum groupe) (le:157) (re:3810) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917751	19067	41223	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917762	19068	41224	537	179

Description

GTC ORF with score 557 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri3) (de:homo sapiens mrna for kiaa0017 protein, complete cds.) (nt:similar to human xeroderma pigmentosum groupe) (le:157) (re:3810) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917765	19069	41225	642	213

Description

6500736224 dnan:mg001 dna polymerase iii:beta chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG001 MG001 Mycoplasma genitalium 2097 -11540082 69060 dnan:mg001 (ec:2.7.7.7) (de:dna polymerase iii, beta chain,) (db:swissprot) DP3B_MYCGE P47247 MYCOPLASMA GENITALIUM 2097 -11540082 172333 dnan dna polymerase iii beta chain (db:pir2.dat) A64200 A64200 Mycoplasma genitalium 2097 -11540082 7500880550 dnan dna polymerase iii beta subunit (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium cdc8, dnae_1, dnah_1, dnaj_1, dnan, gyra,gyrb, rimk, sers, tdhf genes from bases 1 to 14345 (section 1 of56) of the complete genome.) (nt:identified by ... U39679 U39679 g1045669 Mycoplasma genitalium 2097 -11540082 5000697369 (de:(mg001) (pn:dna polymerase iii, beta chain) (gn:dnan) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dp3b_mycge) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG001 MG001 Mycoplasma genitalium 2097 10011643

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917776	19070	41226	954	317

Description

6500736225 rpoe:mg022 rna polymerase delta subunit:probable dna-directed rna polymerase delta subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG022 MG022 Mycoplasma genitalium 2097 -11540083 96274 rpoe:mg022 (ec:2.7.7.6) (de:probable dna-directed rna polymerase delta subunit,) (db:swissprot) RPOE_MYCGE P47268 MYCOPLASMA GENITALIUM 2097 -11540083 172342 dna-directed rna polymerase:delta chain rpoe (ec:2.7.7.6) (db:pir2.dat) D64202 D64202 Mycoplasma genitalium 2097 -11540083 7500890650 mg022 dna-directed rna polymerase:subunit delta (db:genpept-bct2) (de:mycoplasma genitalium section 3 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75090 pid:1673789 percent) (le:5616) (re:6053) (di:direct) U39681 U39681 g3844631 Mycoplasma genitalium 2097 -11540083 5000697370 (de:(mg022) (pn:probable dna-directed rna polymerase delta subunit:rna polymerase delta subunit:rpoe) (gn:rpoe) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpoe_mycge) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium)) MG022 MG022 Mycoplasma genitalium 2097 10038217

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917779	19071	41227	1137	378

Description

GTC ORF with score 406 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmids 9781, 8198, 9115,9981, and lambda clones 3955 and 6052.) (nt:similar to endosome membrane protein p24b from s.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917781	19072	41228	345	114

Description

GTC ORF with score 217 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f08f1.) (nt:strong similarity to saccharomyces cerevisiae) (le:12974:13463:13738) (re:13105:13682:14227) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917790	19073	41229	282	93

Description

GTC ORF with score 196 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f08f1.) (nt:strong similarity to saccharomyces cerevisiae) (le:12974:13463:13738) (re:13105:13682:14227) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917791	19074	41230	534	177

Description

GTC ORF with score 403 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0255 gene, complete cds.) (nt:similar to s.cerevisiae emp70 protein precursor) (le:341) (re:2218) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917807	19075	41231	885	294

Description

6500736226 polc:mg031 dna polymerase iii:dna polymerase iii:alpha chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG031 MG031 Mycoplasma genitalium 2097 -11540084 69045 polc:mg031 (ec:2.7.7.7) (de:dna polymerase iii, alpha chain polc-type, (poliii)) (db:swissprot) DPO3_MYCGE P47277 MYCOPLASMA GENITALIUM 2097 -11540084 172331 dna polymerase iii polc homolog (cl:dna-directed dna polymerase iii alpha chain polc) (db:pir2.dat) D64203 D64203 Mycoplasma genitalium 2097 -11540084 7500880539 mg031 dna polymerase iii:subunit alpha polc-1 (db:genpept-bct2) (de:mycoplasma genitalium section 4 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75080 pid:1673778 percent) (le:3839) (re:8194) (di:complement) U39682 U39682 g3844641 Mycoplasma genitalium 2097 -11540084 5000697371 (de:(mg031) (pn:dna polymerase iii, alpha chain:dna polymerase iii:polc) (gn:polc) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dp3a_mycge) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG031 MG031 Mycoplasma genitalium 2097 10011628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917815	19076	41232	603	200

Description

6500736227 deod:mg049 purine-nucleoside phosphorylase:purine nucleoside phosphorylase:inosine phosphorylase:pnp (gtcfc:4.1:4.2:4.4:9.4) (ec:2.4.2.1) (keggfc:4.1:4.2:9.4) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG049 MG049 Mycoplasma genitalium 2097 -11540085 172614 purine-nucleoside phosphorylase (cl:purine-nucleoside phosphorylase pnp) (db:pir2.dat) D64205 D64205 Mycoplasma genitalium 2097 -11540085 7500965563 mg049 purine-nucleoside phosphorylase deod (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75053 pid:1673747 percent) (le:8406) (re:9368) (di:direct) U39684 U39684 g1045722 Mycoplasma genitalium 2097 -11540085 5000697372 (de:(mg049) (pn:purine nucleoside phosphorylase:inosine phosphorylase:pnp:purine-nucleoside phosphorylase:deod) (gn:deod) (gtcfc:4.1:4.2:9.4) (ec:2.4.2.1) (deod_mycge) (keggfc:4.1:4.2:9.4) (tigrfc:8.4) (db:gtc-mycoplasma genital) MG049 MG049 Mycoplasma genitalium 2097 10010855

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917833	19077	41233	537	178

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917836	19078	41234	264	87

Description

6500736228 deoa:mg051 thymidine phosphorylase:tdrpase (gtcfc:4.1:4.2:4.4) (ec:2.4.2.4) (keggfc:4.1:4.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG051 MG051 Mycoplasma genitalium 2097 -11540086 102894 deoa:mg051 (ec:2.4.2.4) (de:thymidine phosphorylase, (tdrpase)) (db:swissprot) TYPH_MYCGE P47297 MYCOPLASMA GENITALIUM 2097 -11540086 172679 thymidine phosphorylase (cl:thymidine phosphorylase) (ec:2.4.2.4) (db:pir1.dat) F64205 F64205 Mycoplasma genitalium 2097 -11540086 7500893603 mg051 thymidine phosphorylase deoa (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75052 pid:1673745 percent) (le:10030) (re:11295) (di:direct) U39684 U39684 g1045724 Mycoplasma genitalium 2097 -11540086 5000697373 (de:(mg051) (pn:tdrpase:thymidine phosphorylase:deoa) (gn:deoa) (gtcfc:4.1:4.2) (ec:2.4.2.4) (typh_mycge) (keggfc:4.1:4.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium)) MG051 MG051 Mycoplasma genitalium 2097 10044706

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917841	19079	41235	1029	342

Description

6500736229 gmk:mg107 5guanylate kinase:guanylate kinase:gmp kinase (gtcfc:4.1) (ec:2.7.4.8) (keggfc:4.1) (tigrfc:8.3) (db:gtc-mycoplasma genitalium) MG107 MG107 Mycoplasma genitalium 2097 -11540087 172367 guanylate kinase (cl:guanylate kinase:guanylate kinase homology) (ec:2.7.4.8) (db:pir2.dat) H64211 H64211 Mycoplasma genitalium 2097 -11540087 7500965552 gmk 5guanylate kinase (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium asns, cfxec, def, gmk, pgib, pgsa, ptc1, vacbgenes from bases 131230 to 142208 (section 12 of 56) of thecomplete genome.) (nt:identified by sequence sim... U39690 U39690 g1045786 Mycoplasma genitalium 2097 -11540087 5000697374 (de:(mg107) (pn:guanylate kinase:gmp kinase:5"guanylate kinase:gmk) (gn:gmk) (gtcfc:4.1) (ec:2.7.4.8) (kgua_mycge) (keggfc:4.1) (tigrfc:8.3) (db:gtc-mycoplasma genitalium)) MG107 MG107 Mycoplasma genitalium 2097 10022898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917855	19080	41236	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917862	19081	41237	1125	374

Description

6500736230 adk:mg171 adenylate kinase:atp-amp transphosphorylase (gtcfc:4.1) (ec:2.7.4.3) (keggfc:4.1) (tigrfc:8.3) (db:gtc-mycoplasma genitalium) MG171 MG171 Mycoplasma genitalium 2097 -11540088 80337 adk:mg171 (ec:2.7.4.3) (de:adenylate kinase, (atp-amp transphosphorylase)) (db:swissprot) KAD_MYCGE P47417 MYCOPLASMA GENITALIUM 2097 -11540088 172288 adenylate kinase (cl:adenylate kinase) (ec:2.7.4.3) (db:pir2.dat) I64218 I64218 Mycoplasma genitalium 2097 -11540088 7500884461 mg171 adenylate kinase adk (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215703 gb:u00089 sp:q50299) (le:12493) (re:13137) (di:direct) U39696 U39696 g3844765 Mycoplasma genitalium 2097 -11540088 5000697375 (de:(mg171) (pn:atp-amp transphosphorylase:adenylate kinase:adk) (gn:adk) (gtcfc:4.1) (ec:2.7.4.3) (kad_mycge) (keggfc:4.1) (tigrfc:8.3) (db:gtc-mycoplasma genitalium)) MG171 MG171 Mycoplasma genitalium 2097 10022587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917885	19082	41238	1368	455

Description

6500736231 rpoa:mg177 rna polymerase alpha core subunit:dna-directed rna polymerase alpha chain:transcriptase alpha chain:rna polymerase alpha subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG177 MG177 Mycoplasma genitalium 2097 -11540089 96174 rpoa:mg177 (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA_MYCGE P47423 MYCOPLASMA GENITALIUM 2097 -11540089 172339 dna-directed rna polymerase:alpha core chain (cl:dna-directed rna polymerase alpha chain) (ec:2.7.7.6) (db:pir2.dat) F64219 F64219 Mycoplasma genitalium 2097 -11540089 7500890604 mg177 dna-directed rna polymerase:subunit alpha (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215697 gb:u00089 sp:q50295) (le:878) (re:1864) (di:direct) U39697 U39697 g3844773 Mycoplasma genitalium 2097 -11540089 5000697376 (de:(mg177) (pn:dna-directed rna polymerase alpha chain:transcriptase alpha chain:rna polymerase alpha subunit:rna polymerase alpha core subunit:rpoa) (gn:rpoa) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpoa_mycge) (keggfc:4.1:4.2) (tigrfc:) MG177 MG177 Mycoplasma genitalium 2097 10038117

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917911	19083	41239	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917918	19084	41240	2361	786

Description

6500736232 nrdf:mg229 ribonucleotide reductase 2:ribonucleoside-diphosphate reductase beta chain:ribonucleotide reductase (gtcfc:4.1:4.2) (ec:1.17.4.1) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-mycoplasma genitalium) (tigrfc:purines, pyrimidines, nucleosides, and nucleotides-2'-deoxyribonucleotide metabolism) MG229 MG229 Mycoplasma genitalium 2097 -11540090 94454 nrdf:mg229 (ec:1.17.4.1) (de:(ribonucleotide reductase)) (db:swissprot) RIR2_MYCGE P47471 MYCOPLASMA GENITALIUM 2097 -11540090 172623 ribonucleotide reductase 2 nrdf homolog (cl:ribonucleoside-diphosphate reductase beta) (db:pir2.dat) C64225 C64225 Mycoplasma genitalium 2097 -11540090 7500889807 mg229 ribonucleoside-diphosphate reductase:beta chain (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75461 pid:1674208 percent) (le:9088) (re:10110) (di:direct) U39702 U39702 g3844832 Mycoplasma genitalium 2097 -11540090 5000697377 (de:(mg229) (pn:ribonucleoside-diphosphate reductase beta chain:ribonucleotide reductase:ribonucleotide reductase 2:nrdf) (gn:nrdf) (gtcfc:4.1:4.2) (ec:1.17.4.1) (rir2_mycge) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-mycoplasma geni) MG229 MG229 Mycoplasma genitalium 2097 10036434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917937	19085	41241	3162	1053

Description

6500736233 nrde:mg231 ribonucleotide reductase r1 subunit:ribonucleoside-diphosphate reductase alpha chain:ribonucleotide reductase (gtcfc:4.1:4.2) (ec:1.17.4.1) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-mycoplasma genitalium) (tigrfc:purines, pyrimidines, nucleosides, and nucleotides-2'-deoxyribonucleotide metabolism) MG231 MG231 Mycoplasma genitalium 2097 -11540091 94422 nrde:mg231 (ec:1.17.4.1) (de:(ribonucleotide reductase)) (db:swissprot) RIR1_MYCGE P47473 MYCOPLASMA GENITALIUM 2097 -11540091 172622 ribonucleoside-diphosphate reductase (cl:salmonella typhimurium ribonucleoside-diphosphate reductase) (ec:1.17.4.1) (db:pir2.dat) E64225 E64225 Mycoplasma genitalium 2097 -11540091 7500889800 mg231 ribonucleoside-diphosphate reductase:alpha (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78027 pid:1674206 percent) (le:10594) (re:12759) (di:direct) U39702 U39702 g3844834 Mycoplasma genitalium 2097 -11540091 5000697378 (de:(mg231) (pn:ribonucleoside-diphosphate reductase alpha chain:ribonucleotide reductase:ribonucleotide reductase r1 subunit) (gn:nrde) (gtcfc:4.1:4.2) (ec:1.17.4.1) (rir1_mycge) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-mycoplasma) MG231 MG231 Mycoplasma genitalium 2097 10036402

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917938	19086	41242	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917947	19087	41243	2199	732

Description

6500736234 dnae:mg261 dna polymerase iii alpha subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG261 MG261 Mycoplasma genitalium 2097 -11540092 118049 dnae:mg261 (ec:2.7.7.7) (de:dna polymerase iii, alpha chain,) (db:swissprot) DP3A_MYCGE Q49405 MYCOPLASMA GENITALIUM 2097 -11540092 172332 dna polymerase iii alpha chain dnae homolog (cl:polydeoxyribonucleotide synthase (nad+)) (db:pir2.dat) H64228 H64228 Mycoplasma genitalium 2097 -11540092 7500880541 mg261 dna polymerase iii:subunit alpha polc-2 (db:genpept-bct2) (de:mycoplasma genitalium section 27 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75404 pid:1674148 percent) (le:5286) (re:7910) (di:direct) U39705 U39705 g1045954 Mycoplasma genitalium 2097 -11540092 5000697379 (de:(mg261) (pn:dna polymerase iii alpha subunit:dnae) (gn:dnae) (gtcfc:4.1:4.2) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG261 MG261 Mycoplasma genitalium 2097 10060070

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917949	19088	41244	1281	427

Description

6500736235 poli:mg262 dna polymerase i (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG262 MG262 Mycoplasma genitalium 2097 -11540093 118044 pola:mg262 (ec:3.1.11.-) (de:potential 5'-3' exonuclease,) (db:swissprot) EX53_MYCGE Q49406 MYCOPLASMA GENITALIUM 2097 -11540093 172330 dna polymerase i homolog:hypothetical protein mg262:hypothetical protein mg468 (db:pir2.dat) I64228 I64228 Mycoplasma genitalium 2097 -11540093 7500881215 mg262 5-3 exonuclease:putative (db:genpept-bct2) (de:mycoplasma genitalium section 27 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75403 pid:1674147 percent) (le:7917) (re:8792) (di:direct) U39705 U39705 g1045955 Mycoplasma genitalium 2097 -11540093 5000697380 (de:(mg262) (pn:dna polymerase i:poli) (gn:poli) (gtcfc:4.1:4.2) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG262 MG262 Mycoplasma genitalium 2097 10060064

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501917987	19089	41245	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918004	19090	41246	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918014	19091	41247	600	199

Description

6500736236 apt:mg276 adenine phosphoribosyltransferase:aprt (gtcfc:4.1:4.4) (ec:2.4.2.7) (keggfc:4.1) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG276 MG276 Mycoplasma genitalium 2097 -11540094 59905 apt:mg276 (ec:2.4.2.7) (de:adenine phosphoribosyltransferase, (aprt)) (db:swissprot) APT_MYCGE P47518 MYCOPLASMA GENITALIUM 2097 -11540094 172286 adenine phosphoribosyltransferase::amp pyrophosphorylase:transphosphoribosidase (cl:adenine phosphoribosyltransferase) (ec:2.4.2.7) (db:pir2.dat) E64230 E64230 Mycoplasma genitalium 2097 -11540094 7500877009 mg276 adenine phosphoribosyltransferase (db:genpept-bct2) (de:mycoplasma genitalium section 29 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75388 pid:1674131 percent) (le:3777) (re:4319) (di:complement) U39707 U39707 g1045971 Mycoplasma genitalium 2097 -11540094 5000697381 (de:(mg276) (pn:aprt:adenine phosphoribosyltransferase) (gn:apt) (gtcfc:4.1) (ec:2.4.2.7) (apt_mycge) (keggfc:4.1) (tigrfc:8.4) (db:gtc-mycoplasma genitalium)) MG276 MG276 Mycoplasma genitalium 2097 10002638

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918024	19092	41248	402	133

Description

6500736237 spot:mg278 stringent response-like protein:rel:probable guanosine-3:5-bis:diphosphate 3-pyrophosphohydrolase:ppgppase:penta-phosphate guanosine-3-pyrophosphohydrolase (gtcfc:4.1:10.2) (ec:3.1.7.2) (keggfc:4.1) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG278 MG278 Mycoplasma genitalium 2097 -11540095 99300 spot:mg278 (ec:3.1.7.2) (de:pyrophosphohydrolase)) (db:swissprot) SPOT_MYCGE P47520 MYCOPLASMA GENITALIUM 2097 -11540095 172673 stringent response-like protein rel homolog (db:pir2.dat) G64230 G64230 Mycoplasma genitalium 2097 -11540095 7500891990 mg278 guanosine-3:5-bis diphosphate 3- (db:genpept-bct2) (de:mycoplasma genitalium section 29 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75386 pid:1674128 percent) (le:7288) (re:9450) (di:direct) U39707 U39707 g1045973 Mycoplasma genitalium 2097 -11540095 5000697382 (de:(mg278) (pn:probable guanosine-3",5"-bis:diphosphate 3"-pyrophosphohydrolase:ppgppase:penta-phosphate guanosine-3"-pyrophosphohydrolase:stringent response-like protein:rel) (gn:spot) (gtcfc:4.1) (ec:3.1.7.2) (spot_mycge) (k)) MG278 MG278 Mycoplasma genitalium 2097 10041159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918035	19093	41249	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918042	19094	41250	438	145

Description

6500736238 rpoc:mg340 dna-directed rna polymerase beta chain:transcriptase beta chain:rna polymerase beta subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG340 MG340 Mycoplasma genitalium 2097 -11540096 96234 rpoc:mg340 (ec:2.7.7.6) (de:beta' chain) (rna polymerase beta' subunit)) (db:swissprot) RPOC_MYCGE P47582 MYCOPLASMA GENITALIUM 2097 -11540096 172341 rpoc dna-directed rna polymerase:beta chain (ec:2.7.7.6) (db:pir2.dat) F64237 F64237 Mycoplasma genitalium 2097 -11540096 7500890629 mg340 dna-directed rna polymerase:subunit beta (db:genpept-bct2) (de:mycoplasma genitalium section 37 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75271 pid:1674001 percent) (le:9198) (re:13076) (di:complement) U39715 U39715 g3844922 Mycoplasma genitalium 2097 -11540096 5000697383 (de:(mg340) (pn:transcriptase beta" chain:rna polymerase beta" subunit:dna-directed rna polymerase beta" chain:rpoc) (gn:rpoc) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpoc_mycge) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-mycoplasma genitaliu) MG340 MG340 Mycoplasma genitalium 2097 10038177

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918044	19095	41251	843	280

Description

6500736239 rpob:mg341 dna-directed rna polymerase:beta subunit:dna-directed rna polymerase beta chain:transcriptase beta chain:rna polymerase beta subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG341 MG341 Mycoplasma genitalium 2097 -11540097 96200 rpob:mg341 (ec:2.7.7.6) (de:beta chain) (rna polymerase beta subunit)) (db:swissprot) RPOB_MYCGE P47583 MYCOPLASMA GENITALIUM 2097 -11540097 172340 dna-directed rna polymerase:beta chain (cl:dna-directed rna polymerase beta chain) (ec:2.7.7.6) (db:pir2.dat) G64237 G64237 Mycoplasma genitalium 2097 -11540097 7500890618 mg341 dna-directed rna polymerase:subunit beta (db:genpept-bct2) (de:mycoplasma genitalium section 37 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78013 pid:1674000 percent) (le:13086) (re:17258) (di:complement) U39715 U39715 g3844923 Mycoplasma genitalium 2097 -11540097 5000697384 (de:(mg341) (pn:dna-directed rna polymerase beta chain:transcriptase beta chain:rna polymerase beta subunit:dna-directed rna polymerase, beta subunit:rpob) (gn:rpob) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpob_mycge) (keggfc:4.1:4.2) (ti) MG341 MG341 Mycoplasma genitalium 2097 10038143

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918048	19096	41252	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918055	19097	41253	507	168

Description

5000697385 dnax:dnah:mg420 dna polymerase iii subunit:dnah:dna polymerase iii:gamma chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG420 MG420 Mycoplasma genitalium 2097 -11540098 69080 dnax:dnah:mg420 (ec:2.7.7.7) (de:dna polymerase iii, gamma chain,) (db:swissprot) DP3X_MYCGE P47659 MYCOPLASMA GENITALIUM 2097 -11540098 172334 dna polymerase iii chain dnah (db:pir2.dat) D64246 D64246 Mycoplasma genitalium 2097 -11540098 7500880558 mg420 dna polymerase iii:subunit gamma and tau (db:genpept-bct2) (de:mycoplasma genitalium section 46 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75177 pid:1673890 percent) (le:2539) (re:3321) (di:complement) U39724 U39724 g3845015 Mycoplasma genitalium 2097 -11540098 6500736240 dnax:dnah dna polymerase iii subunit:dnah:dna polymerase iii:gamma chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG420 MG420 Mycoplasma genitalium 2097 -11540098

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918057	19098	41254	720	239

Description

6500736241 hpt:mg458 hypoxanthine-guanine phosphoribosyltransferase:hgprt:hgprtase (gtcfc:4.1:4.4) (ec:2.4.2.8) (keggfc:4.1) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG458 MG458 Mycoplasma genitalium 2097 -11540099 77564 hpt:mg458 (ec:2.4.2.8) (de:(hgprtase)) (db:swissprot) HPRT_MYCGE P47696 MYCOPLASMA GENITALIUM 2097 -11540099 172540 hypoxanthine-guanine phosphoribosyltransferase (cl:hypoxanthine phosphoribosyltransferase) (db:pir2.dat) F64250 F64250 Mycoplasma genitalium 2097 -11540099 7500883505 mg458 hypoxanthine-guanine phosphoribosyltransferase (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75119 pid:1673832 percent) (le:8462) (re:8989) (di:complement) U39727 U39727 g3845052 Mycoplasma genitalium 2097 -11540099 5000697386 (de:(mg458) (pn:hgprt:hgprtase:hypoxanthine-guanine phosphoribosyltransferase:hpt) (gn:hpt) (gtcfc:4.1) (ec:2.4.2.8) (hprt_mycge) (keggfc:4.1) (tigrfc:8.4) (db:gtc-mycoplasma genitalium)) MG458 MG458 Mycoplasma genitalium 2097 10019924

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918058	19099	41255	321	106

Description

6500736242 upp:mg030 uracil phosphoribosyltransferase:ump pyrophosphorylase:uprtase (gtcfc:4.2:4.4) (ec:2.4.2.9) (keggfc:4.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG030 MG030 Mycoplasma genitalium 2097 -11540100 103786 upp:mg030 (ec:2.4.2.9) (de:(uprtase)) (db:swissprot) UPP_MYCGE P47276 MYCOPLASMA GENITALIUM 2097 -11540100 172706 uracil phosphoribosyltransferase:upp-type (cl:uracil phosphoribosyltransferase upp) (ec:2.4.2.9) (db:pir2.dat) C64203 C64203 Mycoplasma genitalium 2097 -11540100 7500893828 mg030 uracil phosphoribosyltransferase upp (db:genpept-bct2) (de:mycoplasma genitalium section 4 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75081 pid:1673780 percent) (le:3185) (re:3805) (di:complement) U39682 U39682 g3844640 Mycoplasma genitalium 2097 -11540100 5000697387 (de:(mg030) (pn:ump pyrophosphorylase:uprtase:uracil phosphoribosyltransferase:upp) (gn:upp) (gtcfc:4.2) (ec:2.4.2.9) (upp_mycge) (keggfc:4.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium)) MG030 MG030 Mycoplasma genitalium 2097 10045556

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918071	19100	41256	2625	874

Description

6500736243 tdk:mg034 thymidine kinase (gtcfc:4.2:4.4) (ec:2.7.1.21) (keggfc:4.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG034 MG034 Mycoplasma genitalium 2097 -11540101 80780 tdk:mg034 (ec:2.7.1.21) (de:thymidine kinase,) (db:swissprot) KITH_MYCGE P47280 MYCOPLASMA GENITALIUM 2097 -11540101 172678 thymidine kinase (cl:thymidine kinase) (ec:2.7.1.21) (db:pir2.dat) G64203 G64203 Mycoplasma genitalium 2097 -11540101 7500884639 mg034 thymidine kinase tdk (db:genpept-bct2) (de:mycoplasma genitalium section 5 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75070 pid:1673767 percent) (le:851) (re:1492) (di:complement) U39683 U39683 g3844644 Mycoplasma genitalium 2097 -11540101 5000697388 (de:(mg034) (pn:thymidine kinase:tdk) (gn:tdk) (gtcfc:4.2) (ec:2.7.1.21) (kith_mycge) (keggfc:4.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium)) MG034 MG034 Mycoplasma genitalium 2097 10023021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918073	19101	41257	576	191

Description

6500736244 cdd:mg052 cytidine deaminase:cytidine aminohydrolase:cda (gtcfc:4.2:4.4) (ec:3.5.4.5) (keggfc:4.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG052 MG052 Mycoplasma genitalium 2097 -11540102 63645 cdd:mg052 (ec:3.5.4.5) (de:cytidine deaminase, (cytidine aminohydrolase) (cda)) (db:swissprot) CDD_MYCGE P47298 MYCOPLASMA GENITALIUM 2097 -11540102 172320 cytidine deaminase (cl:cytidine deaminase) (ec:3.5.4.5) (db:pir2.dat) G64205 G64205 Mycoplasma genitalium 2097 -11540102 7500878431 mg052 cytidine deaminase cdd (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75051 pid:1673744 percent) (le:11304) (re:11696) (di:direct) U39684 U39684 g1045725 Mycoplasma genitalium 2097 -11540102 5000697389 (de:(mg052) (pn:cytidine aminohydrolase:cda:cytidine deaminase:cdd) (gn:cdd) (gtcfc:4.2) (ec:3.5.4.5) (cdd_mycge) (keggfc:4.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium)) MG052 MG052 Mycoplasma genitalium 2097 10006314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918074	19102	41258	1581	526

Description

6500736245 trxb:mg102 thioredoxin reductase (gtcfc:9.13) (ec:1.6.4.5) (keggfc:4.2) (tigrfc:8.1) (db:gtc-mycoplasma genitalium) (tigrfc:purines, pyrimidines, nucleosides, and nucleotides-2'-deoxyribonucleotide metabolism) MG102 MG102 Mycoplasma genitalium 2097 -11540103 102509 trxb:mg102 (ec:1.6.4.5) (de:thioredoxin reductase,) (db:swissprot) TRXB_MYCGE P47348 MYCOPLASMA GENITALIUM 2097 -11540103 172676 thioredoxin reductase nadph (cl:thioredoxin reductase:thioredoxin reductase homology) (ec:1.6.4.5) (db:pir1.dat) C64211 C64211 Mycoplasma genitalium 2097 -11540103 7500893540 mg102 thioredoxin reductase trxb (db:genpept-bct2) (de:mycoplasma genitalium section 12 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75531 pid:1674293) (le:7899) (re:8846) (di:direct) U39690 U39690 g3844690 Mycoplasma genitalium 2097 -11540103 5000697390 (de:(mg102) (pn:thioredoxin reductase:trxb) (gn:trxb) (gtcfc:4.2) (ec:1.6.4.5) (trxb_mycge) (keggfc:4.2) (tigrfc:8.1) (db:gtc-mycoplasma genitalium)) MG102 MG102 Mycoplasma genitalium 2097 10044328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918078	19103	41259	681	226

Description

6500736246 thya:mg227 thymidylate synthase:ts (gtcfc:4.2:9.6) (ec:2.1.1.45) (keggfc:4.2:9.7:9.8) (tigrfc:8.1) (db:gtc-mycoplasma genitalium) (gtcfc:nucleotide metabolism-pyrimidine metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) (tigrfc:purines, pyri... MG227 MG227 Mycoplasma genitalium 2097 -11540104 102951 thya:mg227 (ec:2.1.1.45) (de:thymidylate synthase, (ts)) (db:swissprot) TYSY_MYCGE P47469 MYCOPLASMA GENITALIUM 2097 -11540104 137768 thymidylate synthase (cl:thymidylate synthase:thymidylate synthase homology) (ec:2.1.1.45) (db:pir2.dat) A64225 A64225 Mycoplasma genitalium 2097 -11540104 7500893629 mg227 thymidylate synthase thya (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78029 pid:1674210 percent) (le:7737) (re:8600) (di:direct) U39702 U39702 g3844830 Mycoplasma genitalium 2097 -11540104 5000697391 (de:(mg227) (pn:ts:thymidylate synthase:thya) (gn:thya) (gtcfc:4.2) (ec:2.1.1.45) (tysy_mycge) (keggfc:4.2:9.8) (tigrfc:8.1) (db:gtc-mycoplasma genitalium)) MG227 MG227 Mycoplasma genitalium 2097 10044763

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918098	19104	41260	459	152

Description

6500736247 cmk:mg330 cytidylate kinase:ck:cytidine monophosphate kinase:cmp kinase (gtcfc:4.2:4.4) (ec:2.7.4.14) (keggfc:4.2) (tigrfc:8.2) (db:gtc-mycoplasma genitalium) MG330 MG330 Mycoplasma genitalium 2097 -11540105 80556 cmk:mg330 (ec:2.7.4.14) (de:(cmp kinase)) (db:swissprot) KCY_MYCGE P47572 MYCOPLASMA GENITALIUM 2097 -11540105 172321 cytidylate kinase (cl:cytidylate kinase cmk) (ec:2.7.4.14) (db:pir2.dat) E64236 E64236 Mycoplasma genitalium 2097 -11540105 7500884541 mg330 cytidylate kinase cmk (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75308 pid:1674043 percent) (le:5366) (re:6019) (di:complement) U39714 U39714 g3844910 Mycoplasma genitalium 2097 -11540105 5000697392 (de:(mg330) (pn:ck:cytidine monophosphate kinase:cmp kinase:cytidylate kinase:cmk) (gn:cmk) (gtcfc:4.2) (ec:2.7.4.14) (kcy_mycge) (keggfc:4.2) (tigrfc:8.2) (db:gtc-mycoplasma genitalium)) MG330 MG330 Mycoplasma genitalium 2097 10022798

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918105	19105	41261	384	127

Description

6500736248 udk:mg382 uridine kinase:uridine monophosphokinase (gtcfc:4.2:4.4) (ec:2.7.1.48) (keggfc:4.2) (tigrfc:8.2) (db:gtc-mycoplasma genitalium) MG382 MG382 Mycoplasma genitalium 2097 -11540106 103931 udk:mg382 (ec:2.7.1.48) (de:uridine kinase, (uridine monophosphokinase)) (db:swissprot) URK_MYCGE P47622 MYCOPLASMA GENITALIUM 2097 -11540106 172707 uridine kinase (cl:uridine kinase) (ec:2.7.1.48) (db:pir2.dat) C64242 C64242 Mycoplasma genitalium 2097 -11540106 7500893865 mg382 uridine kinase udk (db:genpept-bct2) (de:mycoplasma genitalium section 42 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75217 pid:1673952 percent) (le:219) (re:860) (di:direct) U39720 U39720 g3844971 Mycoplasma genitalium 2097 -11540106 5000697393 (de:(mg382) (pn:uridine kinase:uridine monophosphokinase:udk) (gn:udk) (gtcfc:4.2) (ec:2.7.1.48) (urk_mycge) (keggfc:4.2) (tigrfc:8.2) (db:gtc-mycoplasma genitalium)) MG382 MG382 Mycoplasma genitalium 2097 10045701

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918106	19106	41262	483	160

Description

5000697394 thymidylate kinase:cdc8:hypothetical protein mg006 (gtcfc:4.4) (keggfc:14.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG006 MG006 Mycoplasma genitalium 2097 -11540107 108337 tmk:mg006 (ec:2.7.4.9) (de:thymidylate kinase, (dtmp kinase)) (db:swissprot) KTHY_MYCGE P47252 MYCOPLASMA GENITALIUM 2097 -11540107 172680 thymidylate kinase cdc8 homolog (cl:dtmp kinase) (db:pir2.dat) F64200 F64200 Mycoplasma genitalium 2097 -11540107 7500884761 mg006 thymidylate kinase tmk (db:genpept-bct2) (de:mycoplasma genitalium section 1 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75106 pid:1673808 percent) (le:8552) (re:9184) (di:direct) U39679 U39679 g1045674 Mycoplasma genitalium 2097 -11540107 6500736249 thymidylate kinase:cdc8:hypothetical protein mg006 (gtcfc:4.4) (keggfc:14.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG006 MG006 Mycoplasma genitalium 2097 -11540107

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918130	19107	41263	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918149	19108	41264	1152	383

Description

5000697395 deoxyguanosine/deoxyadenosine kinase:i subunit 2:hypothetical protein mg268 (gtcfc:4.4) (keggfc:14.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG268 MG268 Mycoplasma genitalium 2097 -11540108 109039 mg268 (de:hypothetical protein mg268) (db:swissprot) Y268_MYCGE P47510 MYCOPLASMA GENITALIUM 2097 -11540108 172324 deoxyguanosine/deoxyadenosine kinase i chain 2 homolog (db:pir2.dat) F64229 F64229 Mycoplasma genitalium 2097 -11540108 7500895008 mg268 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75396 pid:1674139 percent) (le:5105) (re:5791) (di:complement) U39706 U39706 g3844864 Mycoplasma genitalium 2097 -11540108 6500736250 deoxyguanosine/deoxyadenosine kinase:i subunit 2:hypothetical protein mg268 (gtcfc:4.4) (keggfc:14.2) (tigrfc:8.4) (db:gtc-mycoplasma genitalium) MG268 MG268 Mycoplasma genitalium 2097 -11540108

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918151	19109	41265	921	306

Description

6500736251 nade:mg383 nh:3-dependent nad+ synthetase:probable nh:3-dependent nad:synthetase (gtcfc:5.1:9.4) (ec:6.3.5.1) (keggfc:5.1:9.4) (tigrfc:2.4) (db:gtc-mycoplasma genitalium) MG383 MG383 Mycoplasma genitalium 2097 -11540109 85147 nade:mg383 (ec:6.3.5.1) (de:probable nh(3)-dependent nad(+) synthetase,) (db:swissprot) NADE_MYCGE P47623 MYCOPLASMA GENITALIUM 2097 -11540109 172672 sporulation protein outb homolog (cl:probable sporulation protein outb) (db:pir2.dat) D64242 D64242 Mycoplasma genitalium 2097 -11540109 7500886248 mg383 nh 3 -dependent nad+ synthetase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 42 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75216 pid:1673951 percent) (le:857) (re:1603) (di:complement) U39720 U39720 g3844972 Mycoplasma genitalium 2097 -11540109 5000697399 (de:(mg383) (pn:probable nh:nh:3-dependent nad) (gn:nade) (gtcfc:5.1:9.4) (ec:6.3.5.1) (nade_mycge) (keggfc:5.1:9.4) (tigrfc:2.4) (db:gtc-mycoplasma genitalium)) MG383 MG383 Mycoplasma genitalium 2097 10027328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918167	19110	41266	3417	1139

Description

6500736252 gltx:mg462 glutamyl-trna synthetase:glutamate--trna ligase:glurs (gtcfc:5.1:9.10:10.6) (ec:6.1.1.17) (keggfc:5.1:9.10:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG462 MG462 Mycoplasma genitalium 2097 -11540110 100022 gltx:mg462 (ec:6.1.1.17) (de:(glurs)) (db:swissprot) SYE_MYCGE P47700 MYCOPLASMA GENITALIUM 2097 -11540110 172357 glutamate--trna ligase::glutamyl-trna synthetase (cl:glutamate--trna ligase:glutamine--trna ligase homology) (ec:6.1.1.17) (db:pir2.dat) A64251 A64251 Mycoplasma genitalium 2097 -11540110 7500892379 mg462 glutamyl-trna synthetase gltx (db:genpept-bct2) (de:mycoplasma genitalium section 50 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75114 pid:1673825 percent) (le:2310) (re:3764) (di:complement) U39728 U39728 g3845057 Mycoplasma genitalium 2097 -11540110 5000697400 (de:(mg462) (pn:glutamate--trna ligase:glurs:glutamyl-trna synthetase:gltx) (gn:gltx) (gtcfc:5.1:9.10:10.6) (ec:6.1.1.17) (sye_mycge) (keggfc:5.1:9.10:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG462 MG462 Mycoplasma genitalium 2097 10041876

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918168	19111	41267	411	136

Description

6500736253 amidase:putative amidase (gtcfc:5.10:5.13:5.14:6.5:11.4) (ec:3.5.1.4) (keggfc:5.10:5.13:5.14:6.5) (tigrfc:3.2) (db:gtc-mycoplasma genitalium) MG099 MG099 Mycoplasma genitalium 2097 -11540111 59316 mg099 (ec:3.5.1.4) (de:putative amidase,) (db:swissprot) AMID_MYCGE P47345 MYCOPLASMA GENITALIUM 2097 -11540111 172384 hydrolase aux2 homolog (cl:indoleacetamide hydrolase) (db:pir2.dat) I64210 I64210 Mycoplasma genitalium 2097 -11540111 7500876808 mg099 glu-trna amidotransferase:subunit a (db:genpept-bct2) (de:mycoplasma genitalium section 12 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75534 pid:1674296 percent) (le:4404) (re:5837) (di:direct) U39690 U39690 g3844687 Mycoplasma genitalium 2097 -11540111 5000697396 (de:(mg099) (pn:putative amidase:amidase) (gtcfc:5.10:6.5) (ec:3.5.1.4) (amid_mycge) (keggfc:5.10:6.5) (tigrfc:3.2) (db:gtc-mycoplasma genitalium)) MG099 MG099 Mycoplasma genitalium 2097 10002054

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918170	19112	41268	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918181	19113	41269	987	328

Description

6500736254 pros:mg283 prolyl-trna synthetase:proline--trna ligase:prors (gtcfc:5.10:10.6) (ec:6.1.1.15) (keggfc:5.10:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG283 MG283 Mycoplasma genitalium 2097 -11540112 100148 pros:mg283 (ec:6.1.1.15) (de:prolyl-trna synthetase, (proline--trna ligase) (prors)) (db:swissprot) SYP_MYCGE P47525 MYCOPLASMA GENITALIUM 2097 -11540112 172604 proline--trna ligase::prolyl-trna synthetase (cl:proline--trna ligase pros) (ec:6.1.1.15) (db:pir2.dat) C64231 C64231 Mycoplasma genitalium 2097 -11540112 7500892549 mg283 prolyl-trna synthetase pros (db:genpept-bct2) (de:mycoplasma genitalium section 30 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75382 pid:1674123 percent) (le:3236) (re:4687) (di:direct) U39708 U39708 g1045979 Mycoplasma genitalium 2097 -11540112 5000697397 (de:(mg283) (pn:proline--trna ligase:prors:prolyl-trna synthetase:pros) (gn:pros) (gtcfc:5.10:10.6) (ec:6.1.1.15) (syp_mycge) (keggfc:5.10:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG283 MG283 Mycoplasma genitalium 2097 10042002

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918183	19114	41270	336	111

Description

6500736255 args:mg378 arginyl-trna synthetase:arginine--trna ligase:argrs (gtcfc:5.10:10.6) (ec:6.1.1.19) (keggfc:5.10:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG378 MG378 Mycoplasma genitalium 2097 -11540113 100167 args:mg378 (ec:6.1.1.19) (de:arginyl-trna synthetase, (arginine--trna ligase) (argrs)) (db:swissprot) SYR_MYCGE P47618 MYCOPLASMA GENITALIUM 2097 -11540113 172291 arginine--trna ligase::arginyl-trna synthetase (ec:6.1.1.19) (db:pir2.dat) H64241 H64241 Mycoplasma genitalium 2097 -11540113 7500892567 mg378 arginyl-trna synthetase args (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75222 pid:1673957 percent) (le:7419) (re:9032) (di:complement) U39719 U39719 g3844966 Mycoplasma genitalium 2097 -11540113 5000697398 (de:(mg378) (pn:arginine--trna ligase:argrs:arginyl-trna synthetase:args) (gn:args) (gtcfc:5.10:10.6) (ec:6.1.1.19) (syr_mycge) (keggfc:5.10:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG378 MG378 Mycoplasma genitalium 2097 10042021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918185	19115	41271	576	191

Description

GTC ORF with score 99 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918190	19116	41272	309	102

Description

6500736256 hiss:mg035 histidyl-trna synthetase:histidine--trna ligase:hisrs (gtcfc:5.11:10.6) (ec:6.1.1.21) (keggfc:5.11:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG035 MG035 Mycoplasma genitalium 2097 -11540114 100063 hiss:mg035 (ec:6.1.1.21) (de:(hisrs)) (db:swissprot) SYH_MYCGE P47281 MYCOPLASMA GENITALIUM 2097 -11540114 172381 histidine--trna ligase::histidyl-trna synthetase (cl:histidine--trna ligase:amino acid--trna ligase repeat homology:histidine--trna ligase homology) (ec:6.1.1.21) (db:pir2.dat) H64203 H64203 Mycoplasma genitalium 2097 -11540114 7500892445 mg035 histidyl-trna synthetase (db:genpept-bct2) (de:mycoplasma genitalium section 5 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75069 pid:1673766 percent) (le:1521) (re:2765) (di:direct) U39683 U39683 g3844645 Mycoplasma genitalium 2097 -11540114 5000697401 (de:(mg035) (pn:histidine--trna ligase:hisrs:histidyl-trna synthetase) (gn:hiss) (gtcfc:5.11:10.6) (ec:6.1.1.21) (syh_mycge) (keggfc:5.11:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG035 MG035 Mycoplasma genitalium 2097 10041917

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918194	19117	41273	624	207

Description

6500736257 trps:mg126 tryptophanyl-trna synthetase:tryptophan--trna ligase:trprs (gtcfc:5.14:10.6) (ec:6.1.1.2) (keggfc:5.14:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG126 MG126 Mycoplasma genitalium 2097 -11540115 100234 trps:mg126 (ec:6.1.1.2) (de:(trprs)) (db:swissprot) SYW_MYCGE P47372 MYCOPLASMA GENITALIUM 2097 -11540115 172701 tryptophan--trna ligase::tryptophanyl-trna synthetase (ec:6.1.1.2) (db:pir2.dat) I64213 I64213 Mycoplasma genitalium 2097 -11540115 7500892643 mg126 tryptophanyl-trna synthetase trps (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75510 pid:1674268 percent) (le:1186) (re:2229) (di:complement) U39693 U39693 g3844717 Mycoplasma genitalium 2097 -11540115 5000697402 (de:(mg126) (pn:tryptophan--trna ligase:trprs:tryptophanyl-trna synthetase:trps) (gn:trps) (gtcfc:5.14:10.6) (ec:6.1.1.2) (syw_mycge) (keggfc:5.14:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG126 MG126 Mycoplasma genitalium 2097 10042088

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918205	19118	41274	408	135

Description

6500736258 phes:mg194 phenylalanyl-trna synthetase:alpha subunit:phenylalanyl-trna synthetase alpha chain:phenylalanine--trna ligase alpha chain:phers (gtcfc:5.15:10.6) (ec:6.1.1.20) (keggfc:5.15:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG194 MG194 Mycoplasma genitalium 2097 -11540116 100030 phes:mg194 (ec:6.1.1.20) (de:-trna ligase alpha chain) (phers)) (db:swissprot) SYFA_MYCGE P47436 MYCOPLASMA GENITALIUM 2097 -11540116 172585 phes phenylalanine--trna ligase:small chain:phenylalanyl-trna synthetase small chain (ec:6.1.1.20) (db:pir2.dat) D64221 D64221 Mycoplasma genitalium 2097 -11540116 7500892387 mg194 phenylalanyl-trna synthetase:subunit alpha (db:genpept-bct2) (de:mycoplasma genitalium section 21 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75564 pid:1673699 percent) (le:1477) (re:2502) (di:direct) U39699 U39699 g3844791 Mycoplasma genitalium 2097 -11540116 5000697403 (de:(mg194) (pn:phenylalanyl-trna synthetase alpha chain:phenylalanine--trna ligase alpha chain:phers:phenylalanyl-trna synthetase, alpha subunit) (gn:phes) (gtcfc:5.15:10.6) (ec:6.1.1.20) (syfa_mycge) (keggfc:5.15:10.1:10.2) (t)) MG194 MG194 Mycoplasma genitalium 2097 10041884

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918206	19119	41275	513	170

Description

6500736259 phet:mg195 phenylalanyl-trna synthetase beta chain:phenylalanine--trna ligase beta chain:phers (gtcfc:5.15:10.6) (ec:6.1.1.20) (keggfc:5.15:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG195 MG195 Mycoplasma genitalium 2097 -11540117 100037 phet:mg195 (ec:6.1.1.20) (de:trna ligase beta chain) (phers)) (db:swissprot) SYFB_MYCGE P47437 MYCOPLASMA GENITALIUM 2097 -11540117 172584 phet phenylalanine--trna ligase:large chain:phenylalanyl-trna synthetase large chain (cl:phenylalanine--trna ligase beta chain) (ec:6.1.1.20) (db:pir2.dat) E64221 E64221 Mycoplasma genitalium 2097 -11540117 7500892395 mg195 phenylalanyl-trna synthetase:subunit beta (db:genpept-bct2) (de:mycoplasma genitalium section 21 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75563 pid:1673698 percent) (le:2506) (re:4926) (di:direct) U39699 U39699 g3844792 Mycoplasma genitalium 2097 -11540117 5000697404 (de:(mg195) (pn:phenylalanine--trna ligase beta chain:phers:phenylalanyl-trna synthetase beta chain:phet) (gn:phet) (gtcfc:5.15:10.6) (ec:6.1.1.20) (syfb_mycge) (keggfc:5.15:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG195 MG195 Mycoplasma genitalium 2097 10041891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918218	19120	41276	243	80

Description

6500736260 tyrs:mg455 tyrosyl trna synthetase:tyrosyl-trna synthetase:tyrosine--trna ligase:tyrrs (gtcfc:5.15:10.6) (ec:6.1.1.1) (keggfc:5.15:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG455 MG455 Mycoplasma genitalium 2097 -11540118 100248 tyrs:mg455 (ec:6.1.1.1) (de:tyrosyl-trna synthetase, (tyrosine--trna ligase) (tyrrs)) (db:swissprot) SYY_MYCGE P47693 MYCOPLASMA GENITALIUM 2097 -11540118 172702 tyrosine--trna ligase::tyrosyl-trna synthetase (cl:tyrosine--trna ligase) (ec:6.1.1.1) (db:pir2.dat) C64250 C64250 Mycoplasma genitalium 2097 -11540118 7500892664 mg455 tyrosyl-trna synthetase tyrs (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75122 pid:1673835 percent) (le:3406) (re:4629) (di:direct) U39727 U39727 g3845049 Mycoplasma genitalium 2097 -11540118 5000697405 (de:(mg455) (pn:tyrosyl-trna synthetase:tyrosine--trna ligase:tyrrs:tyrosyl trna synthetase:tyrs) (gn:tyrs) (gtcfc:5.15:10.6) (ec:6.1.1.1) (syy_mycge) (keggfc:5.15:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG455 MG455 Mycoplasma genitalium 2097 10042102

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918224	19121	41277	834	277

Description

GTC ORF with score 410 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1105.) (nt:similar to saccharomyces cerevisiae unknown, embl) (le:67) (re:906) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918255	19122	41278	231	76

Description

6500736261 asps:mg036 aspartyl-trna synthetase:aspartate--trna ligase:asprs (gtcfc:5.2:10.6) (ec:6.1.1.12) (keggfc:5.2:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG036 MG036 Mycoplasma genitalium 2097 -11540119 100008 asps:mg036 (ec:6.1.1.12) (de:(asprs)) (db:swissprot) SYD_MYCGE P47282 MYCOPLASMA GENITALIUM 2097 -11540119 172294 aspartate--trna ligase::aspartyl-trna synthetase (cl:lysine--trna ligase) (ec:6.1.1.12) (db:pir2.dat) I64203 I64203 Mycoplasma genitalium 2097 -11540119 7500892362 mg036 aspartyl-trna synthetase asps (db:genpept-bct2) (de:mycoplasma genitalium section 5 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75068 pid:1673765 percent) (le:2755) (re:4407) (di:direct) U39683 U39683 g3844646 Mycoplasma genitalium 2097 -11540119 5000697406 (de:(mg036) (pn:aspartate--trna ligase:asprs:aspartyl-trna synthetase:asps) (gn:asps) (gtcfc:5.2:10.6) (ec:6.1.1.12) (syd_mycge) (keggfc:5.2:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG036 MG036 Mycoplasma genitalium 2097 10041862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918267	19123	41279	864	287

Description

GTC ORF with score 984 to: (db:genpept-pln1) (de:emericella nidulans mitochondrial transport protein amc-1 (amc-1)mrna, nuclear gene encoding mitochondrial protein, complete cds.) (nt:mitochondrial carrier) (le:74) (re:1231) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918277	19124	41280	216	71

Description

6500736262 asns:mg113 asparaginyl-trna synthetase:asparagine--trna ligase:asnrs (gtcfc:5.2:10.6) (ec:6.1.1.22) (keggfc:5.2:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG113 MG113 Mycoplasma genitalium 2097 -11540120 100138 asns:mg113 (ec:6.1.1.22) (de:(asnrs)) (db:swissprot) SYN_MYCGE P47359 MYCOPLASMA GENITALIUM 2097 -11540120 172293 asparagine--trna ligase::asparaginyl-trna synthetase (cl:lysine--trna ligase) (ec:6.1.1.22) (db:pir2.dat) E64212 E64212 Mycoplasma genitalium 2097 -11540120 7500892537 mg113 asparaginyl-trna synthetase asns (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75521 pid:1674281 percent) (le:8815) (re:10185) (di:direct) U39691 U39691 g3844702 Mycoplasma genitalium 2097 -11540120 5000697407 (de:(mg113) (pn:asparagine--trna ligase:asnrs:asparaginyl-trna synthetase:asns) (gn:asns) (gtcfc:5.2:10.6) (ec:6.1.1.22) (syn_mycge) (keggfc:5.2:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG113 MG113 Mycoplasma genitalium 2097 10041992

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918280	19125	41281	465	154

Description

6500736263 alas:mg292 alanyl-trna synthetase:alanine--trna ligase:alars (gtcfc:5.2:10.6) (ec:6.1.1.7) (keggfc:5.2:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG292 MG292 Mycoplasma genitalium 2097 -11540121 99980 alas:mg292 (ec:6.1.1.7) (de:alanyl-trna synthetase, (alanine--trna ligase) (alars)) (db:swissprot) SYA_MYCGE P47534 MYCOPLASMA GENITALIUM 2097 -11540121 172289 alanine--trna ligase::alanyl-trna synthetase (cl:alanine--trna ligase) (ec:6.1.1.7) (db:pir2.dat) C64232 C64232 Mycoplasma genitalium 2097 -11540121 7500892326 mg292 alanyl-trna synthetase alas (db:genpept-bct2) (de:mycoplasma genitalium section 31 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75368 pid:1674107 percent) (le:4069) (re:6771) (di:complement) U39709 U39709 g3844871 Mycoplasma genitalium 2097 -11540121 5000697408 (de:(mg292) (pn:alanine--trna ligase:alars:alanyl-trna synthetase:alas) (gn:alas) (gtcfc:5.2:10.6) (ec:6.1.1.7) (sya_mycge) (keggfc:5.2:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG292 MG292 Mycoplasma genitalium 2097 10041835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918296	19126	41282	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918320	19127	41283	309	102

Description

6500736264 sers:mg005 seryl-trna synthetase:serine--trna ligase:serrs (gtcfc:5.3:10.6) (ec:6.1.1.11) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG005 MG005 Mycoplasma genitalium 2097 -11540122 100181 sers:mg005 (ec:6.1.1.11) (de:seryl-trna synthetase, (serine--trna ligase) (serrs)) (db:swissprot) SYS_MYCGE P47251 MYCOPLASMA GENITALIUM 2097 -11540122 172662 serine--trna ligase::seryl-trna synthetase (cl:serine--trna ligase) (ec:6.1.1.11) (db:pir2.dat) E64200 E64200 Mycoplasma genitalium 2097 -11540122 7500892590 mg005 seryl-trna synthetase sers (db:genpept-bct2) (de:mycoplasma genitalium section 1 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75107 pid:1673809 percent) (le:7295) (re:8548) (di:direct) U39679 U39679 g1045673 Mycoplasma genitalium 2097 -11540122 5000697409 (de:(mg005) (pn:serine--trna ligase:serrs:seryl-trna synthetase:sers) (gn:sers) (gtcfc:5.3:10.6) (ec:6.1.1.11) (sys_mycge) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG005 MG005 Mycoplasma genitalium 2097 10042035

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918321	19128	41284	246	81

Description

6500736265 glys:mg251 glycyl-trna synthetase:glycine--trna ligase:glyrs (gtcfc:5.3:10.6) (ec:6.1.1.14) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG251 MG251 Mycoplasma genitalium 2097 -11540123 100054 glys:mg251 (ec:6.1.1.14) (de:glycyl-trna synthetase, (glycine--trna ligase) (glyrs)) (db:swissprot) SYG_MYCGE P47493 MYCOPLASMA GENITALIUM 2097 -11540123 172363 glycine--trna ligase::glycyl-trna synthetase (cl:mycoplasma genitalium glycine--trna ligase) (ec:6.1.1.14) (db:pir2.dat) G64227 G64227 Mycoplasma genitalium 2097 -11540123 7500892427 mg251 glycyl-trna synthetase (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75425 pid:1674173 percent) (le:1841) (re:3181) (di:complement) U39704 U39704 g3844849 Mycoplasma genitalium 2097 -11540123 5000697410 (de:(mg251) (pn:glycine--trna ligase:glyrs:glycyl-trna synthetase) (gn:glys) (gtcfc:5.3:10.6) (ec:6.1.1.14) (syg_mycge) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG251 MG251 Mycoplasma genitalium 2097 10041908

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918324	19129	41285	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918331	19130	41286	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918341	19131	41287	339	113

Description

6500736266 thrs:mg375 thrsv:threonyl-trna synthetase:threonine--trna ligase:thrrs (gtcfc:5.3:10.6) (ec:6.1.1.3) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG375 MG375 Mycoplasma genitalium 2097 -11540124 100204 thrs:mg375 (ec:6.1.1.3) (de:(thrrs)) (db:swissprot) SYT_MYCGE P47615 MYCOPLASMA GENITALIUM 2097 -11540124 172677 threonine--trna ligase::threonyl-trna synthetase (cl:threonine--trna ligase) (ec:6.1.1.3) (db:pir2.dat) E64241 E64241 Mycoplasma genitalium 2097 -11540124 7500892610 mg375 threonyl-trna synthetase thrs (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:m36594 sp:p18255 gb:x04963 pid:143766) (le:4777) (re:6471) (di:complement) U39719 U39719 g3844963 Mycoplasma genitalium 2097 -11540124 5000697411 (de:(mg375) (pn:threonine--trna ligase:thrrs:threonyl-trna synthetase:thrsv) (gn:thrs) (gtcfc:5.3:10.6) (ec:6.1.1.3) (syt_mycge) (keggfc:5.3:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG375 MG375 Mycoplasma genitalium 2097 10042058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918344	19132	41288	402	133

Description

6500736267 mets:mg021 methionyl-trna synthetase:methionine--trna ligase:metrs (gtcfc:5.4:6.4:10.6) (ec:6.1.1.10) (keggfc:5.4:6.4:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG021 MG021 Mycoplasma genitalium 2097 -11540125 100123 mets:mg021 (ec:6.1.1.10) (de:(metrs)) (db:swissprot) SYM_MYCGE P47267 MYCOPLASMA GENITALIUM 2097 -11540125 172559 methionine--trna ligase::methionyl-trna synthetase (ec:6.1.1.10) (db:pir2.dat) C64202 C64202 Mycoplasma genitalium 2097 -11540125 7500892517 mg021 methionyl-trna synthetase mets (db:genpept-bct2) (de:mycoplasma genitalium section 3 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75091 pid:1673790 percent) (le:4048) (re:5586) (di:direct) U39681 U39681 g3844630 Mycoplasma genitalium 2097 -11540125 5000697412 (de:(mg021) (pn:methionine--trna ligase:metrs:methionyl-trna synthetase:mets) (gn:mets) (gtcfc:5.4:6.4:10.6) (ec:6.1.1.10) (sym_mycge) (keggfc:5.4:6.4:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG021 MG021 Mycoplasma genitalium 2097 10041977

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918350	19133	41289	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918358	19134	41290	3042	1013

Description

6500736268 metx:mg047 s-adenosylmethionine synthetase 2:s-adenosylmethionine synthetase:methionine adenosyltransferase:adomet synthetase (gtcfc:5.4:6.4:12.13) (ec:2.5.1.6) (keggfc:5.4:6.4) (tigrfc:5.1) (db:gtc-mycoplasma genitalium) MG047 MG047 Mycoplasma genitalium 2097 -11540126 83595 metk:metx:mg047 (ec:2.5.1.6) (de:adenosyltransferase) (adomet synthetase)) (db:swissprot) METK_MYCGE P47293 MYCOPLASMA GENITALIUM 2097 -11540126 172660 s-adenosylmethionine synthetase 2 metx homolog (db:pir2.dat) B64205 B64205 Mycoplasma genitalium 2097 -11540126 7500885554 mg047 s-adenosylmethionine synthetase metx (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78003 pid:1673749 percent) (le:5878) (re:7029) (di:direct) U39684 U39684 g3844656 Mycoplasma genitalium 2097 -11540126 5000697413 (de:(mg047) (pn:s-adenosylmethionine synthetase:methionine adenosyltransferase:adomet synthetase:s-adenosylmethionine synthetase 2:metx) (gn:metx) (gtcfc:5.4:6.4) (ec:2.5.1.6) (metx_mycge) (keggfc:5.4:6.4) (tigrfc:5.1) (db:gtc-m) MG047 MG047 Mycoplasma genitalium 2097 10025809

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918359	19135	41291	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918360	19136	41292	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918401	19137	41293	315	104

Description

GTC ORF with score 103 to: (sr:pyrococcus horikoshii (strain:ot3) dna) (db:genpept-bct1) (de:pyrococcus horikoshii ot3 genomic dna, 1485001-1738505 nt. position(7/7).) (nt:similar to pir:a64505 percent identity: 33.508 in) (le:78059) (re:81598) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918413	19138	41294	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918415	19139	41295	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918427	19140	41296	1119	372

Description

6500736269 fmt:mg365 methionyl-trna formyltransferase (gtcfc:5.4:9.6:10.6) (ec:2.1.2.9) (keggfc:5.4:9.8:10.1) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) (gtcfc:l-amino acid metabolism-methionine metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of ... MG365 MG365 Mycoplasma genitalium 2097 -11540127 72198 fmt:mg365 (ec:2.1.2.9) (de:methionyl-trna formyltransferase,) (db:swissprot) FMT_MYCGE P47605 MYCOPLASMA GENITALIUM 2097 -11540127 172561 methionyl-trna formyltransferase:homolog (cl:methionyl-trna formyltransferase:phosphoribosylglycinamide formyltransferase homology) (ec:2.1.2.9) (db:pir2.dat) D64240 D64240 Mycoplasma genitalium 2097 -11540127 7500881687 mg365 methionyl-trna formyltransferase fmt (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75235 pid:1673970 percent) (le:2158) (re:3093) (di:direct) U39718 U39718 g3844952 Mycoplasma genitalium 2097 -11540127 5000697414 (de:(mg365) (pn:methionyl-trna formyltransferase:fmt) (gn:fmt) (gtcfc:5.4:10.6) (ec:2.1.2.9) (fmt_mycge) (keggfc:5.4:9.8:10.1) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG365 MG365 Mycoplasma genitalium 2097 10014749

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918430	19141	41297	1674	557

Description

GTC ORF with score 172 to: (db:genpept-inv) (de:caenorhabditis elegans unc-89 (unc-89) gene, complete cds.) (nt:giant ig superfamily member located in the middle) (le:4920:5656:5974:7518) (re:4969:5929:6110:7688) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918432	19142	41298	294	97

Description

6500736270 cyss:mg253 cysteinyl-trna synthetase:cysteine--trna ligase:cysrs (gtcfc:5.5:10.6) (ec:6.1.1.16) (keggfc:5.5:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG253 MG253 Mycoplasma genitalium 2097 -11540128 100000 cyss:mg253 (ec:6.1.1.16) (de:(cysrs)) (db:swissprot) SYC_MYCGE P47495 MYCOPLASMA GENITALIUM 2097 -11540128 172314 cysteine--trna ligase::cysteinyl-trna synthetase (cl:cysteine--trna ligase) (ec:6.1.1.16) (db:pir1.dat) I64227 I64227 Mycoplasma genitalium 2097 -11540128 7500892339 mg253 cysteinyl-trna synthetase cyss (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75423 pid:1674171 percent) (le:3932) (re:5218) (di:complement) U39704 U39704 g3844851 Mycoplasma genitalium 2097 -11540128 5000697415 (de:(mg253) (pn:cysteine--trna ligase:cysrs:cysteinyl-trna synthetase:cyss) (gn:cyss) (gtcfc:5.5:10.6) (ec:6.1.1.16) (syc_mycge) (keggfc:5.5:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG253 MG253 Mycoplasma genitalium 2097 10041854

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918450	19143	41299	339	112

Description

6500736271 leus:mg266 leucyl-trna synthetase:leucine--trna ligase:leurs (gtcfc:5.7:10.6) (ec:6.1.1.4) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG266 MG266 Mycoplasma genitalium 2097 -11540129 100116 leus:mg266 (ec:6.1.1.4) (de:leucyl-trna synthetase, (leucine--trna ligase) (leurs)) (db:swissprot) SYL_MYCGE P47508 MYCOPLASMA GENITALIUM 2097 -11540129 172546 leucine--trna ligase::leucyl-trna synthetase (cl:leucine--trna ligase) (ec:6.1.1.4) (db:pir2.dat) D64229 D64229 Mycoplasma genitalium 2097 -11540129 7500892502 mg266 leucyl-trna synthetase leus (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75398 pid:1674141 percent) (le:2345) (re:4723) (di:complement) U39706 U39706 g3844862 Mycoplasma genitalium 2097 -11540129 5000697416 (de:(mg266) (pn:leucine--trna ligase:leurs:leucyl-trna synthetase:leus) (gn:leus) (gtcfc:5.7:10.6) (ec:6.1.1.4) (syl_mycge) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG266 MG266 Mycoplasma genitalium 2097 10041970

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918496	19144	41300	2289	762

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918497	19145	41301	2835	944

Description

6500736272 vals:mg334 valyl-trna synthetase:valine--trna ligase:valrs (gtcfc:5.7:10.6) (ec:6.1.1.9) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG334 MG334 Mycoplasma genitalium 2097 -11540130 100220 vals:mg334 (ec:6.1.1.9) (de:valyl-trna synthetase, (valine--trna ligase) (valrs)) (db:swissprot) SYV_MYCGE P47576 MYCOPLASMA GENITALIUM 2097 -11540130 172709 valine--trna ligase::valyl-trna synthetase (cl:valine--trna ligase) (ec:6.1.1.9) (db:pir2.dat) I64236 I64236 Mycoplasma genitalium 2097 -11540130 7500892625 mg334 valyl-trna synthetase vals (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75304 pid:1674039 percent) (le:8011) (re:10524) (di:complement) U39714 U39714 g3844913 Mycoplasma genitalium 2097 -11540130 5000697417 (de:(mg334) (pn:valine--trna ligase:valrs:valyl-trna synthetase: vals) (gn:vals) (gtcfc:5.7:10.6) (ec:6.1.1.9) (syv_mycge) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG334 MG334 Mycoplasma genitalium 2097 10042074

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918499	19146	41302	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918546	19147	41303	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918559	19148	41304	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918560	19149	41305	2727	908

Description

6500736273 iles:mg345 isoleucyl-trna synthetase:isoleucine--trna ligase:ilers (gtcfc:5.7:10.6) (ec:6.1.1.5) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG345 MG345 Mycoplasma genitalium 2097 -11540131 100079 iles:mg345 (ec:6.1.1.5) (de:(ilers)) (db:swissprot) SYI_MYCGE P47587 MYCOPLASMA GENITALIUM 2097 -11540131 172543 isoleucine--trna ligase::isoleucyl-trna synthetase (cl:isoleucine--trna ligase) (ec:6.1.1.5) (db:pir2.dat) B64238 B64238 Mycoplasma genitalium 2097 -11540131 7500892464 mg345 isoleucyl-trna synthetase iles (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75258 pid:1673995 percent) (le:2512) (re:5199) (di:complement) U39716 U39716 g3844928 Mycoplasma genitalium 2097 -11540131 5000697418 (de:(mg345) (pn:isoleucine--trna ligase:ilers:isoleucyl-trna synthetase:iles) (gn:iles) (gtcfc:5.7:10.6) (ec:6.1.1.5) (syi_mycge) (keggfc:5.7:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG345 MG345 Mycoplasma genitalium 2097 10041933

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918567	19150	41306	456	151

Description

6500736274 lyss:mg136 lysyl-trna synthetase:lysine--trna ligase:lysrs (gtcfc:5.8:10.6) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG136 MG136 Mycoplasma genitalium 2097 -11540132 100101 lyss:mg136 (ec:6.1.1.6) (de:lysyl-trna synthetase, (lysine--trna ligase) (lysrs)) (db:swissprot) SYK_MYCGE P47382 MYCOPLASMA GENITALIUM 2097 -11540132 172550 lysine--trna ligase::lysyl-trna synthetase (cl:lysine--trna ligase) (ec:6.1.1.6) (db:pir2.dat) A64215 A64215 Mycoplasma genitalium 2097 -11540132 7500892480 mg136 lysyl-trna synthetase lyss (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75500 pid:1674257 percent) (le:8229) (re:9701) (di:direct) U39693 U39693 g3844726 Mycoplasma genitalium 2097 -11540132 5000697419 (de:(mg136) (pn:lysine--trna ligase:lysrs:lysyl-trna synthetase:lyss) (gn:lyss) (gtcfc:5.8:10.6) (ec:6.1.1.6) (syk_mycge) (keggfc:5.8:10.1:10.2) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG136 MG136 Mycoplasma genitalium 2097 10041955

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918573	19151	41307	927	308

Description

5000697420 trxa:trx:mg124 thioredoxin i (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.3) (db:gtc-mycoplasma genitalium) MG124 MG124 Mycoplasma genitalium 2097 -11540133 101386 trxa:trx:mg124 (de:thioredoxin (trx)) (db:swissprot) THIO_MYCGE P47370 MYCOPLASMA GENITALIUM 2097 -11540133 122355 thioredoxin (cl:thioredoxin:thioredoxin homology) (db:pir1.dat) G64213 G64213 Mycoplasma genitalium 2097 -11540133 7500893088 mg124 thioredoxin trxa (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75512 pid:1674270) (le:34) (re:342) (di:direct) U39693 U39693 g3844715 Mycoplasma genitalium 2097 -11540133 6500736275 trxa:trx thioredoxin i (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.3) (db:gtc-mycoplasma genitalium) MG124 MG124 Mycoplasma genitalium 2097 -11540133

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918587	19152	41308	1536	511

Description

5000697790 d-ribulose-5-phosphate 3 epimerase:hypothetical protein mg112 (gtcfc:7.1) (keggfc:14.2) (tigrfc:6.7) (db:gtc-mycoplasma genitalium) MG112 MG112 Mycoplasma genitalium 2097 -11540134 108755 mg112 (de:hypothetical protein mg112) (db:swissprot) Y112_MYCGE P47358 MYCOPLASMA GENITALIUM 2097 -11540134 172323 d-ribulose-5-phosphate 3 epimerase homolog (cl:yeast ribulose-5-phosphate-epimerase) (db:pir2.dat) D64212 D64212 Mycoplasma genitalium 2097 -11540134 7500894723 mg112 d-ribulose-5-phosphate 3-epimerase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:m64172 sp:p40117 sp:q04539 pid:150678) (le:8172) (re:8801) (di:direct) U39691 U39691 g3844701 Mycoplasma genitalium 2097 -11540134 6500736276 d-ribulose-5-phosphate 3 epimerase:hypothetical protein mg112 (gtcfc:7.1) (keggfc:14.2) (tigrfc:6.7) (db:gtc-mycoplasma genitalium) MG112 MG112 Mycoplasma genitalium 2097 -11540134

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918606	19153	41309	354	117

Description

GTC ORF with score 99 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c7d4.) (nt:spac7d4.10, putative atp synthase, len:443aa,) (le:18367:18442:18684:18837) (re:18393:18630:18786:18900) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918611	19154	41310	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918622	19155	41311	1377	458

Description

GTC ORF with score 117 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8083.) (nt:similar to kluyveromyces lactis deoxyribonucleic) (le:23775) (re:26219) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918625	19156	41312	627	208

Description

6500736277 galactosidase acetyltransferase:laca:hypothetical laca/rpib family protein mg396 (gtcfc:7.1) (ec:2.3.1.18) (keggfc:14.1) (tigrfc:6.7) (db:gtc-mycoplasma genitalium) MG396 MG396 Mycoplasma genitalium 2097 -11540135 109143 mg396 (de:hypothetical laca/rpib family protein mg396) (db:swissprot) Y396_MYCGE P47636 MYCOPLASMA GENITALIUM 2097 -11540135 172354 galactoside o-acetyltransferase (cl:galactoside o-acetyltransferase) (ec:2.3.1.18) (db:pir2.dat) H64243 H64243 Mycoplasma genitalium 2097 -11540135 7500895240 mg396 ribose-5-phosphate isomerase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to gb:u14003 sp:p37351 pid:536934) (le:216) (re:674) (di:complement) U39722 U39722 g3844988 Mycoplasma genitalium 2097 -11540135 5000697791 (de:(mg396) (pn:hypothetical laca:galactosidase acetyltransferase:laca) (gtcfc:13.7) (ec:2.3.1.18) (y396_mycge) (keggfc:11.1) (tigrfc:6.7) (db:gtc-mycoplasma genitalium)) MG396 MG396 Mycoplasma genitalium 2097 10050875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918626	19157	41313	624	207

Description

GTC ORF with score 327 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c7d4.) (nt:spac7d4.10, putative atp synthase, len:443aa,) (le:18367:18442:18684:18837) (re:18393:18630:18786:18900) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918627	19158	41314	351	116

Description

GTC ORF with score 131 to: (sr:saccharomyces cerevisiae (strain:grf88) dna, clone_lib:ycp5) (db:genpept-pln1) (de:saccharomyces cerevisiae dna for thi2 positive regulatory proteinof thiamin synthesis, complete cds.) (le:721) (re:2073) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918635	19159	41315	465	154

Description

5000697423 trua:hist:mg182 alkaline endoglucanase:probable pseudouridylate synthase i:pseudouridine synthase i:uracil hydrolyase (gtcfc:7.2) (ec:4.2.1.70) (keggfc:14.1) (tigrfc:5.2) (db:gtc-mycoplasma genitalium) MG182 MG182 Mycoplasma genitalium 2097 -11540136 102499 trua:hist:mg182 (ec:4.2.1.70) (de:i) (pseudouridine synthase i) (uracil hydrolyase)) (db:swissprot) TRUA_MYCGE P47428 MYCOPLASMA GENITALIUM 2097 -11540136 172699 hist trna-pseudouridine synthase i (cl:trna-pseudouridine synthase i) (ec:5.4.99.12) (db:pir2.dat) B64220 B64220 Mycoplasma genitalium 2097 -11540136 7500893518 mg182 pseudouridylate synthase i hist (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215684 gb:u00089 sp:q50291) (le:5206) (re:5940) (di:direct) U39697 U39697 g3844778 Mycoplasma genitalium 2097 -11540136 6500736278 trua:hist alkaline endoglucanase:probable pseudouridylate synthase i:pseudouridine synthase i:uracil hydrolyase (gtcfc:7.2) (ec:4.2.1.70) (keggfc:14.1) (tigrfc:5.2) (db:gtc-mycoplasma genitalium) MG182 MG182 Mycoplasma genitalium 2097 -11540136

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918636	19160	41316	219	72

Description

5000697424 p65 protein:p65 protein homolog (gtcfc:7.2) (keggfc:14.2) (tigrfc:5.2) (db:gtc-mycoplasma genitalium) MG217 MG217 Mycoplasma genitalium 2097 -11540137 88238 mg217 (de:proline-rich p65 protein homolog) (db:swissprot) P65H_MYCGE P47459 MYCOPLASMA GENITALIUM 2097 -11540137 172307 bifunctional endo-1:4-beta-xylanase homolog (db:pir2.dat) I64223 I64223 Mycoplasma genitalium 2097 -11540137 7500887529 mg217 proline-rich p65 protein (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:similar to gb:z32653 pid:474086 pid:556659) (le:7169) (re:8287) (di:direct) U39701 U39701 g3844817 Mycoplasma genitalium 2097 -11540137 6500736279 p65 protein:p65 protein homolog (gtcfc:7.2) (keggfc:14.2) (tigrfc:5.2) (db:gtc-mycoplasma genitalium) MG217 MG217 Mycoplasma genitalium 2097 -11540137

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918646	19161	41317	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918682	19162	41318	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918715	19163	41319	894	297

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918716	19164	41320	615	204

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918735	19165	41321	1584	528

Description

6500736280 glpk:mg038 glycerol kinase:atp:glycerol 3-phosphotransferase:glycerokinase:gk (gtcfc:8.1:12.13) (ec:2.7.1.30) (keggfc:8.1) (tigrfc:5.1) (db:gtc-mycoplasma genitalium) MG038 MG038 Mycoplasma genitalium 2097 -11540138 74040 glpk:mg038 (ec:2.7.1.30) (de:(glycerokinase) (gk)) (db:swissprot) GLPK_MYCGE P47284 MYCOPLASMA GENITALIUM 2097 -11540138 172359 glycerol kinase (cl:xylulokinase) (ec:2.7.1.30) (db:pir2.dat) B64204 B64204 Mycoplasma genitalium 2097 -11540138 7500882506 mg038 glycerol kinase glpk (db:genpept-bct2) (de:mycoplasma genitalium section 5 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75064 pid:1673760 percent) (le:5729) (re:7255) (di:complement) U39683 U39683 g3844648 Mycoplasma genitalium 2097 -11540138 5000697425 (de:(mg038) (pn:atp:glycerol 3-phosphotransferase:glycerokinase:gk:glycerol kinase:glpk) (gn:glpk) (gtcfc:8.1) (ec:2.7.1.30) (glpk_mycge) (keggfc:8.1) (tigrfc:5.1) (db:gtc-mycoplasma genitalium)) MG038 MG038 Mycoplasma genitalium 2097 10016570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918753	19166	41322	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918773	19167	41323	384	127

Description

5000697422 glycerophosphoryl diester phosphodiesterase:glpq:hypothetical protein mg293 (gtcfc:8.1) (keggfc:14.2) (tigrfc:5.4) (db:gtc-mycoplasma genitalium) MG293 MG293 Mycoplasma genitalium 2097 -11540139 109057 mg293 (de:hypothetical protein mg293) (db:swissprot) Y293_MYCGE P47535 MYCOPLASMA GENITALIUM 2097 -11540139 172362 glycerophosphoryl diester phosphodiesterase glpq homolog (db:pir2.dat) D64232 D64232 Mycoplasma genitalium 2097 -11540139 7500895081 mg293 glycerophosphoryl diester phosphodiesterase (db:genpept-bct2) (de:mycoplasma genitalium section 31 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75367 pid:1674106 percent) (le:6829) (re:7563) (di:complement) U39709 U39709 g3844872 Mycoplasma genitalium 2097 -11540139 6500736281 glycerophosphoryl diester phosphodiesterase:glpq:hypothetical protein mg293 (gtcfc:8.1) (keggfc:14.2) (tigrfc:5.4) (db:gtc-mycoplasma genitalium) MG293 MG293 Mycoplasma genitalium 2097 -11540139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918775	19168	41324	2952	983

Description

GTC ORF with score 1473 to: (sr:saccharomyces carlsbergensis dna) (db:genpept-pln1) (ec:1.8.1.2) (de:saccharomyces carlsbergensis assimilatory sulfite reductase (met10)gene, complete cds.) (nt:flavin-binding subunit) (le:215) (re:3322) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918778	19169	41325	2232	743

Description

6500736282 lgt:mg086 prolipoprotein diacylglyceryl transferase:putative prolipoprotein diacylglyceryl transferase (gtcfc:8.5:11.1) (ec:2.4.99.-) (keggfc:8.5) (tigrfc:3.1) (db:gtc-mycoplasma genitalium) MG086 MG086 Mycoplasma genitalium 2097 -11540140 82007 lgt:mg086 (ec:2.4.99.-) (de:probable prolipoprotein diacylglyceryl transferase,) (db:swissprot) LGT_MYCGE P47332 MYCOPLASMA GENITALIUM 2097 -11540140 172605 prolipoprotein diacylglyceryl transferase homolog (db:pir2.dat) E64209 E64209 Mycoplasma genitalium 2097 -11540140 7500884988 mg086 prolipoprotein diacylglyceryl transferase lgt (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75547 pid:1674309 percent) (le:3495) (re:4643) (di:direct) U39689 U39689 g3844673 Mycoplasma genitalium 2097 -11540140 5000697430 (de:(mg086) (pn:putative prolipoprotein diacylglyceryl transferase:prolipoprotein diacylglyceryl transferase:lgt) (gn:lgt) (gtcfc:8.5) (ec:2.4.99.-) (lgt_mycge) (keggfc:8.5) (tigrfc:3.1) (db:gtc-mycoplasma genitalium)) MG086 MG086 Mycoplasma genitalium 2097 10024241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918788	19170	41326	1284	427

Description

6500736283 protein serine/threonine kinase:putative serine/threonine-protein kinase (gtcfc:8.5:9.4:10.7) (ec:2.7.1.-) (keggfc:8.5:9.4) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG109 MG109 Mycoplasma genitalium 2097 -11540141 172610 protein serine/threonine kinase (db:pir2.dat) A64212 A64212 Mycoplasma genitalium 2097 -11540141 7500965562 mg109 serine/threonine protein kinase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75524 pid:1674285 percent) (le:4955) (re:6043) (di:direct) U39691 U39691 g3844698 Mycoplasma genitalium 2097 -11540141 5000697421 (de:(mg109) (pn:putative serine:protein serine) (gtcfc:7.2:8.5:9.4) (ec:2.7.1.-) (pkns_mycge) (keggfc:7.1:8.5:9.4) (tigrfc:12.4) (db:gtc-mycoplasma genitalium)) MG109 MG109 Mycoplasma genitalium 2097 10032005

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918804	19171	41327	987	328

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918805	19172	41328	606	201

Description

6500736284 hemk:mg259 protoporphyrinogen oxidase (gtcfc:9.10) (ec:1.3.3.4) (keggfc:9.10) (tigrfc:2.2) (db:gtc-mycoplasma genitalium) MG259 MG259 Mycoplasma genitalium 2097 -11540142 119038 mg259 (de:hypothetical protein mg259) (db:swissprot) Y259_MYCGE Q49404 MYCOPLASMA GENITALIUM 2097 -11540142 172613 protoporphyrinogen oxidase (ec:1.3.3.4) (db:pir2.dat) F64228 F64228 Mycoplasma genitalium 2097 -11540142 7500894985 mg259 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75419 pid:1674165 percent) (le:11387) (re:12757) (di:direct) U39704 U39704 g1045951 Mycoplasma genitalium 2097 -11540142 5000697431 (de:(mg259) (pn:protoporphyrinogen oxidase:hemk) (gn:hemk) (gtcfc:9.10) (ec:1.3.3.4) (keggfc:9.10) (tigrfc:2.2) (db:gtc-mycoplasma genitalium)) MG259 MG259 Mycoplasma genitalium 2097 10061483

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918806	19173	41329	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918818	19174	41330	285	94

Description

5000697432 dnag:dnae:mg250 dnae:dna primase (gtcfc:9.12:10.8) (ec:2.7.7.-) (keggfc:9.13) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG250 MG250 Mycoplasma genitalium 2097 -11540143 91039 dnag:dnae:mg250 (ec:2.7.7.-) (de:dna primase,) (db:swissprot) PRIM_MYCGE P47492 MYCOPLASMA GENITALIUM 2097 -11540143 172337 dna primase dnae homolog mg250 (cl:probable dna primase mg250) (db:pir2.dat) F64227 F64227 Mycoplasma genitalium 2097 -11540143 7500888464 mg250 dna primase dnae (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75426 pid:1674174 percent) (le:28) (re:1851) (di:complement) U39704 U39704 g3844848 Mycoplasma genitalium 2097 -11540143 6500736285 dnag:dnae dnae:dna primase (gtcfc:9.12:10.8) (ec:2.7.7.-) (keggfc:9.13) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG250 MG250 Mycoplasma genitalium 2097 -11540143

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918822	19175	41331	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918827	19176	41332	726	241

Description

6500736286 lpla:mg270 lipoate-protein ligase:probable lipoate-protein ligase a (gtcfc:9.12:9.6:14.1) (ec:6.-.-.-) (keggfc:9.7:9.13) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) (gtcfc:metabolism of cofactors and vitamins-quinone biosynthesis:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:unkno... MG270 MG270 Mycoplasma genitalium 2097 -11540144 82405 lpla:mg270 (ec:6.-.-.-) (de:probable lipoate-protein ligase a,) (db:swissprot) LPLA_MYCGE P47512 MYCOPLASMA GENITALIUM 2097 -11540144 172420 hypothetical protein homolog mg270 (cl:lipoate-protein ligase) (db:pir2.dat) H64229 H64229 Mycoplasma genitalium 2097 -11540144 7500885127 mg270 lipoate protein ligase lpla (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75394 pid:1674137 percent) (le:7346) (re:8356) (di:complement) U39706 U39706 g1045964 Mycoplasma genitalium 2097 -11540144 5000697433 (de:(mg270) (pn:probable lipoate-protein ligase a:lipoate-protein ligase) (gn:lpla) (gtcfc:9.12) (ec:6.-.-.-) (lpla_mycge) (keggfc:9.13) (tigrfc:15.1) (db:gtc-mycoplasma genitalium)) MG270 MG270 Mycoplasma genitalium 2097 10024629

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918828	19177	41333	225	74

Description

6500736287 pacl:mg071 cation-transporting atpase:probable cation-transporting p-type atpase (gtcfc:9.6:12.5) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:13.5) (db:gtc-mycoplasma genitalium) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:cell processes-transport of cations (na_k_ca_nh4_etc_)) MG071 MG071 Mycoplasma genitalium 2097 -11540145 60475 pacl:mg071 (ec:3.6.1.-) (de:probable cation-transporting p-type atpase,) (db:swissprot) ATCL_MYCGE P47317 MYCOPLASMA GENITALIUM 2097 -11540145 172308 probable cation-transporting atpase::pacl homolog (cl:atpase nucleotide-binding domain homology) (ec:3.6.1.-) (db:pir2.dat) H64207 H64207 Mycoplasma genitalium 2097 -11540145 7500877285 mg071 cation-transporting p-type atpase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 9 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78036 pid:1674325 percent) (le:5818) (re:8442) (di:direct) U39687 U39687 g1045747 Mycoplasma genitalium 2097 -11540145 5000697434 (de:(mg071) (pn:probable cation-transporting p-type atpase:cation-transporting atpase:pacl) (gn:pacl) (gtcfc:9.6) (ec:3.6.1.-) (atcl_mycge) (keggfc:9.7) (tigrfc:13.5) (db:gtc-mycoplasma genitalium)) MG071 MG071 Mycoplasma genitalium 2097 10003201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918830	19178	41334	504	167

Description

6500736288 dnab:mg094 replicative dna helicase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) MG094 MG094 Mycoplasma genitalium 2097 -11540146 172619 replicative dna helicase dnab homolog (db:pir2.dat) D64210 D64210 Mycoplasma genitalium 2097 -11540146 7500965564 mg094 replicative dna helicase dnab (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75539 pid:1674301 percent) (le:9624) (re:10964) (di:direct) U39689 U39689 g3844681 Mycoplasma genitalium 2097 -11540146 5000697435 (de:(mg094) (pn:replicative dna helicase:dnab) (gn:dnab) (gtcfc:9.6) (ec:3.6.1.-) (dnab_mycge) (keggfc:9.7) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG094 MG094 Mycoplasma genitalium 2097 10011440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918840	19179	41335	243	80

Description

5000697436 fola:dhfr:mg228 dihydrofolate reductase:dihydrofolate reductase type i (gtcfc:9.6) (ec:1.5.1.3) (keggfc:9.7:9.8) (tigrfc:2.1) (db:gtc-mycoplasma genitalium) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MG228 MG228 Mycoplasma genitalium 2097 -11540147 69449 fola:dhfr:mg228 (ec:1.5.1.3) (de:dihydrofolate reductase,) (db:swissprot) DYR_MYCGE P47470 MYCOPLASMA GENITALIUM 2097 -11540147 172325 dihydrofolate reductase (cl:type i dihydrofolate reductase:type i dihydrofolate reductase homology) (ec:1.5.1.3) (db:pir2.dat) B64225 B64225 Mycoplasma genitalium 2097 -11540147 7500880747 mg228 dihydrofolate reductase dhfr (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78028 pid:1674209 percent) (le:8600) (re:9082) (di:direct) U39702 U39702 g3844831 Mycoplasma genitalium 2097 -11540147 6500736289 fola:dhfr dihydrofolate reductase:dihydrofolate reductase type i (gtcfc:9.6) (ec:1.5.1.3) (keggfc:9.7:9.8) (tigrfc:2.1) (db:gtc-mycoplasma genitalium) MG228 MG228 Mycoplasma genitalium 2097 -11540147

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918847	19180	41336	330	109

Description

6500736290 rep helicase:single-stranded dna-dependent atpase:rep:probable dna helicase (gtcfc:9.6:10.8) (ec:3.6.1.-) (keggfc:9.7) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-dna replication--recombination/repair) MG244 MG244 Mycoplasma genitalium 2097 -11540148 109015 uvrd:mg244 (ec:3.6.1.-) (de:putative dna helicase ii homolog,) (db:swissprot) UVRD_MYCGE P47486 MYCOPLASMA GENITALIUM 2097 -11540148 172328 dna helicase ii mutb1 homolog (db:pir2.dat) I64226 I64226 Mycoplasma genitalium 2097 -11540148 7500893925 mg244 dna helicase ii:putative (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75437 pid:1674187 percent) (le:12505) (re:14616) (di:direct) U39703 U39703 g1045935 Mycoplasma genitalium 2097 -11540148 5000697437 (de:(mg244) (pn:probable dna helicase:rep helicase, single-stranded dna-dependent atpase:rep) (gtcfc:9.6) (ec:3.6.1.-) (y244_mycge) (keggfc:9.7) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG244 MG244 Mycoplasma genitalium 2097 10050747

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918849	19181	41337	1062	353

Description

GTC ORF with score 208 to: (sr:norway rat strain=sprague dawley) (db:genpept-rod) (de:rattus norvegicus cytochrome p450 4f5 (cyp4f5) mrna, complete cds.) (nt:method: conceptual translation supplied by author) (le:74) (re:1654) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918850	19182	41338	513	170

Description

5000697438 atp-dependent nuclease:adda:hypothetical protein mg032 (gtcfc:10.10) (keggfc:14.2) (tigrfc:10.1) (db:gtc-mycoplasma genitalium) MG032 MG032 Mycoplasma genitalium 2097 -11540149 108445 mg032 (de:hypothetical protein mg032) (db:swissprot) Y032_MYCGE P47278 MYCOPLASMA GENITALIUM 2097 -11540149 172302 atp-dependent nuclease adda homolog (db:pir2.dat) E64203 E64203 Mycoplasma genitalium 2097 -11540149 7500894560 mg032 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 4 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75078 pid:1673776 percent) (le:8459) (re:10459) (di:direct) U39682 U39682 g1045703 Mycoplasma genitalium 2097 -11540149 6500736291 atp-dependent nuclease:adda:hypothetical protein mg032 (gtcfc:10.10) (keggfc:14.2) (tigrfc:10.1) (db:gtc-mycoplasma genitalium) MG032 MG032 Mycoplasma genitalium 2097 -11540149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918852	19183	41339	675	224

Description

6500736292 uvra:mg421 excinuclease abc subunit a (gtcfc:10.10) (keggfc:14.2) (tigrfc:10.1) (db:gtc-mycoplasma genitalium) MG421 MG421 Mycoplasma genitalium 2097 -11540150 172346 excinuclease abc chain a:excision endonuclease abc::chain a:uvra protein (cl:excinuclease abc chain a:atp-binding cassette homology) (ec:3.1.-.-) (db:pir2.dat) E64246 E64246 Mycoplasma genitalium 2097 -11540150 7500955283 uvra excinuclease abc subunit a (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium bs18, dnah_2, uvra genes from bases 523263 to531597 (section 50 of 56) of the complete genome.) (nt:identified by sequence similarity; similar to) (le:8... U39728 U39728 g1046136 Mycoplasma genitalium 2097 -11540150 5000697439 (de:(mg421) (pn:excinuclease abc subunit a:uvra) (gn:uvra) (gtcfc:10.10) (ec:) (uvra_mycge) (keggfc:11.2) (tigrfc:10.1) (db:gtc-mycoplasma genitalium)) MG421 MG421 Mycoplasma genitalium 2097 10045805

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918864	19184	41340	456	151

Description

6500736293 pip:mg020 proline iminopeptidase:putative proline iminopeptidase:prolyl aminopeptidase (gtcfc:10.11) (ec:3.4.11.5) (keggfc:14.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG020 MG020 Mycoplasma genitalium 2097 -11540151 89827 pip:mg020 (ec:3.4.11.5) (de:putative proline iminopeptidase, (prolyl aminopeptidase)) (db:swissprot) PIP_MYCGE P47266 MYCOPLASMA GENITALIUM 2097 -11540151 172602 proline iminopeptidase homolog mg020 (cl:proline aminopeptidase) (db:pir2.dat) B64202 B64202 Mycoplasma genitalium 2097 -11540151 7500888104 mg020 proline iminopeptidase pip (db:genpept-bct2) (de:mycoplasma genitalium section 3 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75092 pid:1673791 percent) (le:3122) (re:4048) (di:direct) U39681 U39681 g3844629 Mycoplasma genitalium 2097 -11540151 5000697440 (de:(mg020) (pn:putative proline iminopeptidase:prolyl aminopeptidase:proline iminopeptidase:pip) (gn:pip) (gtcfc:10.11) (ec:3.4.11.5) (pip_mycge) (keggfc:11.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium)) MG020 MG020 Mycoplasma genitalium 2097 10031947

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918904	19185	41341	879	292

Description

GTC ORF with score 249 to: (db:genpept-bct1) (de:streptomyces lividans amplifiable element aud4: putativetranscriptional regulator, putative ferredoxin, putative cytochromep450 oxidoreductase, and putative oxidoreductase genes, completecds; and unknown...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918908	19186	41342	1209	402

Description

6500736294 gcp:mg046 o-sialoglycoprotein endopeptidase:probable o-sialoglycoprotein endopeptidase:glycoprotease (gtcfc:10.11) (ec:3.4.24.57) (keggfc:14.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG046 MG046 Mycoplasma genitalium 2097 -11540152 73424 gcp:mg046 (ec:3.4.24.57) (de:(glycoprotease)) (db:swissprot) GCP_MYCGE P47292 MYCOPLASMA GENITALIUM 2097 -11540152 172663 o-sialoglycoprotein endopeptidase:homolog (cl:o-sialoglycoprotein endopeptidase) (ec:3.4.24.57) (db:pir2.dat) A64205 A64205 Mycoplasma genitalium 2097 -11540152 7500882264 mg046 o-sialoglycoprotein endopeptidase (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75055 pid:1673750 percent) (le:4947) (re:5894) (di:direct) U39684 U39684 g3844655 Mycoplasma genitalium 2097 -11540152 5000697441 (de:(mg046) (pn:probable o-sialoglycoprotein endopeptidase:o-sialoglycoprotein endopeptidase:glycoprotease) (gn:gcp) (gtcfc:10.11) (ec:3.4.24.57) (gcp_mycge) (keggfc:11.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium)) MG046 MG046 Mycoplasma genitalium 2097 10015958

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918921	19187	41343	405	134

Description

5000697442 glutamic acid specific protease:spase:hypothetical lipoprotein mg067 precursor (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG067 MG067 Mycoplasma genitalium 2097 -11540153 108594 mg067 (de:hypothetical lipoprotein mg067 precursor) (db:swissprot) Y067_MYCGE P47313 MYCOPLASMA GENITALIUM 2097 -11540153 172358 glutamic acid specific proteinase homolog (db:pir2.dat) D64207 D64207 Mycoplasma genitalium 2097 -11540153 7500894628 mg067 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 8 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75610 pid:1673725 percent) (le:7515) (re:9065) (di:direct) U39686 U39686 g1045742 Mycoplasma genitalium 2097 -11540153 6500736295 glutamic acid specific protease:spase:hypothetical lipoprotein mg067 precursor (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG067 MG067 Mycoplasma genitalium 2097 -11540153

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918961	19188	41344	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501918992	19189	41345	957	318

Description

6500736296 ligoendopepti...:pepf:mg183:f gt9_orf611:oligoendopeptidase f homolog (gtcfc:10.11) (ec:3.4.24.-) (keggfc:14.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG183 MG183 Mycoplasma genitalium 2097 -11540154 89022 pepf:mg183 (ec:3.4.24.-) (de:oligoendopeptidase f homolog,) (db:swissprot) PEPF_MYCGE P47429 MYCOPLASMA GENITALIUM 2097 -11540154 172572 oligoendopeptidase f homolog (cl:oligoendopeptidase f) (db:pir2.dat) C64220 C64220 Mycoplasma genitalium 2097 -11540154 7500887819 mg183 oligoendopeptidase f pepf (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215691 sp:p54125 gb:u00089) (le:5930) (re:7753) (di:direct) U39697 U39697 g3844779 Mycoplasma genitalium 2097 -11540154 5000697443 (de:(mg183) (pn:oligoendopeptidase f homolog:gt9_orf611) (gn:pepf:ligoendopeptidase f) (gtcfc:10.11) (ec:3.4.24.-) (pepf_mycge) (keggfc:11.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium)) MG183 MG183 Mycoplasma genitalium 2097 10031148

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919007	19190	41346	282	93

Description

5000697444 iga1 protease:hypothetical protein mg219 (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG219 MG219 Mycoplasma genitalium 2097 -11540155 108991 mg219 (de:hypothetical protein mg219) (db:swissprot) Y219_MYCGE P47461 MYCOPLASMA GENITALIUM 2097 -11540155 172541 iga-specific metalloendopeptidase:type 1 precursor homolog (ec:3.4.24.13) (db:pir2.dat) B64224 B64224 Mycoplasma genitalium 2097 -11540155 7500894896 mg219 m. genitalium predicted coding region mg219 (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:14725) (re:15171) (di:direct) U39701 U39701 g3844821 Mycoplasma genitalium 2097 -11540155 6500736297 iga1 protease:hypothetical protein mg219 (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG219 MG219 Mycoplasma genitalium 2097 -11540155

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919013	19191	41347	798	265

Description

6500736298 lon:mg239 atp-dependent protease:atp-dependent protease la (gtcfc:10.11) (ec:3.4.21.53) (keggfc:14.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG239 MG239 Mycoplasma genitalium 2097 -11540156 82324 lon:mg239 (ec:3.4.21.53) (de:atp-dependent protease la,) (db:swissprot) LON_MYCGE P47481 MYCOPLASMA GENITALIUM 2097 -11540156 172304 endopeptidase la:homolog (cl:atp-dependent serine proteinase la) (ec:3.4.21.53) (db:pir2.dat) D64226 D64226 Mycoplasma genitalium 2097 -11540156 7500885104 mg239 atp-dependent protease la lon (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78025 pid:1674198 percent) (le:4568) (re:6955) (di:direct) U39703 U39703 g3844843 Mycoplasma genitalium 2097 -11540156 5000697445 (de:(mg239) (pn:atp-dependent protease la:atp-dependent protease:lon) (gn:lon) (gtcfc:10.11) (ec:3.4.21.53) (lon_mycge) (keggfc:11.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium)) MG239 MG239 Mycoplasma genitalium 2097 10024554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919022	19192	41348	402	133

Description

5000697446 hypothetical protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG310 MG310 Mycoplasma genitalium 2097 -11540157 118144 mg310 (ec:3.1.-.-) (de:putative esterase/lipase 1,) (db:swissprot) ESL1_MYCGE Q49412 MYCOPLASMA GENITALIUM 2097 -11540157 172603 proline iminopeptidase homolog mg310 (cl:triacylglycerol lipase 1) (db:pir2.dat) C64234 C64234 Mycoplasma genitalium 2097 -11540157 7500881166 mg310 lipase/esterase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75333 pid:1674078 percent) (le:38) (re:844) (di:direct) U39712 U39712 g1046010 Mycoplasma genitalium 2097 -11540157 6500736299 hypothetical protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG310 MG310 Mycoplasma genitalium 2097 -11540157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919047	19193	41349	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919054	19194	41350	561	186

Description

6500736300 pepp:mg324 putative xaa-pro aminopeptidase:x-pro aminopeptidase:aminopeptidase p:app:aminoacylproline aminopeptidase (gtcfc:10.11) (ec:3.4.11.9) (keggfc:14.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG324 MG324 Mycoplasma genitalium 2097 -11540158 59403 pepp:mg324 (ec:3.4.11.9) (de:(aminopeptidase p) (app) (aminoacylproline aminopeptidase)) (db:swissprot) AMPP_MYCGE P47566 MYCOPLASMA GENITALIUM 2097 -11540158 172711 x-pro aminopeptidase (cl:x-pro aminopeptidase) (ec:3.4.11.9) (db:pir2.dat) H64235 H64235 Mycoplasma genitalium 2097 -11540158 7500876867 mg324 aminopeptidase p pepp (db:genpept-bct2) (de:mycoplasma genitalium section 35 of 51 of the complete genome.) (nt:similar to gb:d00398 sp:p15034 pid:216529) (le:8874) (re:9938) (di:complement) U39713 U39713 g3844901 Mycoplasma genitalium 2097 -11540158 5000697447 (de:(mg324) (pn:putative xaa-pro aminopeptidase:x-pro aminopeptidase:app:aminoacylproline aminopeptidase:aminopeptidase p:pepp) (gn:pepp) (gtcfc:10.11) (ec:3.4.11.9) (ampp_mycge) (keggfc:11.1) (tigrfc:12.3) (db:gtc-mycoplasma ge) MG324 MG324 Mycoplasma genitalium 2097 10002140

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919061	19195	41351	600	199

Description

6500736301 clpb:mg355 atp-dependent protease binding subunit:protein (gtcfc:10.11) (keggfc:14.2) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG355 MG355 Mycoplasma genitalium 2097 -11540159 64809 clpb:mg355 (de:clpb protein) (db:swissprot) CLPB_MYCGE P47597 MYCOPLASMA GENITALIUM 2097 -11540159 172303 atp-dependent proteinase clpb regulator component homolog (db:pir2.dat) C64239 C64239 Mycoplasma genitalium 2097 -11540159 7500878855 mg355 atp-dependent clp protease:atpase subunit (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75247 pid:1673983 percent) (le:2742) (re:4886) (di:complement) U39717 U39717 g3844939 Mycoplasma genitalium 2097 -11540159 5000697448 (de:(mg355) (pn:protein:atp-dependent protease binding subunit:clpb) (gn:clpb) (gtcfc:10.11) (ec:) (clpb_mycge) (keggfc:11.2) (tigrfc:12.3) (db:gtc-mycoplasma genitalium)) MG355 MG355 Mycoplasma genitalium 2097 10007470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919062	19196	41352	363	120

Description

6500736302 aminopeptidase:probable cytosol aminopeptidase:leucine aminopeptidase:lap (gtcfc:10.11) (ec:3.4.11.1) (keggfc:14.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium) MG391 MG391 Mycoplasma genitalium 2097 -11540160 59374 mg391 (ec:3.4.11.1) (de:(lap)) (db:swissprot) AMPL_MYCGE P47631 MYCOPLASMA GENITALIUM 2097 -11540160 172290 aminopeptidase (ec:3.4.-.-) (db:pir2.dat) C64243 C64243 Mycoplasma genitalium 2097 -11540160 7500876839 mg391 cytosol aminopeptidase (db:genpept-bct2) (de:mycoplasma genitalium section 43 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75206 pid:1673940 percent) (le:2579) (re:3922) (di:complement) U39721 U39721 g3844982 Mycoplasma genitalium 2097 -11540160 5000697449 (de:(mg391) (pn:probable cytosol aminopeptidase:leucine aminopeptidase:lap:aminopeptidase) (gtcfc:10.11) (ec:3.4.11.1) (ampl_mycge) (keggfc:11.1) (tigrfc:12.3) (db:gtc-mycoplasma genitalium)) MG391 MG391 Mycoplasma genitalium 2097 10002111

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919074	19197	41353	1389	462

Description

5000697581 hypothetical protein:sp:p31216:probable gtp-binding protein mg024 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG024 MG024 Mycoplasma genitalium 2097 -11540161 110786 mg024 (de:probable gtp-binding protein mg024) (db:swissprot) Y024_MYCGE P47270 MYCOPLASMA GENITALIUM 2097 -11540161 172364 probable gtp-binding protein (cl:yeast probable purine nucleotide-binding protein ybr025c) (db:pir2.dat) F64202 F64202 Mycoplasma genitalium 2097 -11540161 7500894537 mg024 gtp-binding protein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 3 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75088 pid:1673787 percent) (le:6926) (re:8029) (di:direct) U39681 U39681 g3844633 Mycoplasma genitalium 2097 -11540161 6500736303 hypothetical protein:sp:p31216:probable gtp-binding protein mg024 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG024 MG024 Mycoplasma genitalium 2097 -11540161

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919079	19198	41354	3696	1231

Description

6500736304 vacb:mg104 virulence associated protein homolog:protein homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG104 MG104 Mycoplasma genitalium 2097 -11540162 104383 vacb:mg104 (de:vacb protein homolog) (db:swissprot) VACB_MYCGE P47350 MYCOPLASMA GENITALIUM 2097 -11540162 172710 virulence-associated protein vacb homolog (cl:virulence-associated protein vacb homolog) (db:pir2.dat) E64211 E64211 Mycoplasma genitalium 2097 -11540162 7500893951 mg104 virulence-associated protein homolog vacb (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75529 pid:1674290 percent) (le:160) (re:2337) (di:direct) U39691 U39691 g3844693 Mycoplasma genitalium 2097 -11540162 5000697582 (de:(mg104) (pn:protein homolog:virulence associated protein homolog:vacb) (gn:vacb) (gtcfc:12.13) (ec:) (vacb_mycge) (keggfc:11.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium)) MG104 MG104 Mycoplasma genitalium 2097 10046150

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919086	19199	41355	462	153

Description

5000697583 major sigma factor:rpod:hypothetical protein mg248 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG248 MG248 Mycoplasma genitalium 2097 -11540163 109021 mg248 (de:hypothetical protein mg248) (db:swissprot) Y248_MYCGE P47490 MYCOPLASMA GENITALIUM 2097 -11540163 172552 major sigma factor (db:pir2.dat) D64227 D64227 Mycoplasma genitalium 2097 -11540163 7500894967 mg248 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75427 pid:1674176 percent) (le:16644) (re:17300) (di:complement) U39703 U39703 g1045939 Mycoplasma genitalium 2097 -11540163 6500736305 major sigma factor:rpod:hypothetical protein mg248 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG248 MG248 Mycoplasma genitalium 2097 -11540163

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919119	19200	41356	1386	461

Description

5000697584 gtp-binding protein:obg:probable gtp-binding protein mg384 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG384 MG384 Mycoplasma genitalium 2097 -11540164 109132 mg384 (de:probable gtp-binding protein mg384) (db:swissprot) Y384_MYCGE P47624 MYCOPLASMA GENITALIUM 2097 -11540164 172365 gtp-binding protein obg (cl:gtp-binding protein obg:translation elongation factor tu homology) (db:pir1.dat) E64242 E64242 Mycoplasma genitalium 2097 -11540164 7500895218 mg384 gtp-binding protein obg (db:genpept-bct2) (de:mycoplasma genitalium section 42 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75215 pid:1673950 percent) (le:1596) (re:2897) (di:complement) U39720 U39720 g3844973 Mycoplasma genitalium 2097 -11540164 6500736306 gtp-binding protein:obg:probable gtp-binding protein mg384 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG384 MG384 Mycoplasma genitalium 2097 -11540164

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919122	19201	41357	756	251

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919124	19202	41358	303	100

Description

5000697585 era:spg:mg387 spg:gtp-binding protein era homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG387 MG387 Mycoplasma genitalium 2097 -11540165 70481 era:spg:mg387 (de:gtp-binding protein era homolog) (db:swissprot) ERA_MYCGE P47627 MYCOPLASMA GENITALIUM 2097 -11540165 172366 gtp-binding protein era homolog spg homolog (cl:translation elongation factor tu homology) (db:pir2.dat) H64242 H64242 Mycoplasma genitalium 2097 -11540165 7500881110 mg387 gtp-binding protein era (db:genpept-bct2) (de:mycoplasma genitalium section 42 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75210 pid:1673945 percent) (le:9367) (re:10239) (di:complement) U39720 U39720 g3844976 Mycoplasma genitalium 2097 -11540165 6500736307 era:spg spg:gtp-binding protein era homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG387 MG387 Mycoplasma genitalium 2097 -11540165

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919131	19203	41359	339	112

Description

5000697586 pilin repressor:pilb:putative peptide methionine sulfoxide reductase:peptide met:o reductase (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG408 MG408 Mycoplasma genitalium 2097 -11540166 90141 mg408 (de:reductase)) (db:swissprot) PMSR_MYCGE P47648 MYCOPLASMA GENITALIUM 2097 -11540166 172596 pilin repressor pilb homolog mg408 (cl:peptide methionine sulfoxide reductase) (db:pir2.dat) B64245 B64245 Mycoplasma genitalium 2097 -11540166 7500888211 mg408 peptide methionine sulfoxide reductase pmsr (db:genpept-bct2) (de:mycoplasma genitalium section 45 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75188 pid:1673902 percent) (le:1544) (re:2017) (di:direct) U39723 U39723 g3845001 Mycoplasma genitalium 2097 -11540166 6500736308 pilin repressor:pilb:putative peptide methionine sulfoxide reductase:peptide met:o reductase (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG408 MG408 Mycoplasma genitalium 2097 -11540166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919136	19204	41360	312	103

Description

5000697587 peripheral membrane protein u:phou:hypothetical protein mg409 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG409 MG409 Mycoplasma genitalium 2097 -11540167 109149 mg409 (de:hypothetical protein mg409) (db:swissprot) Y409_MYCGE P47649 MYCOPLASMA GENITALIUM 2097 -11540167 172581 peripheral membrane protein u homolog (cl:phou protein) (db:pir2.dat) C64245 C64245 Mycoplasma genitalium 2097 -11540167 7500895252 mg409 regulatory protein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 45 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75187 pid:1673901 percent) (le:2014) (re:2691) (di:complement) U39723 U39723 g3845002 Mycoplasma genitalium 2097 -11540167 6500736309 peripheral membrane protein u:phou:hypothetical protein mg409 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG409 MG409 Mycoplasma genitalium 2097 -11540167

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919139	19205	41361	510	169

Description

5000697588 pilin repressor:pilb:hypothetical protein mg448 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG448 MG448 Mycoplasma genitalium 2097 -11540168 109174 mg448 (de:hypothetical protein mg448) (db:swissprot) Y448_MYCGE P47686 MYCOPLASMA GENITALIUM 2097 -11540168 172597 pilin repressor pilb homolog mg448 (cl:hypthetical protein ycl033c) (db:pir2.dat) E64249 E64249 Mycoplasma genitalium 2097 -11540168 7500895312 mg448 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75129 pid:1673843 percent) (le:8118) (re:8570) (di:complement) U39726 U39726 g3845041 Mycoplasma genitalium 2097 -11540168 6500736310 pilin repressor:pilb:hypothetical protein mg448 (gtcfc:10.2) (keggfc:14.2) (tigrfc:9.1) (db:gtc-mycoplasma genitalium) MG448 MG448 Mycoplasma genitalium 2097 -11540168

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919158	19206	41362	768	255

Description

5000697450 probable helicase mot1:hypothetical helicase mg018 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG018 MG018 Mycoplasma genitalium 2097 -11540169 172374 helicase mot1 homolog (db:pir2.dat) I64201 I64201 Mycoplasma genitalium 2097 -11540169 7500965553 mot1 helicase (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium dnaj_2, fold, gtp1, mets, mot1, msba, pip_1,rpoe, trna-ala, trna-ile_1, tsr genes from bases 14296 to 28573(section 2 of 56) of the complete genome.) (n... U39680 U39680 g1045687 Mycoplasma genitalium 2097 -11540169 6500736311 probable helicase mot1:hypothetical helicase mg018 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG018 MG018 Mycoplasma genitalium 2097 -11540169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919163	19207	41363	1122	374

Description

6500736312 nusa:mg141 n-utilization substance protein a homolog (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG141 MG141 Mycoplasma genitalium 2097 -11540170 87232 nusa:mg141 (de:n-utilization substance protein a homolog) (db:swissprot) NUSA_MYCGE P47387 MYCOPLASMA GENITALIUM 2097 -11540170 172567 n-utilization substance protein a homolog (cl:transcription termination factor nusa homology) (db:pir2.dat) F64215 F64215 Mycoplasma genitalium 2097 -11540170 7500887010 mg141 n-utilization substance protein a nusa (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to sp:p75591 pid:1674384 percent identity:) (le:3883) (re:5478) (di:direct) U39695 U39695 g3844734 Mycoplasma genitalium 2097 -11540170 5000697451 (de:(mg141) (pn:n-utilization substance protein a homolog:nusa) (gn:nusa) (gtcfc:10.2) (ec:) (nusa_mycge) (keggfc:11.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium)) MG141 MG141 Mycoplasma genitalium 2097 10029383

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919168	19208	41364	456	151

Description

5000697452 rpod:siga:mg249 rna polymerase sigma-43 factor:rpod:rna polymerase sigma factor rpod:sigma-a (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG249 MG249 Mycoplasma genitalium 2097 -11540171 96334 rpod:siga:mg249 (de:rna polymerase sigma factor rpod (sigma-a)) (db:swissprot) RPSD_MYCGE P47491 MYCOPLASMA GENITALIUM 2097 -11540171 172685 transcription initiation factor sigma a:rna polymerase sigma-a factor (cl:transcription initiation factor sigma katf homology) (db:pir2.dat) E64227 E64227 Mycoplasma genitalium 2097 -11540171 7500890688 mg249 rna polymerase sigma-43 factor rpod (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78022 pid:1674175 percent) (le:17284) (re:18777) (di:complement) U39703 U39703 g1045940 Mycoplasma genitalium 2097 -11540171 6500736313 rpod:siga rna polymerase sigma-43 factor:rpod:rna polymerase sigma factor rpod:sigma-a (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG249 MG249 Mycoplasma genitalium 2097 -11540171

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919175	19209	41365	468	155

Description

5000697453 atp-dependent rna helicase:dead:probable rna helicase mg425 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG425 MG425 Mycoplasma genitalium 2097 -11540172 109162 mg425 (de:probable rna helicase mg425) (db:swissprot) Y425_MYCGE P47664 MYCOPLASMA GENITALIUM 2097 -11540172 172306 atp-dependent rna helicase dead homolog mg425 (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) I64246 I64246 Mycoplasma genitalium 2097 -11540172 7500895277 mg425 atp-dependent rna helicase dead (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75172 pid:1673885 percent) (le:125) (re:1474) (di:direct) U39725 U39725 g3845018 Mycoplasma genitalium 2097 -11540172 6500736314 atp-dependent rna helicase:dead:probable rna helicase mg425 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.2) (db:gtc-mycoplasma genitalium) MG425 MG425 Mycoplasma genitalium 2097 -11540172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919176	19210	41366	312	103

Description

5000697454 transcription antitermination factor:nusg:hypothetical protein mg054 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-mycoplasma genitalium) MG054 MG054 Mycoplasma genitalium 2097 -11540173 108537 mg054 (de:hypothetical protein mg054) (db:swissprot) Y054_MYCGE P47300 MYCOPLASMA GENITALIUM 2097 -11540173 172683 transcription antitermination factor nusg (db:pir2.dat) I64205 I64205 Mycoplasma genitalium 2097 -11540173 7500894597 mg054 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75049 pid:1673742 percent) (le:13325) (re:14275) (di:complement) U39684 U39684 g1045727 Mycoplasma genitalium 2097 -11540173 6500736315 transcription antitermination factor:nusg:hypothetical protein mg054 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-mycoplasma genitalium) MG054 MG054 Mycoplasma genitalium 2097 -11540173

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919180	19211	41367	222	73

Description

6500736316 grea:mg282 transcription elongation factor:transcript cleavage factor grea (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-mycoplasma genitalium) MG282 MG282 Mycoplasma genitalium 2097 -11540174 74477 grea:mg282 (de:grea)) (db:swissprot) GREA_MYCGE P47524 MYCOPLASMA GENITALIUM 2097 -11540174 172684 transcription elongation factor grea homolog (cl:transcription elongation factor greb) (db:pir2.dat) B64231 B64231 Mycoplasma genitalium 2097 -11540174 7500882725 mg282 transcription elongation factor grea (db:genpept-bct2) (de:mycoplasma genitalium section 30 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78019 pid:1674124 percent) (le:2419) (re:2904) (di:complement) U39708 U39708 g1045978 Mycoplasma genitalium 2097 -11540174 5000697455 (de:(mg282) (pn:transcription elongation factor :transcript cleavage factor grea:transcription elongation factor:grea) (gn:grea) (gtcfc:10.2) (ec:) (grea_mycge) (keggfc:11.2) (tigrfc:11.3) (db:gtc-mycoplasma genitalium)) MG282 MG282 Mycoplasma genitalium 2097 10016993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919184	19212	41368	1512	504

Description

5000697456 atp-dependent rna helicase:dead:probable rna helicase mg308 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-mycoplasma genitalium) MG308 MG308 Mycoplasma genitalium 2097 -11540175 109069 mg308 (de:probable rna helicase mg308) (db:swissprot) Y308_MYCGE P52271 MYCOPLASMA GENITALIUM 2097 -11540175 172305 atp-dependent rna helicase dead homolog mg308 (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) A64234 A64234 Mycoplasma genitalium 2097 -11540175 7500895102 mg308 atp-dependent rna helicase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 33 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75335 pid:1674080 percent) (le:6693) (re:7925) (di:complement) U39711 U39711 g3844887 Mycoplasma genitalium 2097 -11540175 6500736317 atp-dependent rna helicase:dead:probable rna helicase mg308 (gtcfc:10.2) (keggfc:14.2) (tigrfc:11.3) (db:gtc-mycoplasma genitalium) MG308 MG308 Mycoplasma genitalium 2097 -11540175

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919193	19213	41369	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919211	19214	41370	291	96

Description

5000697520 ribosomal protein s6 modification protein:rimk:hypothetical protein mg012 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.1) (db:gtc-mycoplasma genitalium) MG012 MG012 Mycoplasma genitalium 2097 -11540176 172655 ribosomal protein s6 modification protein rimk homolog (db:pir2.dat) C64201 C64201 Mycoplasma genitalium 2097 -11540176 7500965567 rimk ribosomal protein s6 modification protein (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium cdc8, dnae_1, dnah_1, dnaj_1, dnan, gyra,gyrb, rimk, sers, tdhf genes from bases 1 to 14345 (section 1 of56) of the complete genome.) (nt:identified by ... U39679 U39679 g1045680 Mycoplasma genitalium 2097 -11540176 6500736318 ribosomal protein s6 modification protein:rimk:hypothetical protein mg012 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.1) (db:gtc-mycoplasma genitalium) MG012 MG012 Mycoplasma genitalium 2097 -11540176

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919213	19215	41371	603	200

Description

5000697521 pet112 protein:hypothetical protein mg100 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.1) (db:gtc-mycoplasma genitalium) MG100 MG100 Mycoplasma genitalium 2097 -11540177 108721 mg100 (de:hypothetical protein mg100) (db:swissprot) Y100_MYCGE P47346 MYCOPLASMA GENITALIUM 2097 -11540177 172583 pet112 protein homolog (cl:pet112 protein) (db:pir2.dat) A64211 A64211 Mycoplasma genitalium 2097 -11540177 7500894695 mg100 glu-trna amidotransferase:subunit b gatb (db:genpept-bct2) (de:mycoplasma genitalium section 12 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75533 pid:1674295 percent) (le:5830) (re:7263) (di:direct) U39690 U39690 g3844688 Mycoplasma genitalium 2097 -11540177 6500736319 pet112 protein:hypothetical protein mg100 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.1) (db:gtc-mycoplasma genitalium) MG100 MG100 Mycoplasma genitalium 2097 -11540177

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919216	19216	41372	897	298

Description

5000697522 ribosome-binding factor a:p15b protein:hypothetical protein mg143 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.1) (db:gtc-mycoplasma genitalium) MG143 MG143 Mycoplasma genitalium 2097 -11540178 108869 mg143 (de:hypothetical protein mg143) (db:swissprot) Y143_MYCGE P47389 MYCOPLASMA GENITALIUM 2097 -11540178 172405 hypothetical protein homolog mg143 (db:pir2.dat) H64215 H64215 Mycoplasma genitalium 2097 -11540178 7500894777 mg143 ribosome-binding factor a:putative (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75589 pid:1674381 percent) (le:7583) (re:7921) (di:direct) U39695 U39695 g3844736 Mycoplasma genitalium 2097 -11540178 6500736320 ribosome-binding factor a:p15b protein:hypothetical protein mg143 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.1) (db:gtc-mycoplasma genitalium) MG143 MG143 Mycoplasma genitalium 2097 -11540178

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919218	19217	41373	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919225	19218	41374	405	134

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919226	19219	41375	651	216

Description

5000697457 rpsb:rps2:mg070 ribosomal protein s2:30s ribosomal protein s2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG070 MG070 Mycoplasma genitalium 2097 -11540179 97238 rpsb:rps2:mg070 (de:30s ribosomal protein s2) (db:swissprot) RS2_MYCGE P47316 MYCOPLASMA GENITALIUM 2097 -11540179 172651 ribosomal protein s2 (cl:escherichia coli ribosomal protein s2) (db:pir2.dat) G64207 G64207 Mycoplasma genitalium 2097 -11540179 7500891031 mg070 ribosomal protein s2 rps2 (db:genpept-bct2) (de:mycoplasma genitalium section 9 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75560 pid:1674326 percent) (le:4959) (re:5813) (di:direct) U39687 U39687 g1045746 Mycoplasma genitalium 2097 -11540179 6500736321 rpsb:rps2 ribosomal protein s2:30s ribosomal protein s2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG070 MG070 Mycoplasma genitalium 2097 -11540179

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919230	19220	41376	330	109

Description

5000697458 rplk:rpl11:mg081 ribosomal protein l11:50s ribosomal protein l11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG081 MG081 Mycoplasma genitalium 2097 -11540180 148863 ribosomal protein l11 (cl:escherichia coli ribosomal protein l11) (db:pir2.dat) I64208 I64208 Mycoplasma genitalium 2097 -11540180 7500954919 mg081 ribosomal protein l11 rpl11 (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75550 pid:1674314 percent) (le:39) (re:452) (di:direct) U39689 U39689 g3844668 Mycoplasma genitalium 2097 -11540180 6500736322 rplk:rpl11 ribosomal protein l11:50s ribosomal protein l11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG081 MG081 Mycoplasma genitalium 2097 -11540180

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919235	19221	41377	2175	724

Description

5000697459 rpla:rpl1:mg082 ribosomal protein l1:rpl1:50s ribosomal protein l1 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG082 MG082 Mycoplasma genitalium 2097 -11540181 94931 rpla:rpl1:mg082 (de:50s ribosomal protein l1) (db:swissprot) RL1_MYCGE P47328 MYCOPLASMA GENITALIUM 2097 -11540181 172625 ribosomal protein l1 (cl:escherichia coli ribosomal protein l1) (db:pir2.dat) A64209 A64209 Mycoplasma genitalium 2097 -11540181 7500890040 mg082 ribosomal protein l1 rpl1 (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78035 pid:1674313 percent) (le:452) (re:1132) (di:direct) U39689 U39689 g3844669 Mycoplasma genitalium 2097 -11540181 6500736323 rpla:rpl1 ribosomal protein l1:rpl1:50s ribosomal protein l1 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG082 MG082 Mycoplasma genitalium 2097 -11540181

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919254	19222	41378	3477	1158

Description

5000697460 rpsl:rps12:mg087 ribosomal protein s12:30s ribosomal protein s12 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG087 MG087 Mycoplasma genitalium 2097 -11540182 96954 rpsl:rps12:mg087 (de:30s ribosomal protein s12) (db:swissprot) RS12_MYCGE P47333 MYCOPLASMA GENITALIUM 2097 -11540182 148529 ribosomal protein s12 (cl:escherichia coli ribosomal protein s12) (db:pir2.dat) F64209 F64209 Mycoplasma genitalium 2097 -11540182 7500890875 mg087 ribosomal protein s12 rps12 (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75546 pid:1674308 percent) (le:4672) (re:5091) (di:direct) U39689 U39689 g3844674 Mycoplasma genitalium 2097 -11540182 6500736324 rpsl:rps12 ribosomal protein s12:30s ribosomal protein s12 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG087 MG087 Mycoplasma genitalium 2097 -11540182

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919256	19223	41379	2583	860

Description

5000697461 rpsg:rps7:mg088 ribosomal protein s7:rps7:30s ribosomal protein s7 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG088 MG088 Mycoplasma genitalium 2097 -11540183 97394 rpsg:rps7:mg088 (de:30s ribosomal protein s7) (db:swissprot) RS7_MYCGE P47334 MYCOPLASMA GENITALIUM 2097 -11540183 148414 ribosomal protein s7 (cl:escherichia coli ribosomal protein s7) (db:pir2.dat) G64209 G64209 Mycoplasma genitalium 2097 -11540183 7500891105 mg088 ribosomal protein s7 rps7 (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75545 pid:1674307 percent) (le:5108) (re:5575) (di:direct) U39689 U39689 g3844675 Mycoplasma genitalium 2097 -11540183 6500736325 rpsg:rps7 ribosomal protein s7:rps7:30s ribosomal protein s7 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG088 MG088 Mycoplasma genitalium 2097 -11540183

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919320	19224	41380	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919332	19225	41381	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919334	19226	41382	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919347	19227	41383	1215	404

Description

5000697462 rpsf:rps6:mg090 ribosomal protein s6:rps6:30s ribosomal protein s6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG090 MG090 Mycoplasma genitalium 2097 -11540184 97367 rpsf:rps6:mg090 (de:30s ribosomal protein s6) (db:swissprot) RS6_MYCGE P47336 MYCOPLASMA GENITALIUM 2097 -11540184 172654 ribosomal protein s6 (db:pir2.dat) I64209 I64209 Mycoplasma genitalium 2097 -11540184 7500891091 mg090 ribosomal protein s6 rps6 (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75543 pid:1674305 percent) (le:7703) (re:8329) (di:direct) U39689 U39689 g3844677 Mycoplasma genitalium 2097 -11540184 6500736326 rpsf:rps6 ribosomal protein s6:rps6:30s ribosomal protein s6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG090 MG090 Mycoplasma genitalium 2097 -11540184

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919352	19228	41384	5718	1905

Description

5000697463 rpsr:rps18:mg092 ribosomal protein s18:rps18:30s ribosomal protein s18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG092 MG092 Mycoplasma genitalium 2097 -11540185 97102 rpsr:rps18:mg092 (de:30s ribosomal protein s18) (db:swissprot) RS18_MYCGE P47338 MYCOPLASMA GENITALIUM 2097 -11540185 172650 ribosomal protein s18 (cl:escherichia coli ribosomal protein s18) (db:pir2.dat) B64210 B64210 Mycoplasma genitalium 2097 -11540185 7500890957 mg092 ribosomal protein s18 rps18 (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75541 pid:1674303 percent) (le:8802) (re:9119) (di:direct) U39689 U39689 g3844679 Mycoplasma genitalium 2097 -11540185 6500736327 rpsr:rps18 ribosomal protein s18:rps18:30s ribosomal protein s18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG092 MG092 Mycoplasma genitalium 2097 -11540185

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919353	19229	41385	456	151

Description

5000697464 rpli:rpl9:mg093 ribosomal protein l9:rpl9:50s ribosomal protein l9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG093 MG093 Mycoplasma genitalium 2097 -11540186 95499 rpli:rpl9:mg093 (de:50s ribosomal protein l9) (db:swissprot) RL9_MYCGE P47339 MYCOPLASMA GENITALIUM 2097 -11540186 172645 ribosomal protein l9 (db:pir2.dat) C64210 C64210 Mycoplasma genitalium 2097 -11540186 7500890367 mg093 ribosomal protein l9 rpl9 (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75540 pid:1674302 percent) (le:9122) (re:9574) (di:direct) U39689 U39689 g3844680 Mycoplasma genitalium 2097 -11540186 6500736328 rpli:rpl9 ribosomal protein l9:rpl9:50s ribosomal protein l9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG093 MG093 Mycoplasma genitalium 2097 -11540186

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919355	19230	41386	2316	771

Description

5000697465 rpsj:rps10:mg150 ribosomal protein s10:rps10:30s ribosomal protein s10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG150 MG150 Mycoplasma genitalium 2097 -11540187 96900 rpsj:rps10:mg150 (de:30s ribosomal protein s10) (db:swissprot) RS10_MYCGE P47396 MYCOPLASMA GENITALIUM 2097 -11540187 172646 ribosomal protein s10 (cl:escherichia coli ribosomal protein s10) (db:pir2.dat) F64216 F64216 Mycoplasma genitalium 2097 -11540187 7500890848 mg150 ribosomal protein s10 rps10 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75581 pid:1674372 percent) (le:1508) (re:1828) (di:direct) U39696 U39696 g3844744 Mycoplasma genitalium 2097 -11540187 6500736329 rpsj:rps10 ribosomal protein s10:rps10:30s ribosomal protein s10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG150 MG150 Mycoplasma genitalium 2097 -11540187

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919358	19231	41387	915	304

Description

5000697466 rplc:rpl3:mg151 ribosomal protein l3:rpl3:50s ribosomal protein l3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG151 MG151 Mycoplasma genitalium 2097 -11540188 95299 rplc:rpl3:mg151 (de:50s ribosomal protein l3) (db:swissprot) RL3_MYCGE P47397 MYCOPLASMA GENITALIUM 2097 -11540188 172639 ribosomal protein l3 (cl:escherichia coli ribosomal protein l3) (db:pir2.dat) G64216 G64216 Mycoplasma genitalium 2097 -11540188 7500890277 mg151 ribosomal protein l3 rpl3 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75580 pid:1674371 percent) (le:1832) (re:2605) (di:direct) U39696 U39696 g3844745 Mycoplasma genitalium 2097 -11540188 6500736330 rplc:rpl3 ribosomal protein l3:rpl3:50s ribosomal protein l3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG151 MG151 Mycoplasma genitalium 2097 -11540188

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919386	19232	41388	612	204

Description

5000697467 rpld:rpl4:mg152 ribosomal protein l4:rpl4:50s ribosomal protein l4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG152 MG152 Mycoplasma genitalium 2097 -11540189 95369 rpld:rpl4:mg152 (de:50s ribosomal protein l4) (db:swissprot) RL4_MYCGE P47398 MYCOPLASMA GENITALIUM 2097 -11540189 172642 ribosomal protein l4 (cl:escherichia coli ribosomal protein l4) (db:pir2.dat) H64216 H64216 Mycoplasma genitalium 2097 -11540189 7500890317 mg152 ribosomal protein l4 rpl4 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75579 pid:1674370 percent) (le:2605) (re:3240) (di:direct) U39696 U39696 g3844746 Mycoplasma genitalium 2097 -11540189 6500736331 rpld:rpl4 ribosomal protein l4:rpl4:50s ribosomal protein l4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG152 MG152 Mycoplasma genitalium 2097 -11540189

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919391	19233	41389	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919418	19234	41390	1164	387

Description

5000697468 rplw:rpl23:mg153 ribosomal protein l23:rpl23:50s ribosomal protein l23 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG153 MG153 Mycoplasma genitalium 2097 -11540190 95005 rplw:rpl23:mg153 (de:50s ribosomal protein l23) (db:swissprot) RL23_MYCGE P47399 MYCOPLASMA GENITALIUM 2097 -11540190 172635 ribosomal protein l23 (cl:escherichia coli ribosomal protein l23) (db:pir1.dat) I64216 I64216 Mycoplasma genitalium 2097 -11540190 7500890095 mg153 ribosomal protein l23 rpl23 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75578 pid:1674369 percent) (le:3244) (re:3564) (di:direct) U39696 U39696 g3844747 Mycoplasma genitalium 2097 -11540190 6500736332 rplw:rpl23 ribosomal protein l23:rpl23:50s ribosomal protein l23 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG153 MG153 Mycoplasma genitalium 2097 -11540190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919427	19235	41391	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919456	19236	41392	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919462	19237	41393	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919463	19238	41394	1827	608

Description

5000697469 rplb:rpl2:mg154 ribosomal protein l2:rpl2:50s ribosomal protein l2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG154 MG154 Mycoplasma genitalium 2097 -11540191 95119 rplb:rpl2:mg154 (de:50s ribosomal protein l2) (db:swissprot) RL2_MYCGE P47400 MYCOPLASMA GENITALIUM 2097 -11540191 148691 ribosomal protein l2 (cl:escherichia coli ribosomal protein l2) (db:pir2.dat) A64217 A64217 Mycoplasma genitalium 2097 -11540191 7500890171 mg154 ribosomal protein l2 rpl2 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75577 pid:1674368 percent) (le:3564) (re:4421) (di:direct) U39696 U39696 g3844748 Mycoplasma genitalium 2097 -11540191 6500736333 rplb:rpl2 ribosomal protein l2:rpl2:50s ribosomal protein l2 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG154 MG154 Mycoplasma genitalium 2097 -11540191

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919465	19239	41395	843	280

Description

5000697470 rpss:rps19:mg155 ribosomal protein s19:rps19:30s ribosomal protein s19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG155 MG155 Mycoplasma genitalium 2097 -11540192 97119 rpss:rps19:mg155 (de:30s ribosomal protein s19) (db:swissprot) RS19_MYCGE P47401 MYCOPLASMA GENITALIUM 2097 -11540192 148630 ribosomal protein s19 (cl:escherichia coli ribosomal protein s19) (db:pir2.dat) B64217 B64217 Mycoplasma genitalium 2097 -11540192 7500890969 mg155 ribosomal protein s19 rps19 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75576 pid:1674367 percent) (le:4421) (re:4684) (di:direct) U39696 U39696 g3844749 Mycoplasma genitalium 2097 -11540192 6500736334 rpss:rps19 ribosomal protein s19:rps19:30s ribosomal protein s19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG155 MG155 Mycoplasma genitalium 2097 -11540192

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919467	19240	41396	435	144

Description

5000697471 rplv:rpl22:mg156 ribosomal protein l22:50s ribosomal protein l22 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG156 MG156 Mycoplasma genitalium 2097 -11540193 94987 rplv:rpl22:mg156 (de:50s ribosomal protein l22) (db:swissprot) RL22_MYCGE P47402 MYCOPLASMA GENITALIUM 2097 -11540193 172634 ribosomal protein l22 (cl:escherichia coli ribosomal protein l22) (db:pir2.dat) C64217 C64217 Mycoplasma genitalium 2097 -11540193 7500890071 mg156 ribosomal protein l22 rpl22 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75575 pid:1674366 percent) (le:4687) (re:5121) (di:direct) U39696 U39696 g3844750 Mycoplasma genitalium 2097 -11540193 6500736335 rplv:rpl22 ribosomal protein l22:50s ribosomal protein l22 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG156 MG156 Mycoplasma genitalium 2097 -11540193

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919487	19241	41397	357	118

Description

5000697472 rpsc:rps3:mg157 ribosomal protein s3:rps3:30s ribosomal protein s3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG157 MG157 Mycoplasma genitalium 2097 -11540194 172652 ribosomal protein s3 (cl:escherichia coli ribosomal protein s3) (db:pir2.dat) D64217 D64217 Mycoplasma genitalium 2097 -11540194 7500965566 mg157 ribosomal protein s3 rps3 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:x67652 sp:p41205 pid:44500 gb:u00089) (le:5124) (re:5930) (di:direct) U39696 U39696 g3844751 Mycoplasma genitalium 2097 -11540194 6500736336 rpsc:rps3 ribosomal protein s3:rps3:30s ribosomal protein s3 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG157 MG157 Mycoplasma genitalium 2097 -11540194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919499	19242	41398	264	87

Description

5000697473 rplp:rpl16:mg158 ribosomal protein l16:rpl16:50s ribosomal protein l16 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG158 MG158 Mycoplasma genitalium 2097 -11540195 94840 rplp:rpl16:mg158 (de:50s ribosomal protein l16) (db:swissprot) RL16_MYCGE P47404 MYCOPLASMA GENITALIUM 2097 -11540195 148908 ribosomal protein l16 (cl:escherichia coli ribosomal protein l16) (db:pir2.dat) E64217 E64217 Mycoplasma genitalium 2097 -11540195 7500889982 mg158 ribosomal protein l16 rpl16 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:x67651 sp:p41204 pid:44498) (le:5936) (re:6352) (di:direct) U39696 U39696 g3844752 Mycoplasma genitalium 2097 -11540195 6500736337 rplp:rpl16 ribosomal protein l16:rpl16:50s ribosomal protein l16 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG158 MG158 Mycoplasma genitalium 2097 -11540195

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919500	19243	41399	339	112

Description

5000697474 rpmc:rpl29:mg159 ribosomal protein l29:rpl29:50s ribosomal protein l29 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG159 MG159 Mycoplasma genitalium 2097 -11540196 95084 rpmc:rpl29:mg159 (de:50s ribosomal protein l29) (db:swissprot) RL29_MYCGE P47405 MYCOPLASMA GENITALIUM 2097 -11540196 172638 ribosomal protein l29 (db:pir2.dat) F64217 F64217 Mycoplasma genitalium 2097 -11540196 7500890152 mg159 ribosomal protein l29 rpl29 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215715 gb:u00089 sp:q50310) (le:6352) (re:6954) (di:direct) U39696 U39696 g3844753 Mycoplasma genitalium 2097 -11540196 6500736338 rpmc:rpl29 ribosomal protein l29:rpl29:50s ribosomal protein l29 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG159 MG159 Mycoplasma genitalium 2097 -11540196

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919507	19244	41400	255	84

Description

5000697475 rpsq:rps17:mg160 ribosomal protein s17:rps17:30s ribosomal protein s17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG160 MG160 Mycoplasma genitalium 2097 -11540197 97085 rpsq:rps17:mg160 (de:30s ribosomal protein s17) (db:swissprot) RS17_MYCGE P47406 MYCOPLASMA GENITALIUM 2097 -11540197 148600 ribosomal protein s17 (cl:escherichia coli ribosomal protein s17) (db:pir2.dat) G64217 G64217 Mycoplasma genitalium 2097 -11540197 7500890941 mg160 ribosomal protein s17 rps17 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215714 gb:u00089 sp:q50309) (le:6954) (re:7211) (di:direct) U39696 U39696 g3844754 Mycoplasma genitalium 2097 -11540197 6500736339 rpsq:rps17 ribosomal protein s17:rps17:30s ribosomal protein s17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG160 MG160 Mycoplasma genitalium 2097 -11540197

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919517	19245	41401	336	111

Description

5000697476 rpln:rpl14:mg161 ribosomal protein l14:rpl14:50s ribosomal protein l14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG161 MG161 Mycoplasma genitalium 2097 -11540198 94800 rpln:rpl14:mg161 (de:50s ribosomal protein l14) (db:swissprot) RL14_MYCGE P47407 MYCOPLASMA GENITALIUM 2097 -11540198 148877 ribosomal protein l14 (cl:escherichia coli ribosomal protein l14) (db:pir2.dat) H64217 H64217 Mycoplasma genitalium 2097 -11540198 7500889947 mg161 ribosomal protein l14 rpl14 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215713 gb:u00089 sp:q50308) (le:7215) (re:7583) (di:direct) U39696 U39696 g3844755 Mycoplasma genitalium 2097 -11540198 6500736340 rpln:rpl14 ribosomal protein l14:rpl14:50s ribosomal protein l14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG161 MG161 Mycoplasma genitalium 2097 -11540198

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919518	19246	41402	486	161

Description

5000697477 rplx:rpl24:mg162 ribosomal protein l24:rpl24:50s ribosomal protein l24 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG162 MG162 Mycoplasma genitalium 2097 -11540199 95026 rplx:rpl24:mg162 (de:50s ribosomal protein l24) (db:swissprot) RL24_MYCGE P47408 MYCOPLASMA GENITALIUM 2097 -11540199 172636 ribosomal protein l24 (cl:escherichia coli ribosomal protein l24) (db:pir2.dat) I64217 I64217 Mycoplasma genitalium 2097 -11540199 7500890110 mg162 ribosomal protein l24 rpl24 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215712 gb:u00089 sp:q50307) (le:7583) (re:7909) (di:direct) U39696 U39696 g3844756 Mycoplasma genitalium 2097 -11540199 6500736341 rplx:rpl24 ribosomal protein l24:rpl24:50s ribosomal protein l24 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG162 MG162 Mycoplasma genitalium 2097 -11540199

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919527	19247	41403	312	103

Description

5000697478 rple:rpl5:mg163 ribosomal protein l5:rpl5:50s ribosomal protein l5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG163 MG163 Mycoplasma genitalium 2097 -11540200 95396 rple:rpl5:mg163 (de:50s ribosomal protein l5) (db:swissprot) RL5_MYCGE P47409 MYCOPLASMA GENITALIUM 2097 -11540200 148739 ribosomal protein l5 (cl:escherichia coli ribosomal protein l5) (db:pir2.dat) A64218 A64218 Mycoplasma genitalium 2097 -11540200 7500890331 mg163 ribosomal protein l5 rpl5 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215711 gb:u00089 sp:q50306) (le:7915) (re:8457) (di:direct) U39696 U39696 g3844757 Mycoplasma genitalium 2097 -11540200 6500736342 rple:rpl5 ribosomal protein l5:rpl5:50s ribosomal protein l5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG163 MG163 Mycoplasma genitalium 2097 -11540200

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919528	19248	41404	798	265

Description

5000697479 rpsn:rps14:mg164 ribosomal protein s14:rps14:30s ribosomal protein s14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG164 MG164 Mycoplasma genitalium 2097 -11540201 97020 rpsn:rps14:mg164 (de:30s ribosomal protein s14) (db:swissprot) RS14_MYCGE P47410 MYCOPLASMA GENITALIUM 2097 -11540201 148570 ribosomal protein s14 (cl:escherichia coli ribosomal protein s14) (db:pir2.dat) B64218 B64218 Mycoplasma genitalium 2097 -11540201 7500890901 mg164 ribosomal protein s14 rps14 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215710 gb:u00089 sp:q50305) (le:8460) (re:8645) (di:direct) U39696 U39696 g3844758 Mycoplasma genitalium 2097 -11540201 6500736343 rpsn:rps14 ribosomal protein s14:rps14:30s ribosomal protein s14 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG164 MG164 Mycoplasma genitalium 2097 -11540201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919530	19249	41405	507	168

Description

5000697480 rpsh:rps8:mg165 ribosomal protein s8:rps8:30s ribosomal protein s8 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG165 MG165 Mycoplasma genitalium 2097 -11540202 97429 rpsh:rps8:mg165 (de:30s ribosomal protein s8) (db:swissprot) RS8_MYCGE P47411 MYCOPLASMA GENITALIUM 2097 -11540202 172656 ribosomal protein s8 (cl:escherichia coli ribosomal protein s8) (db:pir2.dat) C64218 C64218 Mycoplasma genitalium 2097 -11540202 7500891117 mg165 ribosomal protein s8 rps8 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215709 gb:u00089 sp:q50304) (le:8639) (re:9064) (di:direct) U39696 U39696 g3844759 Mycoplasma genitalium 2097 -11540202 6500736344 rpsh:rps8 ribosomal protein s8:rps8:30s ribosomal protein s8 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG165 MG165 Mycoplasma genitalium 2097 -11540202

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919532	19250	41406	696	231

Description

5000697481 rplf:rpl6:mg166 ribosomal protein l6:rpl6:50s ribosomal protein l6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG166 MG166 Mycoplasma genitalium 2097 -11540203 95426 rplf:rpl6:mg166 (de:50s ribosomal protein l6) (db:swissprot) RL6_MYCGE P47412 MYCOPLASMA GENITALIUM 2097 -11540203 172643 ribosomal protein l6 (cl:escherichia coli ribosomal protein l6) (db:pir2.dat) D64218 D64218 Mycoplasma genitalium 2097 -11540203 7500890346 mg166 ribosomal protein l6 rpl6 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215708 gb:u00089 sp:q50303) (le:9071) (re:9625) (di:direct) U39696 U39696 g3844760 Mycoplasma genitalium 2097 -11540203 6500736345 rplf:rpl6 ribosomal protein l6:rpl6:50s ribosomal protein l6 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG166 MG166 Mycoplasma genitalium 2097 -11540203

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919533	19251	41407	267	88

Description

5000697482 rplr:rpl18:mg167 ribosomal protein l18:rpl18:50s ribosomal protein l18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG167 MG167 Mycoplasma genitalium 2097 -11540204 94878 rplr:rpl18:mg167 (de:50s ribosomal protein l18) (db:swissprot) RL18_MYCGE P47413 MYCOPLASMA GENITALIUM 2097 -11540204 172630 ribosomal protein l18 (cl:escherichia coli ribosomal protein l18) (db:pir2.dat) E64218 E64218 Mycoplasma genitalium 2097 -11540204 7500890005 mg167 ribosomal protein l18 rpl18 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215707 gb:u00089 sp:q50302) (le:9627) (re:9974) (di:direct) U39696 U39696 g3844761 Mycoplasma genitalium 2097 -11540204 6500736346 rplr:rpl18 ribosomal protein l18:rpl18:50s ribosomal protein l18 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG167 MG167 Mycoplasma genitalium 2097 -11540204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919537	19252	41408	891	296

Description

5000697483 rpse:rps5:mg168 ribosomal protein s5:rps5:30s ribosomal protein s5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG168 MG168 Mycoplasma genitalium 2097 -11540205 97348 rpse:rps5:mg168 (de:30s ribosomal protein s5) (db:swissprot) RS5_MYCGE P47414 MYCOPLASMA GENITALIUM 2097 -11540205 148387 ribosomal protein s5 (cl:escherichia coli ribosomal protein s5) (db:pir2.dat) F64218 F64218 Mycoplasma genitalium 2097 -11540205 7500891068 mg168 ribosomal protein s5 rps5 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215706 gb:u00089 sp:q50301) (le:9979) (re:10614) (di:direct) U39696 U39696 g3844762 Mycoplasma genitalium 2097 -11540205 6500736347 rpse:rps5 ribosomal protein s5:rps5:30s ribosomal protein s5 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG168 MG168 Mycoplasma genitalium 2097 -11540205

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919541	19253	41409	654	217

Description

5000697484 rpmj:rpl36:mg174 ribosomal protein l36:rpl36:50s ribosomal protein l36 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG174 MG174 Mycoplasma genitalium 2097 -11540206 95241 rpmj:rpl36:mg174 (de:50s ribosomal protein l36) (db:swissprot) RL36_MYCGE P47420 MYCOPLASMA GENITALIUM 2097 -11540206 149070 ribosomal protein l36 (cl:escherichia coli ribosomal protein l36) (db:pir2.dat) C64219 C64219 Mycoplasma genitalium 2097 -11540206 7500890245 mg174 ribosomal protein l36 rpl36 (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215700 sp:p52864 gb:u00089) (le:11) (re:124) (di:direct) U39697 U39697 g3844770 Mycoplasma genitalium 2097 -11540206 6500736348 rpmj:rpl36 ribosomal protein l36:rpl36:50s ribosomal protein l36 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG174 MG174 Mycoplasma genitalium 2097 -11540206

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919550	19254	41410	600	199

Description

5000697485 rpsm:rps13:mg175 ribosomal protein s13:rps13:30s ribosomal protein s13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG175 MG175 Mycoplasma genitalium 2097 -11540207 148550 ribosomal protein s13 (cl:escherichia coli ribosomal protein s13) (db:pir2.dat) D64219 D64219 Mycoplasma genitalium 2097 -11540207 7500954831 mg175 ribosomal protein s13 rps13 (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215699 gb:u00089 sp:q50297) (le:124) (re:498) (di:direct) U39697 U39697 g3844771 Mycoplasma genitalium 2097 -11540207 6500736349 rpsm:rps13 ribosomal protein s13:rps13:30s ribosomal protein s13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG175 MG175 Mycoplasma genitalium 2097 -11540207

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919554	19255	41411	483	160

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919555	19256	41412	945	314

Description

5000697486 rpsk:rps11:mg176 ribosomal protein s11:rps11:30s ribosomal protein s11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG176 MG176 Mycoplasma genitalium 2097 -11540208 96928 rpsk:rps11:mg176 (de:30s ribosomal protein s11) (db:swissprot) RS11_MYCGE P47422 MYCOPLASMA GENITALIUM 2097 -11540208 172647 ribosomal protein s11 (cl:escherichia coli ribosomal protein s11) (db:pir2.dat) E64219 E64219 Mycoplasma genitalium 2097 -11540208 7500890862 mg176 ribosomal protein s11 rps11 (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215698 gb:u00089 sp:q50296) (le:498) (re:893) (di:direct) U39697 U39697 g3844772 Mycoplasma genitalium 2097 -11540208 6500736350 rpsk:rps11 ribosomal protein s11:rps11:30s ribosomal protein s11 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG176 MG176 Mycoplasma genitalium 2097 -11540208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919583	19257	41413	498	165

Description

5000697487 rplq:rpl17:mg178 ribosomal protein l17:rpl17:50s ribosomal protein l17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG178 MG178 Mycoplasma genitalium 2097 -11540209 94855 rplq:rpl17:mg178 (de:50s ribosomal protein l17) (db:swissprot) RL17_MYCGE P47424 MYCOPLASMA GENITALIUM 2097 -11540209 172629 ribosomal protein l17 (cl:escherichia coli ribosomal protein l17) (db:pir2.dat) G64219 G64219 Mycoplasma genitalium 2097 -11540209 7500889994 mg178 ribosomal protein l17 rpl17 (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215696 gb:u00089 sp:q59547) (le:1877) (re:2248) (di:direct) U39697 U39697 g3844774 Mycoplasma genitalium 2097 -11540209 6500736351 rplq:rpl17 ribosomal protein l17:rpl17:50s ribosomal protein l17 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG178 MG178 Mycoplasma genitalium 2097 -11540209

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919606	19258	41414	855	285

Description

5000697488 rpmi:rpl35:mg197 ribosomal protein l35:50s ribosomal protein l35 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG197 MG197 Mycoplasma genitalium 2097 -11540210 95224 rpmi:rpl35:mg197 (de:50s ribosomal protein l35) (db:swissprot) RL35_MYCGE P47439 MYCOPLASMA GENITALIUM 2097 -11540210 149073 ribosomal protein l35 (cl:escherichia coli ribosomal protein l35) (db:pir2.dat) G64221 G64221 Mycoplasma genitalium 2097 -11540210 7500890237 mg197 ribosomal protein l35 rpl35 (db:genpept-bct2) (de:mycoplasma genitalium section 21 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75447 pid:1673687 percent) (le:5533) (re:5712) (di:direct) U39699 U39699 g3844794 Mycoplasma genitalium 2097 -11540210 6500736352 rpmi:rpl35 ribosomal protein l35:50s ribosomal protein l35 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG197 MG197 Mycoplasma genitalium 2097 -11540210

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919612	19259	41415	213	70

Description

5000697489 rplt:rpl20:mg198 ribosomal protein l20:rpl20:50s ribosomal protein l20 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG198 MG198 Mycoplasma genitalium 2097 -11540211 94952 rplt:rpl20:mg198 (de:50s ribosomal protein l20) (db:swissprot) RL20_MYCGE P47440 MYCOPLASMA GENITALIUM 2097 -11540211 148941 ribosomal protein l20 (cl:escherichia coli ribosomal protein l20) (db:pir2.dat) H64221 H64221 Mycoplasma genitalium 2097 -11540211 7500890044 mg198 ribosomal protein l20 rpl20 (db:genpept-bct2) (de:mycoplasma genitalium section 21 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78023 pid:1673686 percent) (le:5715) (re:6089) (di:direct) U39699 U39699 g3844795 Mycoplasma genitalium 2097 -11540211 6500736353 rplt:rpl20 ribosomal protein l20:rpl20:50s ribosomal protein l20 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG198 MG198 Mycoplasma genitalium 2097 -11540211

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919614	19260	41416	360	119

Description

5000697490 rplu:rpl21:mg232 ribosomal protein l21:rpl21:50s ribosomal protein l21 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG232 MG232 Mycoplasma genitalium 2097 -11540212 94964 rplu:rpl21:mg232 (de:50s ribosomal protein l21) (db:swissprot) RL21_MYCGE P47474 MYCOPLASMA GENITALIUM 2097 -11540212 172632 ribosomal protein l21 (cl:escherichia coli ribosomal protein l21) (db:pir2.dat) F64225 F64225 Mycoplasma genitalium 2097 -11540212 246085 (db:genpept-bct1) (de:mycoplasma genitalium random genomic clone sc12a ribosomal proteinl21 homolog gene, complete cds.) (nt:homology to ribosomal protein l21 x59528) (le:138) (re:440) (di:direct) MGU02141 U02141 g406334 Mycoplasma genitalium 2097 -11540212 7500890061 mg232 ribosomal protein l21 rpl21 (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78026 pid:1674205 percent) (le:77) (re:379) (di:direct) U39703 U39703 g3844836 Mycoplasma genitalium 2097 -11540212 7502853921 (db:genpept) (de:mycoplasma genitalium random genomic clone sc12a ribosomal proteinl21 homolog gene, complete cds.) (nt:homology to ribosomal protein l21 x59528) (le:138) (re:440) (di:direct) MGU02141 U02141 g406334 Mycoplasma genitalium 2097 -11540212 6500736354 rplu:rpl21 ribosomal protein l21:rpl21:50s ribosomal protein l21 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG232 MG232 Mycoplasma genitalium 2097 -11540212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919622	19261	41417	303	100

Description

5000697491 ribosomal protein l21 homolog:hypothetical protein mg233 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG233 MG233 Mycoplasma genitalium 2097 -11540213 109003 mg233 (de:hypothetical protein mg233) (db:swissprot) Y233_MYCGE P47475 MYCOPLASMA GENITALIUM 2097 -11540213 172633 ribosomal protein l21 homolog (cl:hypothetical protein ysxb) (db:pir2.dat) G64225 G64225 Mycoplasma genitalium 2097 -11540213 246086 (db:genpept-bct1) (de:mycoplasma genitalium random genomic clone sc12a ribosomal proteinl21 homolog gene, complete cds.) (nt:homology to orfx x59528) (le:433) (re:732) (di:direct) MGU02141 U02141 g406335 Mycoplasma genitalium 2097 -11540213 7500894933 mg233 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75459 pid:1674204 percent) (le:372) (re:671) (di:direct) U39703 U39703 g3844837 Mycoplasma genitalium 2097 -11540213 7502853922 (db:genpept) (de:mycoplasma genitalium random genomic clone sc12a ribosomal proteinl21 homolog gene, complete cds.) (nt:homology to orfx x59528) (le:433) (re:732) (di:direct) MGU02141 U02141 g406335 Mycoplasma genitalium 2097 -11540213 6500736355 ribosomal protein l21 homolog:hypothetical protein mg233 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG233 MG233 Mycoplasma genitalium 2097 -11540213

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919623	19262	41418	786	261

Description

GTC ORF with score 581 to: (sr:yeast (s.cerevisiae) dna, clones pn21 and p-92) (db:genpept-pln1) (de:yeast (s.cerevisiae) gal7 gene encodingalpha-d-galactose-1-phosphate uridyltraneferase, complete cds.) (nt:galactose-1-phosphate uridyltransferase (ec)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919636	19263	41419	819	272

Description

5000697492 rpma:rpl27:mg234 ribosomal protein l27:bl30:50s ribosomal protein l27 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG234 MG234 Mycoplasma genitalium 2097 -11540214 95056 rpma:rpl27:mg234 (de:50s ribosomal protein l27) (db:swissprot) RL27_MYCGE P47476 MYCOPLASMA GENITALIUM 2097 -11540214 149002 ribosomal protein l27 (cl:escherichia coli ribosomal protein l27:eubacterial ribosomal protein l27 homology) (db:pir2.dat) H64225 H64225 Mycoplasma genitalium 2097 -11540214 7500890131 mg234 ribosomal protein l27 rpl27 (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75458 pid:1674203 percent) (le:664) (re:978) (di:direct) U39703 U39703 g3844838 Mycoplasma genitalium 2097 -11540214 6500736356 rpma:rpl27 ribosomal protein l27:bl30:50s ribosomal protein l27 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG234 MG234 Mycoplasma genitalium 2097 -11540214

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919639	19264	41420	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919641	19265	41421	402	133

Description

5000697493 rrna methylase:hypothetical rrna methylase mg252 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG252 MG252 Mycoplasma genitalium 2097 -11540215 109026 mg252 (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase mg252,) (db:swissprot) Y252_MYCGE P47494 MYCOPLASMA GENITALIUM 2097 -11540215 172659 rrna methylase (cl:conserved hypothetical protein hi0860) (db:pir2.dat) H64227 H64227 Mycoplasma genitalium 2097 -11540215 7500894975 mg252 rrna methylase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75424 pid:1674172 percent) (le:3201) (re:3929) (di:complement) U39704 U39704 g3844850 Mycoplasma genitalium 2097 -11540215 6500736357 rrna methylase:hypothetical rrna methylase mg252 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG252 MG252 Mycoplasma genitalium 2097 -11540215

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919658	19266	41422	543	181

Description

5000697494 rpme:rpl31:mg257 ribosomal protein l31:rpl31:50s ribosomal protein l31 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG257 MG257 Mycoplasma genitalium 2097 -11540216 95152 rpme:rpl31:mg257 (de:50s ribosomal protein l31) (db:swissprot) RL31_MYCGE P47499 MYCOPLASMA GENITALIUM 2097 -11540216 172640 ribosomal protein l31 (db:pir2.dat) D64228 D64228 Mycoplasma genitalium 2097 -11540216 7500890196 mg257 ribosomal protein l31 rpl31 (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78020 pid:1674167 percent) (le:10014) (re:10307) (di:direct) U39704 U39704 g1045949 Mycoplasma genitalium 2097 -11540216 6500736358 rpme:rpl31 ribosomal protein l31:rpl31:50s ribosomal protein l31 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG257 MG257 Mycoplasma genitalium 2097 -11540216

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919669	19267	41423	417	138

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919685	19268	41424	741	246

Description

5000697495 rpsd:rps4:mg311 ribosomal protein s4:30s ribosomal protein s4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG311 MG311 Mycoplasma genitalium 2097 -11540217 97325 rpsd:rps4:mg311 (de:30s ribosomal protein s4) (db:swissprot) RS4_MYCGE P47553 MYCOPLASMA GENITALIUM 2097 -11540217 172653 ribosomal protein s4 (cl:escherichia coli ribosomal protein s4) (db:pir2.dat) D64234 D64234 Mycoplasma genitalium 2097 -11540217 7500891053 mg311 ribosomal protein s4 (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to sp:p46775 pid:639791 gb:u00089) (le:851) (re:1468) (di:complement) U39712 U39712 g1046011 Mycoplasma genitalium 2097 -11540217 6500736359 rpsd:rps4 ribosomal protein s4:30s ribosomal protein s4 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG311 MG311 Mycoplasma genitalium 2097 -11540217

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919686	19269	41425	189	62

Description

5000697496 rpmg:rpl33:mg325 ribosomal protein l33:rpl33:50s ribosomal protein l33 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG325 MG325 Mycoplasma genitalium 2097 -11540218 95186 rpmg:rpl33:mg325 (de:50s ribosomal protein l33) (db:swissprot) RL33_MYCGE P47567 MYCOPLASMA GENITALIUM 2097 -11540218 149044 ribosomal protein l33 (cl:escherichia coli ribosomal protein l33) (db:pir2.dat) I64235 I64235 Mycoplasma genitalium 2097 -11540218 7500890215 mg325 ribosomal protein l33 rpl33 (db:genpept-bct2) (de:mycoplasma genitalium section 35 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78015 pid:1674049 percent) (le:9938) (re:10099) (di:complement) U39713 U39713 g3844902 Mycoplasma genitalium 2097 -11540218 6500736360 rpmg:rpl33 ribosomal protein l33:rpl33:50s ribosomal protein l33 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG325 MG325 Mycoplasma genitalium 2097 -11540218

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919689	19270	41426	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919690	19271	41427	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919692	19272	41428	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919696	19273	41429	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919703	19274	41430	1917	638

Description

5000697497 rplj:rpl10:mg361 ribosomal protein l10:bl5:50s ribosomal protein l10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG361 MG361 Mycoplasma genitalium 2097 -11540219 94714 rplj:rpl10:mg361 (de:50s ribosomal protein l10) (db:swissprot) RL10_MYCGE P36263 MYCOPLASMA GENITALIUM 2097 -11540219 172626 ribosomal protein l10 (cl:escherichia coli ribosomal protein l10) (db:pir2.dat) I64239 I64239 Mycoplasma genitalium 2097 -11540219 7500889908 mg361 ribosomal protein l10 rpl10 (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75240 pid:1673976 percent) (le:91) (re:579) (di:direct) U39718 U39718 g3844947 Mycoplasma genitalium 2097 -11540219 6500736361 rplj:rpl10 ribosomal protein l10:bl5:50s ribosomal protein l10 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG361 MG361 Mycoplasma genitalium 2097 -11540219

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919705	19275	41431	687	228

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919722	19276	41432	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919724	19277	41433	366	121

Description

5000697498 rpll:rpl7:mg362 ribosomal protein l7/l12:bl13:a type:50s ribosomal protein l7/l12 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG362 MG362 Mycoplasma genitalium 2097 -11540220 95468 rpll:rpl7:mg362 (de:50s ribosomal protein l7/l12) (db:swissprot) RL7_MYCGE P36255 MYCOPLASMA GENITALIUM 2097 -11540220 172644 ribosomal protein l7/l12 a type (cl:escherichia coli ribosomal protein l12) (db:pir2.dat) A64240 A64240 Mycoplasma genitalium 2097 -11540220 7500890357 mg362 ribosomal protein l7/l12 rpl7 (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75239 pid:1673975 percent) (le:602) (re:970) (di:direct) U39718 U39718 g3844948 Mycoplasma genitalium 2097 -11540220 6500736362 rpll:rpl7 ribosomal protein l7/l12:bl13:a type:50s ribosomal protein l7/l12 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG362 MG362 Mycoplasma genitalium 2097 -11540220

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919726	19278	41434	1545	514

Description

GTC ORF with score 276 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v lambda clones 6592, 4678,4742, and 3612.) (nt:similar to hypothetical protein from s. cerevisiae,) (le:11964) (re:13226) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919739	19279	41435	357	118

Description

5000697499 rpmf:rpl32:mg363 ribosomal protein l32:rpl32:50s ribosomal protein l32 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG363 MG363 Mycoplasma genitalium 2097 -11540221 172641 ribosomal protein l32 (cl:escherichia coli ribosomal protein l32) (db:pir1.dat) B64240 B64240 Mycoplasma genitalium 2097 -11540221 7500965565 mg363 ribosomal protein l32 rpl32 (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75238 pid:1673974 percent) (le:973) (re:1146) (di:direct) U39718 U39718 g3844949 Mycoplasma genitalium 2097 -11540221 6500736363 rpmf:rpl32 ribosomal protein l32:rpl32:50s ribosomal protein l32 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG363 MG363 Mycoplasma genitalium 2097 -11540221

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919777	19280	41436	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919781	19281	41437	642	213

Description

5000697500 rpsi:rps9:mg417 ribosomal protein s9:rps9:30s ribosomal protein s9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG417 MG417 Mycoplasma genitalium 2097 -11540222 97443 rpsi:rps9:mg417 (de:30s ribosomal protein s9) (db:swissprot) RS9_MYCGE P47656 MYCOPLASMA GENITALIUM 2097 -11540222 148446 ribosomal protein s9 (cl:escherichia coli ribosomal protein s9) (db:pir2.dat) A64246 A64246 Mycoplasma genitalium 2097 -11540222 7500891126 mg417 ribosomal protein s9 rps9 (db:genpept-bct2) (de:mycoplasma genitalium section 46 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75179 pid:1673892 percent) (le:647) (re:1045) (di:complement) U39724 U39724 g3845009 Mycoplasma genitalium 2097 -11540222 6500736364 rpsi:rps9 ribosomal protein s9:rps9:30s ribosomal protein s9 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG417 MG417 Mycoplasma genitalium 2097 -11540222

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919785	19282	41438	1206	401

Description

5000697501 rplm:rpl13:mg418 ribosomal protein l13:rpl13:50s ribosomal protein l13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG418 MG418 Mycoplasma genitalium 2097 -11540223 94781 rplm:rpl13:mg418 (de:50s ribosomal protein l13) (db:swissprot) RL13_MYCGE P47657 MYCOPLASMA GENITALIUM 2097 -11540223 172627 ribosomal protein l13 (db:pir2.dat) B64246 B64246 Mycoplasma genitalium 2097 -11540223 7500889934 mg418 ribosomal protein l13 rpl13 (db:genpept-bct2) (de:mycoplasma genitalium section 46 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75178 pid:1673891 percent) (le:1051) (re:1491) (di:complement) U39724 U39724 g3845010 Mycoplasma genitalium 2097 -11540223 6500736365 rplm:rpl13 ribosomal protein l13:rpl13:50s ribosomal protein l13 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG418 MG418 Mycoplasma genitalium 2097 -11540223

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919789	19283	41439	441	146

Description

5000697502 rpso:rps15:mg424 ribosomal protein s15:bs18:30s ribosomal protein s15 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG424 MG424 Mycoplasma genitalium 2097 -11540224 97044 rpso:rps15:mg424 (de:30s ribosomal protein s15) (db:swissprot) RS15_MYCGE P47663 MYCOPLASMA GENITALIUM 2097 -11540224 172648 ribosomal protein s15 (cl:escherichia coli ribosomal protein s15:eubacterial ribosomal protein s15 homology) (db:pir2.dat) H64246 H64246 Mycoplasma genitalium 2097 -11540224 7500890910 mg424 ribosomal protein s15 rps15 (db:genpept-bct2) (de:mycoplasma genitalium section 46 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75173 pid:1673886 percent) (le:10396) (re:10656) (di:complement) U39724 U39724 g3845014 Mycoplasma genitalium 2097 -11540224 6500736366 rpso:rps15 ribosomal protein s15:bs18:30s ribosomal protein s15 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG424 MG424 Mycoplasma genitalium 2097 -11540224

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919791	19284	41440	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919804	19285	41441	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919811	19286	41442	516	171

Description

5000697503 rpmb:rpl28:mg426 ribosomal protein l28:rpl28:50s ribosomal protein l28 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG426 MG426 Mycoplasma genitalium 2097 -11540225 95068 rpmb:rpl28:mg426 (de:50s ribosomal protein l28) (db:swissprot) RL28_MYCGE P47665 MYCOPLASMA GENITALIUM 2097 -11540225 172637 ribosomal protein l28 (cl:escherichia coli ribosomal protein l28) (db:pir2.dat) A64247 A64247 Mycoplasma genitalium 2097 -11540225 7500890140 mg426 ribosomal protein l28 rpl28 (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75171 pid:1673884 percent) (le:1497) (re:1691) (di:direct) U39725 U39725 g3845019 Mycoplasma genitalium 2097 -11540225 6500736367 rpmb:rpl28 ribosomal protein l28:rpl28:50s ribosomal protein l28 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG426 MG426 Mycoplasma genitalium 2097 -11540225

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919812	19287	41443	579	192

Description

5000697504 rpls:rpl19:mg444 ribosomal protein l19:rpl19:50s ribosomal protein l19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG444 MG444 Mycoplasma genitalium 2097 -11540226 94901 rpls:rpl19:mg444 (de:50s ribosomal protein l19) (db:swissprot) RL19_MYCGE P47682 MYCOPLASMA GENITALIUM 2097 -11540226 172631 ribosomal protein l19 (cl:escherichia coli ribosomal protein l19) (db:pir2.dat) A64249 A64249 Mycoplasma genitalium 2097 -11540226 7500890027 mg444 ribosomal protein l19 rpl19 (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75133 pid:1673847 percent) (le:4538) (re:4897) (di:complement) U39726 U39726 g3845037 Mycoplasma genitalium 2097 -11540226 6500736368 rpls:rpl19 ribosomal protein l19:rpl19:50s ribosomal protein l19 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG444 MG444 Mycoplasma genitalium 2097 -11540226

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919820	19288	41444	255	84

Description

6500736369 rpsp:rps16:mg446 ribosomal protein s16:bs17:30s ribosomal protein s16 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG446 MG446 Mycoplasma genitalium 2097 -11540227 97062 rpsp:rps16:mg446 (de:30s ribosomal protein s16) (db:swissprot) RS16_MYCGE P47684 MYCOPLASMA GENITALIUM 2097 -11540227 172649 ribosomal protein s16 (cl:escherichia coli ribosomal protein s16) (db:pir2.dat) C64249 C64249 Mycoplasma genitalium 2097 -11540227 7500890924 mg446 ribosomal protein s16 rps16 (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75131 pid:1673845 percent) (le:5576) (re:5845) (di:complement) U39726 U39726 g3845039 Mycoplasma genitalium 2097 -11540227 5000697505 (de:(mg446) (pn:30s ribosomal protein s16:ribosomal protein s16:bs17) (gn:rprps16) (gtcfc:10.4:10.5) (ec:) (rs16_mycge) (keggfc:11.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium)) MG446 MG446 Mycoplasma genitalium 2097 10038983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919821	19289	41445	279	92

Description

5000697506 rpmh:rpl34:mg466 ribosomal protein l34:rpl34:50s ribosomal protein l34 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG466 MG466 Mycoplasma genitalium 2097 -11540228 95202 rpmh:rpl34:mg466 (de:50s ribosomal protein l34) (db:swissprot) RL34_MYCGE P47704 MYCOPLASMA GENITALIUM 2097 -11540228 149054 ribosomal protein l34 (cl:escherichia coli ribosomal protein l34) (db:pir2.dat) E64251 E64251 Mycoplasma genitalium 2097 -11540228 7500890228 mg466 ribosomal protein l34 rpl34 (db:genpept-bct2) (de:mycoplasma genitalium section 50 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78006 pid:1673821 percent) (le:6007) (re:6153) (di:complement) U39728 U39728 g3845061 Mycoplasma genitalium 2097 -11540228 6500736370 rpmh:rpl34 ribosomal protein l34:rpl34:50s ribosomal protein l34 (gtcfc:10.4) (keggfc:14.2) (tigrfc:12.5) (db:gtc-mycoplasma genitalium) MG466 MG466 Mycoplasma genitalium 2097 -11540228

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919822	19290	41446	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919826	19291	41447	195	64

Description

5000697518 pth:mg083 peptidyl-trna hydrolase homolog:peptidyl-trna hydrolase:pth (gtcfc:10.6) (ec:3.1.1.29) (keggfc:14.1) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG083 MG083 Mycoplasma genitalium 2097 -11540229 92200 pth:mg083 (ec:3.1.1.29) (de:peptidyl-trna hydrolase, (pth)) (db:swissprot) PTH_MYCGE P47329 MYCOPLASMA GENITALIUM 2097 -11540229 172579 peptidyl-trna hydrolase homolog (cl:peptidyl-trna hydrolase) (db:pir2.dat) B64209 B64209 Mycoplasma genitalium 2097 -11540229 7500888968 mg083 peptidyl-trna hydrolase pth (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78034 pid:1674312 percent) (le:1132) (re:1701) (di:direct) U39689 U39689 g3844670 Mycoplasma genitalium 2097 -11540229 6500736371 pth peptidyl-trna hydrolase homolog:peptidyl-trna hydrolase:pth (gtcfc:10.6) (ec:3.1.1.29) (keggfc:14.1) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG083 MG083 Mycoplasma genitalium 2097 -11540229

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919838	19292	41448	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919840	19293	41449	213	70

Description

6500736372 trmd:mg445 trna:guanine-n1-methyltransferase:m1g-methyltransferase (gtcfc:10.6) (ec:2.1.1.31) (keggfc:14.1) (tigrfc:12.2) (db:gtc-mycoplasma genitalium) MG445 MG445 Mycoplasma genitalium 2097 -11540230 102278 trmd:mg445 (ec:2.1.1.31) (de:methyltransferase) (trna (gm37) methyltransferase)) (db:swissprot) TRMD_MYCGE P47683 MYCOPLASMA GENITALIUM 2097 -11540230 172698 trna guanine-n1--methyltransferase (cl:trna (guanine-n1) methyltransferase) (ec:2.1.1.31) (db:pir2.dat) B64249 B64249 Mycoplasma genitalium 2097 -11540230 7500893407 mg445 trna guanine-n1 -methyltransferase trmd (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75132 pid:1673846 percent) (le:4881) (re:5576) (di:complement) U39726 U39726 g3845038 Mycoplasma genitalium 2097 -11540230 5000697519 (de:(mg445) (pn:m1g-methyltransferase:trna:guanine-n1-methyltransferase:trmd) (gn:trmd) (gtcfc:10.6) (ec:2.1.1.31) (trmd_mycge) (keggfc:11.1) (tigrfc:12.2) (db:gtc-mycoplasma genitalium)) MG445 MG445 Mycoplasma genitalium 2097 10044097

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919847	19294	41450	549	182

Description

6500736373 efp:mg026 elongation factor p:ef-p (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG026 MG026 Mycoplasma genitalium 2097 -11540231 69868 efp:mg026 (de:elongation factor p (ef-p)) (db:swissprot) EFP_MYCGE P47272 MYCOPLASMA GENITALIUM 2097 -11540231 172687 translation elongation factor ef-p homolog (cl:translation elongation factor ef-p) (db:pir2.dat) H64202 H64202 Mycoplasma genitalium 2097 -11540231 7500880941 mg026 elongation factor p efp (db:genpept-bct2) (de:mycoplasma genitalium section 4 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75085 pid:1673784 percent) (le:1032) (re:1604) (di:direct) U39682 U39682 g3844636 Mycoplasma genitalium 2097 -11540231 5000697507 (de:(mg026) (pn:ef-p:elongation factor p:efp) (gn:efp) (gtcfc:10.5) (ec:) (efp_mycge) (keggfc:11.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium)) MG026 MG026 Mycoplasma genitalium 2097 10012446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919859	19295	41451	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919868	19296	41452	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919893	19297	41453	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919901	19298	41454	957	318

Description

5000697508 fusa:fus:mg089 fus:elongation factor g:ef-g (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG089 MG089 Mycoplasma genitalium 2097 -11540232 69849 fusa:fus:mg089 (de:elongation factor g (ef-g)) (db:swissprot) EFG_MYCGE P47335 MYCOPLASMA GENITALIUM 2097 -11540232 154240 translation elongation factor ef-g (cl:translation elongation factor g:translation elongation factor tu homology) (db:pir2.dat) H64209 H64209 Mycoplasma genitalium 2097 -11540232 7500880937 mg089 elongation factor g fus (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75544 pid:1674306 percent) (le:5585) (re:7651) (di:direct) U39689 U39689 g3844676 Mycoplasma genitalium 2097 -11540232 6500736374 fusa:fus fus:elongation factor g:ef-g (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG089 MG089 Mycoplasma genitalium 2097 -11540232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919903	19299	41455	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919909	19300	41456	825	274

Description

GTC ORF with score 278 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c338.) (nt:spcc338.15, dolichyl-diphosphooligosaccharide) (le:28405:28581:28779:29565) (re:28534:28691:29434:29981) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919921	19301	41457	465	154

Description

5000697509 protein phosphatase 2c homolog:ptc1:hypothetical protein mg108 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG108 MG108 Mycoplasma genitalium 2097 -11540233 108737 mg108 (ec:3.1.3.16) (de:putative protein phosphatase,) (db:swissprot) PPH_MYCGE P47354 MYCOPLASMA GENITALIUM 2097 -11540233 172609 protein phosphatase 2c homolog (cl:conserved hypothetical protein yloo:conserved hypothetical protein yloo homology) (db:pir2.dat) I64211 I64211 Mycoplasma genitalium 2097 -11540233 7500888360 mg108 protein phosphatase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75525 pid:1674286 percent) (le:4113) (re:4895) (di:direct) U39691 U39691 g3844697 Mycoplasma genitalium 2097 -11540233 6500736375 protein phosphatase 2c homolog:ptc1:hypothetical protein mg108 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG108 MG108 Mycoplasma genitalium 2097 -11540233

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919922	19302	41458	516	171

Description

6500736376 infb:mg142 protein synthesis initiation factor 2:initiation factor if-2 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG142 MG142 Mycoplasma genitalium 2097 -11540234 78884 infb:mg142 (de:translation initiation factor if-2) (db:swissprot) IF2_MYCGE P47388 MYCOPLASMA GENITALIUM 2097 -11540234 172690 translation initiation factor if-2:infb:protein synthesis initiation factor 2 (cl:translation elongation factor tu homology) (db:pir2.dat) G64215 G64215 Mycoplasma genitalium 2097 -11540234 7500883891 mg142 translation initiation factor 2 infb (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75590 pid:1674382 percent) (le:5737) (re:7596) (di:direct) U39695 U39695 g3844735 Mycoplasma genitalium 2097 -11540234 5000697510 (de:(mg142) (pn:initiation factor if-2:protein synthesis initiation factor 2:infb) (gn:infb) (gtcfc:10.5) (ec:) (if2_mycge) (keggfc:11.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium)) MG142 MG142 Mycoplasma genitalium 2097 10021219

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919932	19303	41459	189	62

Description

5000697511 map:mg172 methionine amino peptidase:methionine aminopeptidase:map:peptidase m (gtcfc:10.7) (ec:3.4.11.18) (keggfc:14.1) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG172 MG172 Mycoplasma genitalium 2097 -11540235 59387 map:mg172 (ec:3.4.11.18) (de:methionine aminopeptidase, (map) (peptidase m)) (db:swissprot) AMPM_MYCGE P47418 MYCOPLASMA GENITALIUM 2097 -11540235 172560 methionyl aminopeptidase (ec:3.4.11.18) (db:pir2.dat) A64219 A64219 Mycoplasma genitalium 2097 -11540235 7500876853 mg172 methionine aminopeptidase map (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215702 sp:q11132 gb:u00089) (le:13140) (re:13886) (di:direct) U39696 U39696 g3844766 Mycoplasma genitalium 2097 -11540235 6500736377 map methionine amino peptidase:methionine aminopeptidase:map:peptidase m (gtcfc:10.7) (ec:3.4.11.18) (keggfc:14.1) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG172 MG172 Mycoplasma genitalium 2097 -11540235

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919944	19304	41460	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919959	19305	41461	369	122

Description

GTC ORF with score 222 to: (sr:neurospora crassa) (db:genpept-pln1) (de:nadh:ubiquinone reductase (complex i) 9.5 kda ubiquinone-bindingprotein (neurospora crassa, mrna, 812 nt).) (nt:method: conceptual translation with partial peptide) (le:143) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919986	19306	41462	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919989	19307	41463	471	156

Description

GTC ORF with score 142 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f56a11.) (nt:coded for by c. elegans cdna yk171d3.5) (le:32282:33079:33163) (re:33024:33112:33414) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501919991	19308	41464	1995	664

Description

6500736378 infa:mg173 initiation factor 1:initiation factor if-1 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG173 MG173 Mycoplasma genitalium 2097 -11540236 78856 infa:mg173 (de:translation initiation factor if-1) (db:swissprot) IF1_MYCGE P47419 MYCOPLASMA GENITALIUM 2097 -11540236 172689 translation initiation factor if-1 (cl:translation initiation factor if-1) (db:pir2.dat) B64219 B64219 Mycoplasma genitalium 2097 -11540236 7500883853 mg173 translation initiation factor 1 infa (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215701 gb:u00089 sp:q50298) (le:13886) (re:14098) (di:direct) U39696 U39696 g3844767 Mycoplasma genitalium 2097 -11540236 5000697512 (de:(mg173) (pn:initiation factor if-1:initiation factor 1:infa) (gn:infa) (gtcfc:10.5) (ec:) (if1_mycge) (keggfc:11.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium)) MG173 MG173 Mycoplasma genitalium 2097 10021192

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920017	19309	41465	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920118	19310	41466	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920119	19311	41467	1266	421

Description

6500736379 infc:mg196 initiation factor if-3 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG196 MG196 Mycoplasma genitalium 2097 -11540237 172691 translation initiation factor if-3 (cl:translation initiation factor if-3) (db:pir2.dat) F64221 F64221 Mycoplasma genitalium 2097 -11540237 7500965570 infc translation initiation factor if3 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium dnaj_3, grpe, infc, parc, pare, phes, phet,rpl20, rpl35, trna-thr_1 genes from bases 230511 to 245885 (section19 of 56) of the complete genome.) (nt:ide... U39697 U39697 g1045881 Mycoplasma genitalium 2097 -11540237 5000697513 (de:(mg196) (pn:initiation factor if-3) (gn:infc) (gtcfc:10.5) (ec:) (if3_mycge) (keggfc:11.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium)) MG196 MG196 Mycoplasma genitalium 2097 10021232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920122	19312	41468	1575	524

Description

6500736380 prfa:mg258 polypeptide chain release factor 1:peptide chain release factor 1:rf-1 (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG258 MG258 Mycoplasma genitalium 2097 -11540238 94089 prfa:mg258 (de:peptide chain release factor 1 (rf-1)) (db:swissprot) RF1_MYCGE P47500 MYCOPLASMA GENITALIUM 2097 -11540238 172578 prfa:rf-1 translation releasing factor rf-1:peptide chain release factor 1 (cl:translation releasing factor) (db:pir1.dat) E64228 E64228 Mycoplasma genitalium 2097 -11540238 7500889657 mg258 peptide chain release factor 1 prfa (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75420 pid:1674166 percent) (le:10307) (re:11386) (di:direct) U39704 U39704 g1045950 Mycoplasma genitalium 2097 -11540238 5000697514 (de:(mg258) (pn:peptide chain release factor 1:rf-1:polypeptide chain release factor 1:prfa) (gn:prfa) (gtcfc:10.5) (ec:) (rf1_mycge) (keggfc:11.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium)) MG258 MG258 Mycoplasma genitalium 2097 10036072

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920125	19313	41469	525	174

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920133	19314	41470	1275	424

Description

6500736381 tsf:mg433 elongation factor ts:ef-ts (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG433 MG433 Mycoplasma genitalium 2097 -11540239 69881 tsf:mg433 (de:elongation factor ts (ef-ts)) (db:swissprot) EFTS_MYCGE P47246 MYCOPLASMA GENITALIUM 2097 -11540239 172688 translation elongation factor ef-ts (db:pir2.dat) H64247 H64247 Mycoplasma genitalium 2097 -11540239 7500880946 mg433 elongation factor ts tsf (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78009 pid:1673876 percent) (le:8089) (re:8985) (di:direct) U39725 U39725 g3845026 Mycoplasma genitalium 2097 -11540239 5000697515 (de:(mg433) (pn:ef-ts:elongation factor ts:tsf) (gn:tsf) (gtcfc:10.5) (ec:) (efts_mycge) (keggfc:11.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium)) MG433 MG433 Mycoplasma genitalium 2097 10012459

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920134	19315	41471	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920136	19316	41472	291	96

Description

6500736382 frr:mg435 ribosome recycling factor:ribosome releasing factor:rrf (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG435 MG435 Mycoplasma genitalium 2097 -11540240 96610 frr:mg435 (de:ribosome recycling factor (ribosome releasing factor) (rrf)) (db:swissprot) RRF_MYCGE P47673 MYCOPLASMA GENITALIUM 2097 -11540240 172657 ribosome releasing factor (cl:ribosome releasing factor) (db:pir2.dat) A64248 A64248 Mycoplasma genitalium 2097 -11540240 7500890815 mg435 ribosome releasing factor frr (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75161 pid:1673870 percent) (le:9697) (re:10248) (di:direct) U39725 U39725 g3845028 Mycoplasma genitalium 2097 -11540240 5000697516 (de:(mg435) (pn:ribosome recycling factor:rrf:ribosome releasing factor:frr) (gn:frr) (gtcfc:10.5) (ec:) (rrf_mycge) (keggfc:11.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium)) MG435 MG435 Mycoplasma genitalium 2097 10038542

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920137	19317	41473	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920140	19318	41474	4260	1420

Description

6500736383 tuf:mg451 elongation factor tu:ef-tu (gtcfc:10.7) (keggfc:14.2) (tigrfc:12.4) (db:gtc-mycoplasma genitalium) MG451 MG451 Mycoplasma genitalium 2097 -11540241 245924 tuf:mg451 (de:elongation factor tu (ef-tu)) (db:swissprot) EFTU_MYCGE P13927 MYCOPLASMA GENITALIUM 2097 -11540241 131216 tuf translation elongation factor ef-tu (cl:translation elongation factor tu:translation elongation factor tu homology) (db:pir1.dat) EFYMTG S14909 Mycoplasma genitalium 2097 -11540241 7500880959 (db:genpept-bct1) (de:mycoplasma gentalium tuf gene for elongation factor tu.) (nt:elongation factor tu (aa 1-394)) (le:92) (re:1276) (di:direct) MGENTUF X16463 g44306 Mycoplasma capricolum 2095 -11540241 5000697517 mg451 elongation factor tu tuf (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:u00089 pid:1673840 percent identity:) (le:110) (re:1294) (di:complement) U39727 U39727 g3845045 Mycoplasma genitalium 2097 -11540241 69933 tuf:mg451 (de:elongation factor tu (ef-tu)) (db:swissprot) EFTU_MYCGE P13927 MYCOPLASMA GENITALIUM 2097 -11540241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920159	19319	41475	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920161	19320	41476	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920191	19321	41477	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920192	19322	41478	240	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920194	19323	41479	291	96

Description

6500736384 gyrb:mg003 dna gyrase subunit b (gtcfc:10.8) (ec:5.99.1.3) (keggfc:14.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG003 MG003 Mycoplasma genitalium 2097 -11540242 75224 gyrb:mg003 (ec:5.99.1.3) (de:dna gyrase subunit b,) (db:swissprot) GYRB_MYCGE P47249 MYCOPLASMA GENITALIUM 2097 -11540242 142223 dna gyrase chain b gyrb (cl:dna topoisomerase (atp-hydrolyzing) chain b) (db:pir2.dat) C64200 C64200 Mycoplasma genitalium 2097 -11540242 246237 gyrb dna gyrase subunit b (db:genpept-bct1) (de:mycoplasma genitalium dna gyrase subunit b (gyrb), dna gyrasesubunit a (gyra) and orf311 genes, complete cds, dna polymeraseiii beta subunit (dnan) and seryl-trna synthetase (sers) genes,partial cds.) (nt:similar to dna gyrase b, ... MGU09251 U09251 g497647 Mycoplasma genitalium 2097 -11540242 7500882884 mg003 dna gyrase subunit b gyrb (db:genpept-bct2) (de:mycoplasma genitalium section 1 of 51 of the complete genome.) (nt:similar to gb:u09251 gb:u02187 gb:u02199 gb:x61522) (le:2846) (re:4798) (di:direct) U39679 U39679 g1045671 Mycoplasma genitalium 2097 -11540242 5000697523 (de:(mg003) (pn:dna gyrase subunit b:gyrb) (gn:gyrb) (gtcfc:10.8) (ec:5.99.1.3) (gyrb_mycge) (keggfc:11.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG003 MG003 Mycoplasma genitalium 2097 10017735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920202	19324	41480	216	72

Description

6500736385 gyra:mg004 dna gyrase subunit a (gtcfc:10.8) (ec:5.99.1.3) (keggfc:14.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG004 MG004 Mycoplasma genitalium 2097 -11540243 75202 gyra:mg004 (ec:5.99.1.3) (de:dna gyrase subunit a,) (db:swissprot) GYRA_MYCGE P47250 MYCOPLASMA GENITALIUM 2097 -11540243 142239 gyra dna topoisomerase atp-hydrolyzing:chain a:dna-gyrase:type ii dna topoisomerase (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (ec:5.99.1.3) (db:pir2.dat) D64200 D64200 Mycoplasma genitalium 2097 -11540243 7500882876 mg004 dna gyrase subunit a gyra (db:genpept-bct2) (de:mycoplasma genitalium section 1 of 51 of the complete genome.) (nt:similar to gb:u09251 gb:u02211 gb:x61522 gb:x61535) (le:4813) (re:7323) (di:direct) U39679 U39679 g1045672 Mycoplasma genitalium 2097 -11540243 5000697524 (de:(mg004) (pn:dna gyrase subunit a:gyra) (gn:gyra) (gtcfc:10.8) (ec:5.99.1.3) (gyra_mycge) (keggfc:11.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG004 MG004 Mycoplasma genitalium 2097 10017713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920212	19325	41481	591	196

Description

5000697525 dna polymerase iii subunit:dnah:hypothetical protein mg007 (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG007 MG007 Mycoplasma genitalium 2097 -11540244 108339 mg007 (de:hypothetical protein mg007) (db:swissprot) Y007_MYCGE P47253 MYCOPLASMA GENITALIUM 2097 -11540244 172335 dna polymerase iii chain dnah homolog mg007 (db:pir2.dat) G64200 G64200 Mycoplasma genitalium 2097 -11540244 7500894511 mg007 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 1 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75105 pid:1673807 percent) (le:9157) (re:9921) (di:direct) U39679 U39679 g1045675 Mycoplasma genitalium 2097 -11540244 6500736386 dna polymerase iii subunit:dnah:hypothetical protein mg007 (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG007 MG007 Mycoplasma genitalium 2097 -11540244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920223	19326	41482	543	180

Description

5000697526 dna primase:dnae:hypothetical protein mg010 (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG010 MG010 Mycoplasma genitalium 2097 -11540245 108365 mg010 (de:hypothetical protein mg010) (db:swissprot) Y010_MYCGE P47256 MYCOPLASMA GENITALIUM 2097 -11540245 172336 dna primase dnae homolog mg010 (db:pir2.dat) A64201 A64201 Mycoplasma genitalium 2097 -11540245 7500894519 mg010 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 2 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75099 pid:1673800 percent) (le:20) (re:676) (di:direct) U39680 U39680 g3844622 Mycoplasma genitalium 2097 -11540245 6500736387 dna primase:dnae:hypothetical protein mg010 (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG010 MG010 Mycoplasma genitalium 2097 -11540245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920228	19327	41483	381	126

Description

6500736388 uvrb:mg073 excinuclease abc subunit b (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG073 MG073 Mycoplasma genitalium 2097 -11540246 104046 uvrb:mg073 (de:excinuclease abc subunit b) (db:swissprot) UVRB_MYCGE P47319 MYCOPLASMA GENITALIUM 2097 -11540246 172347 excinuclease abc chain b (cl:excinuclease abc chain b:dead/h box helicase homology) (db:pir2.dat) A64208 A64208 Mycoplasma genitalium 2097 -11540246 7500893902 mg073 excinuclease abc subunit b uvrb (db:genpept-bct2) (de:mycoplasma genitalium section 9 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75558 pid:1674323 percent) (le:10827) (re:12797) (di:direct) U39687 U39687 g1045749 Mycoplasma genitalium 2097 -11540246 5000697527 (de:(mg073) (pn:excinuclease abc subunit b:uvrb) (gn:uvrb) (gtcfc:10.8) (ec:) (uvrb_mycge) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG073 MG073 Mycoplasma genitalium 2097 10045816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920229	19328	41484	462	153

Description

6500736389 ssb:mg091 single-stranded dna binding protein:putative single-stranded dna binding protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG091 MG091 Mycoplasma genitalium 2097 -11540247 99531 ssb:mg091 (de:putative single-stranded dna binding protein) (db:swissprot) SSB_MYCGE P47337 MYCOPLASMA GENITALIUM 2097 -11540247 172665 single-stranded dna binding protein ssb homolog (db:pir2.dat) A64210 A64210 Mycoplasma genitalium 2097 -11540247 7500892120 mg091 single-stranded dna-binding protein ssb (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:z32660 pid:474074 gb:u00089 sp:p75542) (le:8330) (re:8812) (di:direct) U39689 U39689 g3844678 Mycoplasma genitalium 2097 -11540247 5000697528 (de:(mg091) (pn:putative single-stranded dna binding protein:single-stranded dna binding protein:ssb) (gn:ssb) (gtcfc:10.8) (ec:) (ssb_mycge) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG091 MG091 Mycoplasma genitalium 2097 10041389

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920232	19329	41485	246	81

Description

GTC ORF with score 130 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c17d11.) (nt:spbc17d11.06, len:459aa, similar eg. to ykl045w,) (le:13651:13875:14270:14905) (re:13816:14070:14861:15330) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920234	19330	41486	612	203

Description

6500736390 ung:mg097 uracil dna glycosylase:uracil-dna glycosylase (gtcfc:10.8) (ec:3.2.2.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG097 MG097 Mycoplasma genitalium 2097 -11540248 103729 ung:mg097 (ec:3.2.2.-) (de:uracil-dna glycosylase, (udg)) (db:swissprot) UNG_MYCGE P47343 MYCOPLASMA GENITALIUM 2097 -11540248 172705 uracil dna glycosylase (db:pir2.dat) G64210 G64210 Mycoplasma genitalium 2097 -11540248 7500893815 mg097 uracil dna glycosylase ung (db:genpept-bct2) (de:mycoplasma genitalium section 12 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75536 pid:1674298 percent) (le:2131) (re:2868) (di:direct) U39690 U39690 g3844685 Mycoplasma genitalium 2097 -11540248 5000697529 (de:(mg097) (pn:uracil-dna glycosylase:uracil dna glycosylase:ung) (gn:ung) (gtcfc:10.8) (ec:3.2.2.-) (ung_mycge) (keggfc:11.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG097 MG097 Mycoplasma genitalium 2097 10045499

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920248	19331	41487	1047	348

Description

6500736391 topa:mg122 dna topoisomerase i:omega-protein:relaxing enzyme:untwisting enzyme:swivelase (gtcfc:10.8) (ec:5.99.1.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG122 MG122 Mycoplasma genitalium 2097 -11540249 101789 topa:mg122 (ec:5.99.1.2) (de:(untwisting enzyme) (swivelase)) (db:swissprot) TOP1_MYCGE P47368 MYCOPLASMA GENITALIUM 2097 -11540249 172338 dna topoisomerase::type i dna topoisomerase (ec:5.99.1.2) (db:pir2.dat) E64213 E64213 Mycoplasma genitalium 2097 -11540249 7500893258 mg122 dna topoisomerase i topa (db:genpept-bct2) (de:mycoplasma genitalium section 14 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78032 pid:1674272 percent) (le:7136) (re:9265) (di:direct) U39692 U39692 g3844712 Mycoplasma genitalium 2097 -11540249 5000697530 (de:(mg122) (pn:omega-protein:relaxing enzyme:untwisting enzyme:swivelase:dna topoisomerase i:topa) (gn:topa) (gtcfc:10.8) (ec:5.99.1.2) (top1_mycge) (keggfc:11.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG122 MG122 Mycoplasma genitalium 2097 10043618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920262	19332	41488	564	188

Description

6500736392 ssoim:mg184 adenine specific dna modification methylase:methyltransferase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG184 MG184 Mycoplasma genitalium 2097 -11540250 121049 mg184 (ec:2.1.1.72) (de:hypothetical adenine-specific methylase mg184,) (db:swissprot) Y184_MYCGE Q49400 MYCOPLASMA GENITALIUM 2097 -11540250 172563 methyltransferase ssoim homolog (db:pir2.dat) D64220 D64220 Mycoplasma genitalium 2097 -11540250 7500894835 mg184 adenine-specific dna modification methylase (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215690 gb:u00089 sp:q50290) (le:7754) (re:8707) (di:direct) U39697 U39697 g3844780 Mycoplasma genitalium 2097 -11540250 5000697531 (de:(mg184) (pn:methyltransferase:adenine specific dna modification methylase) (gn:ssoim) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG184 MG184 Mycoplasma genitalium 2097 10064304

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920278	19333	41489	684	227

Description

GTC ORF with score 279 to: (db:genpept-bct2) (de:streptomyces venezuelae methymycin/pikromycin polyketide synthasegene cluster, complete sequence.) (nt:multifunctional polyketide synthase; contains a) (le:2912) (re:16753) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920280	19334	41490	3717	1238

Description

GTC ORF with score 503 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920295	19335	41491	372	123

Description

GTC ORF with score 143 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920298	19336	41492	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920300	19337	41493	1503	500

Description

GTC ORF with score 750 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920323	19338	41494	432	143

Description

GTC ORF with score 182 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f49e8.) (nt:coded for by c. elegans cdna yk2g1.3; coded for by) (le:1296:1429:2136) (re:1382:2089:3064) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920324	19339	41495	351	116

Description

6500736393 pare:mg203 topoisomerase iv subunit b (gtcfc:10.8) (ec:5.99.1.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG203 MG203 Mycoplasma genitalium 2097 -11540251 88651 pare:mg203 (ec:5.99.1.-) (de:topoisomerase iv subunit b,) (db:swissprot) PARE_MYCGE P47445 MYCOPLASMA GENITALIUM 2097 -11540251 172682 pare topoisomerase iv chain b (cl:dna topoisomerase (atp-hydrolyzing) chain b) (db:pir2.dat) D64222 D64222 Mycoplasma genitalium 2097 -11540251 7500887669 mg203 topoisomerase iv subunit b pare (db:genpept-bct2) (de:mycoplasma genitalium section 22 of 51 of the complete genome.) (nt:similar to gb:l43967 sp:p47445 pid:806906) (le:29) (re:1930) (di:direct) U39700 U39700 g3844801 Mycoplasma genitalium 2097 -11540251 5000697532 (de:(mg203) (pn:topoisomerase iv subunit b:pare) (gn:pare) (gtcfc:10.8) (ec:5.99.1.-) (pare_mycge) (keggfc:11.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG203 MG203 Mycoplasma genitalium 2097 10030778

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920325	19340	41496	939	312

Description

6500736394 parc:mg204 topoisomerase iv subunit a (gtcfc:10.8) (ec:5.99.1.-) (keggfc:14.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG204 MG204 Mycoplasma genitalium 2097 -11540252 88642 parc:mg204 (ec:5.99.1.-) (de:topoisomerase iv subunit a,) (db:swissprot) PARC_MYCGE P47446 MYCOPLASMA GENITALIUM 2097 -11540252 172681 parc topoisomerase iv chain a (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (db:pir2.dat) E64222 E64222 Mycoplasma genitalium 2097 -11540252 7500887665 mg204 topoisomerase iv:subunit a parc (db:genpept-bct2) (de:mycoplasma genitalium section 22 of 51 of the complete genome.) (nt:similar to gb:l43967 sp:p47446 pid:806907) (le:1930) (re:4275) (di:direct) U39700 U39700 g3844802 Mycoplasma genitalium 2097 -11540252 5000697533 (de:(mg204) (pn:topoisomerase iv subunit a:parc) (gn:parc) (gtcfc:10.8) (ec:5.99.1.-) (parc_mycge) (keggfc:11.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG204 MG204 Mycoplasma genitalium 2097 10030769

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920328	19341	41497	216	71

Description

6500736395 uvrc:mg206 excinuclease abc subunit c (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG206 MG206 Mycoplasma genitalium 2097 -11540253 172348 excinuclease abc chain c (db:pir2.dat) G64222 G64222 Mycoplasma genitalium 2097 -11540253 7500965550 excinuclease abc subunit c uvrc (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium lsp, pfk, plsc, pyk, trna-asp, trna-cys,trna-f-met, trna-ile_2, trna-met, trna-phe, trna-pro, trna-ser_2genes from bases 245836 to 257984 (section 20 of... U39698 U39698 g1045892 Mycoplasma genitalium 2097 -11540253 5000697534 (de:(mg206) (pn:excinuclease abc subunit c:uvrc) (gn:uvrc) (gtcfc:10.8) (ec:) (uvrc_mycge) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG206 MG206 Mycoplasma genitalium 2097 10045820

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920329	19342	41498	279	92

Description

6500736396 nfo:mg235 apurinic endonuclease:apn1:probable endonuclease iv:endodeoxyribonuclease iv (gtcfc:10.8) (ec:3.1.21.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG235 MG235 Mycoplasma genitalium 2097 -11540254 70160 nfo:mg235 (ec:3.1.21.2) (de:probable endonuclease iv, (endodeoxyribonuclease iv)) (db:swissprot) END4_MYCGE P47477 MYCOPLASMA GENITALIUM 2097 -11540254 172345 endonuclease iv homolog (cl:deoxyribonuclease iv (phage t4-induced)) (db:pir2.dat) I64225 I64225 Mycoplasma genitalium 2097 -11540254 7500881025 mg235 endonuclease iv:putative (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75457 pid:1674202 percent) (le:971) (re:1846) (di:direct) U39703 U39703 g3844839 Mycoplasma genitalium 2097 -11540254 5000697535 (de:(mg235) (pn:probable endonuclease iv:endodeoxyribonuclease iv:apurinic endonuclease:apn1) (gn:nfo) (gtcfc:10.8) (ec:3.1.21.2) (end4_mycge) (keggfc:11.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG235 MG235 Mycoplasma genitalium 2097 10012738

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920335	19343	41499	495	164

Description

6500736397 lig:mg254 dna ligase:dna ase:polydeoxyribonucleotide synthase:nad+ (gtcfc:10.8) (ec:6.5.1.2) (keggfc:14.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG254 MG254 Mycoplasma genitalium 2097 -11540255 69003 liga:lig:mg254 (ec:6.5.1.2) (de:dna ligase, (polydeoxyribonucleotide synthase (nad+))) (db:swissprot) DNLJ_MYCGE P47496 MYCOPLASMA GENITALIUM 2097 -11540255 172329 dna ligase nad+ (cl:polydeoxyribonucleotide synthase (nad+)) (ec:6.5.1.2) (db:pir1.dat) A64228 A64228 Mycoplasma genitalium 2097 -11540255 7500880527 mg254 dna ligase (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to sp:p49421 pid:607820 percent identity:) (le:5223) (re:7202) (di:complement) U39704 U39704 g3844852 Mycoplasma genitalium 2097 -11540255 5000697536 (de:(mg254) (pn:dna ase:polydeoxyribonucleotide synthase:nad:dna ligase) (gn:lig) (gtcfc:10.8) (ec:6.5.1.2) (dnlj_mycge) (keggfc:11.1) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG254 MG254 Mycoplasma genitalium 2097 10011587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920336	19344	41500	267	88

Description

GTC ORF with score 139 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f49e8.) (nt:coded for by c. elegans cdna yk2g1.3; coded for by) (le:1296:1429:2136) (re:1382:2089:3064) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920338	19345	41501	270	89

Description

6500736398 reca:mg339 reca protein:protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG339 MG339 Mycoplasma genitalium 2097 -11540256 93754 reca:mg339 (de:reca protein) (db:swissprot) RECA_MYCGE P47581 MYCOPLASMA GENITALIUM 2097 -11540256 172618 reca protein (cl:reca protein) (db:pir2.dat) E64237 E64237 Mycoplasma genitalium 2097 -11540256 7500889544 mg339 reca protein reca (db:genpept-bct2) (de:mycoplasma genitalium section 37 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78014 pid:1674029 percent) (le:5711) (re:6733) (di:complement) U39715 U39715 g3844921 Mycoplasma genitalium 2097 -11540256 5000697537 (de:(mg339) (pn:protein:reca protein) (gn:reca) (gtcfc:10.8) (ec:) (reca_mycge) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG339 MG339 Mycoplasma genitalium 2097 10035745

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920340	19346	41502	291	96

Description

6500736399 ruva:mg358 holliday junction dna helicase (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG358 MG358 Mycoplasma genitalium 2097 -11540257 172382 holliday junction dna helicase ruva homolog (db:pir2.dat) F64239 F64239 Mycoplasma genitalium 2097 -11540257 7500965554 mg358 holliday junction dna helicase ruva (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75243 pid:1673979 percent) (le:7719) (re:8501) (di:direct) U39717 U39717 g3844942 Mycoplasma genitalium 2097 -11540257 5000697538 (de:(mg358) (pn:holliday junction dna helicase:holliday junction dna helicase:ruva) (gn:ruva) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG358 MG358 Mycoplasma genitalium 2097 10091236

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920346	19347	41503	195	64

Description

6500736400 ruvb:mg359 uv-tolerance/filament formation protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG359 MG359 Mycoplasma genitalium 2097 -11540258 120420 ruvb:mg359 (de:probable holliday junction dna helicase ruvb) (db:swissprot) RUVB_MYCGE Q49425 MYCOPLASMA GENITALIUM 2097 -11540258 172383 holliday junction dna helicase ruvb homolog (cl:ruvb protein) (db:pir2.dat) G64239 G64239 Mycoplasma genitalium 2097 -11540258 7500891239 mg359 holliday junction dna helicase ruvb (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75242 pid:1673978 percent) (le:8476) (re:9399) (di:direct) U39717 U39717 g3844943 Mycoplasma genitalium 2097 -11540258 5000697539 (de:(mg359) (pn:uv-tolerance) (gn:ruvb) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG359 MG359 Mycoplasma genitalium 2097 10063421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920353	19348	41504	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920355	19349	41505	357	118

Description

6500736401 gida:mg379 glucose inhibited division protein:glucose inhibited division protein a (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG379 MG379 Mycoplasma genitalium 2097 -11540259 73608 gida:mg379 (de:glucose inhibited division protein a) (db:swissprot) GIDA_MYCGE P47619 MYCOPLASMA GENITALIUM 2097 -11540259 172355 glucose inhibited division protein a homolog (cl:gida protein) (db:pir2.dat) I64241 I64241 Mycoplasma genitalium 2097 -11540259 7500882342 mg379 glucose-inhibited division protein a gida (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75221 pid:1673956 percent) (le:9061) (re:10899) (di:direct) U39719 U39719 g3844967 Mycoplasma genitalium 2097 -11540259 5000697540 (de:(mg379) (pn:glucose inhibited division protein a:glucose inhibited division protein:gida) (gn:gida) (gtcfc:10.8) (ec:) (gida_mycge) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG379 MG379 Mycoplasma genitalium 2097 10016142

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920361	19350	41506	819	272

Description

6500736402 gidb:mg380 glucose-inhibited division protein:glucose inhibited division protein b (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG380 MG380 Mycoplasma genitalium 2097 -11540260 73614 gidb:mg380 (de:glucose inhibited division protein b) (db:swissprot) GIDB_MYCGE P47620 MYCOPLASMA GENITALIUM 2097 -11540260 172356 glucose inhibited division protein b homolog (cl:gidb protein) (db:pir2.dat) A64242 A64242 Mycoplasma genitalium 2097 -11540260 7500882355 mg380 glucose-inhibited division protein b gidb (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75220 pid:1673955 percent) (le:10892) (re:11470) (di:direct) U39719 U39719 g3844968 Mycoplasma genitalium 2097 -11540260 5000697541 (de:(mg380) (pn:glucose inhibited division protein b:glucose-inhibited division protein:gidb) (gn:gidb) (gtcfc:10.8) (ec:) (gidb_mycge) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG380 MG380 Mycoplasma genitalium 2097 10016148

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920366	19351	41507	228	75

Description

6500736403 hsds:mg438 restriction-modification enzyme ecod specificity subunit (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG438 MG438 Mycoplasma genitalium 2097 -11540261 119121 mg438 (de:hypothetical protein mg438) (db:swissprot) Y438_MYCGE Q49434 MYCOPLASMA GENITALIUM 2097 -11540261 172620 restriction-modification enzyme ecod specificity chain homolog (db:pir2.dat) D64248 D64248 Mycoplasma genitalium 2097 -11540261 7500895293 mg438 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75159 pid:1673868 percent) (le:11461) (re:12612) (di:direct) U39725 U39725 g3845029 Mycoplasma genitalium 2097 -11540261 5000697542 (de:(mg438) (pn:restriction-modification enzyme ecod specificity subunit:hsds) (gn:hsds) (gtcfc:10.8) (ec:) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG438 MG438 Mycoplasma genitalium 2097 10061564

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920370	19352	41508	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920371	19353	41509	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920376	19354	41510	411	136

Description

6500736404 dnaa:mg469 chromosomal replication initiator protein (gtcfc:10.8) (keggfc:14.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium) MG469 MG469 Mycoplasma genitalium 2097 -11540262 68833 dnaa:mg469 (de:chromosomal replication initiator protein dnaa) (db:swissprot) DNAA_MYCGE P35888 MYCOPLASMA GENITALIUM 2097 -11540262 172312 replication initiation protein dnaa (cl:replication initiation protein dnaa) (db:pir2.dat) H64251 H64251 Mycoplasma genitalium 2097 -11540262 7500880395 mg469 chromosomal replication initiator protein (db:genpept-bct2) (de:mycoplasma genitalium section 51 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:q59549 pid:1209520) (le:42) (re:1355) (di:complement) U39729 U39729 g3845066 Mycoplasma genitalium 2097 -11540262 5000697543 (de:(mg469) (pn:chromosomal replication initiator protein :chromosomal replication initiator protein:dnaa) (gn:dnaa) (gtcfc:10.8) (ec:) (dnaa_mycge) (keggfc:11.2) (tigrfc:10.2) (db:gtc-mycoplasma genitalium)) MG469 MG469 Mycoplasma genitalium 2097 10011418

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920389	19355	41511	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920407	19356	41512	363	120

Description

6500736405 rnc:mg367 ribonuclease iii:rnase iii (gtcfc:10.9) (ec:3.1.26.3) (keggfc:14.1) (tigrfc:11.1) (db:gtc-mycoplasma genitalium) MG367 MG367 Mycoplasma genitalium 2097 -11540263 95700 rnc:mg367 (ec:3.1.26.3) (de:ribonuclease iii, (rnase iii)) (db:swissprot) RNC_MYCGE P47607 MYCOPLASMA GENITALIUM 2097 -11540263 172621 ribonuclease iii (cl:ribonuclease iii:double-stranded rna-binding repeat homology) (db:pir2.dat) F64240 F64240 Mycoplasma genitalium 2097 -11540263 7500890441 mg367 ribonuclease iii rnc (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75233 pid:1673968 percent) (le:5122) (re:5910) (di:complement) U39718 U39718 g3844954 Mycoplasma genitalium 2097 -11540263 5000697544 (de:(mg367) (pn:rnase iii:ribonuclease iii:rnc) (gn:rnc) (gtcfc:10.9) (ec:3.1.26.3) (rnc_mycge) (keggfc:11.1) (tigrfc:11.1) (db:gtc-mycoplasma genitalium)) MG367 MG367 Mycoplasma genitalium 2097 10037650

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920411	19357	41513	375	124

Description

GTC ORF with score 408 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c2f3.) (nt:spac2f3.16, unknown, (splicing may be incorrectly) (le:34728:35097:35485:35652) (re:35027:35429:35589:36191) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920412	19358	41514	630	209

Description

6500736406 rnpa:mg465 rnasep c5 subunit:ribonuclease p protein component:protein c5:rnase p (gtcfc:10.9) (ec:3.1.26.5) (keggfc:14.1) (tigrfc:11.1) (db:gtc-mycoplasma genitalium) MG465 MG465 Mycoplasma genitalium 2097 -11540264 95764 rnpa:mg465 (ec:3.1.26.5) (de:ribonuclease p protein component, (protein c5) (rnase p)) (db:swissprot) RNPA_MYCGE P47703 MYCOPLASMA GENITALIUM 2097 -11540264 172658 rnpa rnasep c5 chain (db:pir2.dat) D64251 D64251 Mycoplasma genitalium 2097 -11540264 7500890466 mg465 ribonuclease p protein component rnpa (db:genpept-bct2) (de:mycoplasma genitalium section 50 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75111 pid:1673822 percent) (le:5652) (re:6038) (di:complement) U39728 U39728 g3845060 Mycoplasma genitalium 2097 -11540264 5000697545 (de:(mg465) (pn:ribonuclease p protein component:protein c5:rnase p:rnasep c5 subunit:rnpa) (gn:rnpa) (gtcfc:10.9) (ec:3.1.26.5) (rnpa_mycge) (keggfc:11.1) (tigrfc:11.1) (db:gtc-mycoplasma genitalium)) MG465 MG465 Mycoplasma genitalium 2097 10037713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920413	19359	41515	471	156

Description

5000697546 membrane lipoprotein:tmpc:hypothetical lipoprotein mg040 precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-mycoplasma genitalium) MG040 MG040 Mycoplasma genitalium 2097 -11540265 108490 mg040 (de:hypothetical lipoprotein mg040 precursor) (db:swissprot) Y040_MYCGE P47286 MYCOPLASMA GENITALIUM 2097 -11540265 172554 membrane lipoprotein tmpc homolog (db:pir2.dat) D64204 D64204 Mycoplasma genitalium 2097 -11540265 7500894574 mg040 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 5 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75062 pid:1673758 percent) (le:8559) (re:10334) (di:direct) U39683 U39683 g1045712 Mycoplasma genitalium 2097 -11540265 6500736407 membrane lipoprotein:tmpc:hypothetical lipoprotein mg040 precursor (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-mycoplasma genitalium) MG040 MG040 Mycoplasma genitalium 2097 -11540265

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920415	19360	41516	354	117

Description

5000697547 adhesin-related protein:30 kda (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-mycoplasma genitalium) MG318 MG318 Mycoplasma genitalium 2097 -11540266 120362 mg318 (de:p32 adhesin (cytadhesin p32)) (db:swissprot) P32_MYCGE Q49417 MYCOPLASMA GENITALIUM 2097 -11540266 172350 fibronectin-binding protein homolog (db:pir2.dat) B64235 B64235 Mycoplasma genitalium 2097 -11540266 7500887512 mg318 adhesin p32 (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to gb:u00089 pid:1674069 pid:1684932) (le:11014) (re:11856) (di:complement) U39712 U39712 g3844895 Mycoplasma genitalium 2097 -11540266 6500736408 adhesin-related protein:30 kda (gtcfc:11.1) (keggfc:14.2) (tigrfc:3.1) (db:gtc-mycoplasma genitalium) MG318 MG318 Mycoplasma genitalium 2097 -11540266

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920418	19361	41517	1314	437

Description

GTC ORF with score 449 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c2f3.) (nt:spac2f3.16, unknown, (splicing may be incorrectly) (le:34728:35097:35485:35652) (re:35027:35429:35589:36191) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920463	19362	41518	318	105

Description

5000697548 trsb protein:hypothetical protein mg025 (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium) MG025 MG025 Mycoplasma genitalium 2097 -11540267 108418 mg025 (de:hypothetical protein mg025) (db:swissprot) Y025_MYCGE P47271 MYCOPLASMA GENITALIUM 2097 -11540267 172700 trsb homolog (db:pir2.dat) G64202 G64202 Mycoplasma genitalium 2097 -11540267 7500894541 mg025 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 4 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75086 pid:1673785 percent) (le:132) (re:1028) (di:direct) U39682 U39682 g3844635 Mycoplasma genitalium 2097 -11540267 6500736409 trsb protein:hypothetical protein mg025 (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium) MG025 MG025 Mycoplasma genitalium 2097 -11540267

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920464	19363	41519	183	60

Description

5000697549 lipopolysaccharide biosynthesis protein:rfbv:hypothetical protein mg060 (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium) MG060 MG060 Mycoplasma genitalium 2097 -11540268 108581 mg060 (de:hypothetical protein mg060) (db:swissprot) Y060_MYCGE P47306 MYCOPLASMA GENITALIUM 2097 -11540268 172549 lipopolysaccharide biosynthesis protein rfbv homolog (db:pir2.dat) F64206 F64206 Mycoplasma genitalium 2097 -11540268 7500894614 mg060 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 7 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75042 pid:1673734 percent) (le:3136) (re:4029) (di:direct) U39685 U39685 g1045734 Mycoplasma genitalium 2097 -11540268 6500736410 lipopolysaccharide biosynthesis protein:rfbv:hypothetical protein mg060 (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium) MG060 MG060 Mycoplasma genitalium 2097 -11540268

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920473	19364	41520	1287	428

Description

6500736411 rfbd:mg137 dtdp-4-dehydrorhamnose reductase (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium) MG137 MG137 Mycoplasma genitalium 2097 -11540269 120214 glf:mg137 (ec:5.4.99.9) (de:udp-galactopyranose mutase,) (db:swissprot) GLF_MYCGE Q49398 MYCOPLASMA GENITALIUM 2097 -11540269 172343 probable dtdp-4-dehydrorhamnose reductase (cl:methanobacterium thermoautotrophicum udp-galactopyranose mutase) (db:pir2.dat) B64215 B64215 Mycoplasma genitalium 2097 -11540269 7500882390 mg137 udp-galactopyranose mutase glf (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75499 pid:1674256 percent) (le:9643) (re:10857) (di:direct) U39693 U39693 g3844727 Mycoplasma genitalium 2097 -11540269 5000697550 (de:(mg137) (pn:dtdp-4-dehydrorhamnose reductase:rfbd) (gn:rfbd) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium)) MG137 MG137 Mycoplasma genitalium 2097 10063105

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920476	19365	41521	780	259

Description

6500736412 pag:mg269 surface protein antigen precursor (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium) MG269 MG269 Mycoplasma genitalium 2097 -11540270 119043 mg269 (de:hypothetical protein mg269) (db:swissprot) Y269_MYCGE Q49407 MYCOPLASMA GENITALIUM 2097 -11540270 172674 surface protein antigen precursor homolog (db:pir2.dat) G64229 G64229 Mycoplasma genitalium 2097 -11540270 7500895011 mg269 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75395 pid:1674138 percent) (le:5942) (re:6964) (di:complement) U39706 U39706 g1045963 Mycoplasma genitalium 2097 -11540270 5000697551 (de:(mg269) (pn:surface protein antigen precursor:pag) (gn:pag) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium)) MG269 MG269 Mycoplasma genitalium 2097 10061488

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920484	19366	41522	543	180

Description

GTC ORF with score 129 to: (fn:actin patch assembly and localization) (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe wiskott-aldrich syndrome protein homolog(wsp1+) gene, complete cds, and btf3/beta-nac gene, partialsequence.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920486	19367	41523	279	92

Description

6500736413 lica:mg356 lic-1 operon protein (gtcfc:11.2) (keggfc:14.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium) MG356 MG356 Mycoplasma genitalium 2097 -11540271 119090 mg356 (de:hypothetical protein mg356) (db:swissprot) Y356_MYCGE Q49423 MYCOPLASMA GENITALIUM 2097 -11540271 172547 lic-1 operon protein lica homolog (db:pir2.dat) D64239 D64239 Mycoplasma genitalium 2097 -11540271 7500895184 mg356 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75246 pid:1673982 percent) (le:5040) (re:5882) (di:complement) U39717 U39717 g3844940 Mycoplasma genitalium 2097 -11540271 5000697552 (de:(mg356) (pn:lic-1 operon protein:lica) (gn:lica) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-mycoplasma genitalium)) MG356 MG356 Mycoplasma genitalium 2097 10061535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920497	19368	41524	501	166

Description

6500736414 mgpb:mg191 attachment protein:mgpa operon:mgp:adhesin p1 precursor:cytadhesin p1:attachment protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG191 MG191 Mycoplasma genitalium 2097 -11540272 58797 mgpb:mgpa:mg191 (de:adhesin p1 precursor (cytadhesin p1) (attachment protein)) (db:swissprot) ADP1_MYCGE P20796 MYCOPLASMA GENITALIUM 2097 -11540272 130825 mgpa 140k adhesin precursor:attachment protein mgpa (cl:adhesin p1) (db:pir1.dat) A30588 A30588 Mycoplasma genitalium 2097 -11540272 252035 (sr:m.genitalium (strain g-37, atcc 33530) dna) (db:genpept-bct1) (de:m.genitalium attachment protein (mgpa) gene, complete cds.) (nt:attachment protein mgpa) (le:1066) (re:5400) (di:direct) MYCMGP M31431 g150159 Mycoplasma genitalium 2097 -11540272 7500876600 mg191 adhesin p1 mgpb (db:genpept-bct2) (de:mycoplasma genitalium section 20 of 51 of the complete genome.) (nt:similar to sp:p20796 gb:m31431 gb:u01694 gb:u01779) (le:6818) (re:11152) (di:direct) U39698 U39698 g3844788 Mycoplasma genitalium 2097 -11540272 5000697553 (de:(mg191) (pn:adhesin p1 precursor:cytadhesin p1:attachment protein:attachment protein, mgpa operon:mgp) (gn:mgpb) (gtcfc:11.3) (ec:) (adp1_mycge) (keggfc:11.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium)) MG191 MG191 Mycoplasma genitalium 2097 10001542

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920509	19369	41525	1134	378

Description

6500736415 mgpc:mg192 hypothetical protein:114 kda:mgpa 3 region:protein precursor (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG192 MG192 Mycoplasma genitalium 2097 -11540273 83656 mgpc:mg192 (de:mgpc protein precursor) (db:swissprot) MGPC_MYCGE P22747 MYCOPLASMA GENITALIUM 2097 -11540273 172386 hypothetical 114k protein mgpa 3 region (db:pir2.dat) C64221 C64221 Mycoplasma genitalium 2097 -11540273 252036 (sr:m.genitalium (strain g-37, atcc 33530) dna) (db:genpept-bct1) (de:m.genitalium attachment protein (mgpa) gene, complete cds.) (nt:114 kd protein) (le:5402) (re:8560) (di:direct) MYCMGP M31431 g150160 Mycoplasma genitalium 2097 -11540273 7500885598 mg192 mgpc protein mgpc (db:genpept-bct2) (de:mycoplasma genitalium section 20 of 51 of the complete genome.) (nt:similar to sp:p22747 gb:u02157 gb:m31431 gb:u02161) (le:11154) (re:14312) (di:direct) U39698 U39698 g3844789 Mycoplasma genitalium 2097 -11540273 5000697554 (de:(mg192) (pn:protein precursor:hypothetical protein, 114 kda:mgpa 3" region) (gn:mgpc) (gtcfc:11.3) (ec:) (mgpc_mycge) (keggfc:11.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium)) MG192 MG192 Mycoplasma genitalium 2097 10025870

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920514	19370	41526	1893	630

Description

5000697555 hmw1 protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG312 MG312 Mycoplasma genitalium 2097 -11540274 120245 hmw1:mg312 (de:protein 1)) (db:swissprot) HMW1_MYCGE Q49413 MYCOPLASMA GENITALIUM 2097 -11540274 172316 cytadherence-accessory protein hmw1 homolog mg312 (db:pir2.dat) E64234 E64234 Mycoplasma genitalium 2097 -11540274 7500883438 mg312 cytadherence accessory protein hmw1 (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to pid:474076 pid:474078 pid:639790) (le:1491) (re:4910) (di:complement) U39712 U39712 g1046012 Mycoplasma genitalium 2097 -11540274 6500736416 hmw1 protein (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG312 MG312 Mycoplasma genitalium 2097 -11540274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920517	19371	41527	450	150

Description

GTC ORF with score 129 to: (sr:mouse (strain cd-1) dna, library of o.smithies, clone pump-2-be) (db:genpept-rod) (de:mouse prp gene encoding proline-rich protein (mp-2) gene, completecds.) (nt:precursor) (le:737:2234) (re:800:2955) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920519	19372	41528	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920533	19373	41529	489	163

Description

5000697556 cytadherence-accessory protein:hmw1 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG313 MG313 Mycoplasma genitalium 2097 -11540275 172317 cytadherence-accessory protein hmw1 homolog mg313 (db:pir2.dat) F64234 F64234 Mycoplasma genitalium 2097 -11540275 7500965549 hmw1_1 cytadherence-accessory protein (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium dead_1, hmw1_1, pip_2, rps4 genes from bases376724 to 392186 (section 34 of 56) of the complete genome.) (nt:identified by sequence similarity; similar ... U39712 U39712 g1046013 Mycoplasma genitalium 2097 -11540275 6500736417 cytadherence-accessory protein:hmw1 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG313 MG313 Mycoplasma genitalium 2097 -11540275

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920536	19374	41530	717	238

Description

5000697557 cytadherence accessory protein:hmw1 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG315 MG315 Mycoplasma genitalium 2097 -11540276 119066 mg315 (de:hypothetical protein mg315) (db:swissprot) Y315_MYCGE Q49416 MYCOPLASMA GENITALIUM 2097 -11540276 172315 cytadherence accessory protein hmw1 homolog mg315 (cl:hypothetical protein mg315) (db:pir2.dat) H64234 H64234 Mycoplasma genitalium 2097 -11540276 7500895112 mg315 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to pid:639787 gb:u00089 sp:q50362) (le:7233) (re:8126) (di:complement) U39712 U39712 g3844892 Mycoplasma genitalium 2097 -11540276 6500736418 cytadherence accessory protein:hmw1 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG315 MG315 Mycoplasma genitalium 2097 -11540276

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920543	19375	41531	204	67

Description

5000697558 phase-variable cytadherence accessory protein:hmw3 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG317 MG317 Mycoplasma genitalium 2097 -11540277 120248 hmw3:mg317 (de:protein 3) (accessory adhesin protein 3) (p69)) (db:swissprot) HMW3_MYCGE Q57081 MYCOPLASMA GENITALIUM 2097 -11540277 172319 cytadherence-accessory protein hmw3 homolog mg317 (db:pir2.dat) A64235 A64235 Mycoplasma genitalium 2097 -11540277 251986 69kda protein (fn:adherence accessory protein homologous to hmw3) (sr:mycoplasma genitalium (strain g-37) (clone library: puc18 base) (db:genpept-bct1) (de:mycoplasma genitalium 20.5 kda nuclear targetting protein gene, p32adhesin gene, p69 protein gene, complete cd... MYCADH L43097 g871802 Mycoplasma genitalium 2097 -11540277 7500883442 mg317 cytadherence accessory protein hmw3 (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to pid:639785 gb:u00089 sp:q50360) (le:9200) (re:10999) (di:complement) U39712 U39712 g3844894 Mycoplasma genitalium 2097 -11540277 6500736419 phase-variable cytadherence accessory protein:hmw3 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG317 MG317 Mycoplasma genitalium 2097 -11540277

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920545	19376	41532	1299	432

Description

5000697559 cytadherence-accessory protein:hmw1 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG386 MG386 Mycoplasma genitalium 2097 -11540278 120360 mg386 (de:protein p200) (db:swissprot) P200_MYCGE Q49429 MYCOPLASMA GENITALIUM 2097 -11540278 172318 cytadherence-accessory protein hmw1 homolog mg386 (db:pir2.dat) G64242 G64242 Mycoplasma genitalium 2097 -11540278 7500887465 mg386 protein p200 (db:genpept-bct2) (de:mycoplasma genitalium section 42 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75211 pid:1673946 percent) (le:4230) (re:9080) (di:complement) U39720 U39720 g3844975 Mycoplasma genitalium 2097 -11540278 6500736420 cytadherence-accessory protein:hmw1 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG386 MG386 Mycoplasma genitalium 2097 -11540278

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920554	19377	41533	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920560	19378	41534	1218	405

Description

5000697560 surface exclusion protein:prga:plasmid pcf10 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG459 MG459 Mycoplasma genitalium 2097 -11540279 119134 mg459 (de:hypothetical protein mg459) (db:swissprot) Y459_MYCGE Q49436 MYCOPLASMA GENITALIUM 2097 -11540279 172598 plsamid surface exclusion protein prga homolog (db:pir2.dat) G64250 G64250 Mycoplasma genitalium 2097 -11540279 7500895331 mg459 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75118 pid:1673831 percent) (le:8991) (re:9500) (di:complement) U39727 U39727 g3845053 Mycoplasma genitalium 2097 -11540279 6500736421 surface exclusion protein:prga:plasmid pcf10 (gtcfc:11.3) (keggfc:14.2) (tigrfc:3.4) (db:gtc-mycoplasma genitalium) MG459 MG459 Mycoplasma genitalium 2097 -11540279

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920579	19379	41535	1650	550

Description

6500736422 tlyc:mg146 hemolysin (gtcfc:12.10:12.11) (keggfc:14.2) (tigrfc:4.2) (db:gtc-mycoplasma genitalium) MG146 MG146 Mycoplasma genitalium 2097 -11540280 500685033 mg146 (de:hypothetical protein mg146) (db:swissprot) Y146_MYCGE Q49399 MYCOPLASMA GENITALIUM 2097 -11540280 172375 hemolysin tlyc homolog (db:pir2.dat) B64216 B64216 Mycoplasma genitalium 2097 -11540280 7500894787 mg146 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75586 pid:1674378 percent) (le:9607) (re:10881) (di:direct) U39695 U39695 g3844739 Mycoplasma genitalium 2097 -11540280 119113 mg146 (de:hypothetical protein mg146) (db:swissprot) Y146_MYCGE Q49399 MYCOPLASMA GENITALIUM 2097 -11540280 5000697567 (de:(mg146) (pn:hemolysin:tlyc) (gn:tlyc) (gtcfc:12.10) (ec:) (keggfc:11.2) (tigrfc:4.2) (db:gtc-mycoplasma genitalium)) MG146 MG146 Mycoplasma genitalium 2097 10061448

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920587	19380	41536	549	182

Description

6500736423 vaca:mg220 pre-procytotoxin (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.2) (db:gtc-mycoplasma genitalium) MG220 MG220 Mycoplasma genitalium 2097 -11540281 119017 mg220 (de:hypothetical protein mg220) (db:swissprot) Y220_MYCGE Q49403 MYCOPLASMA GENITALIUM 2097 -11540281 172322 cytotoxin vaca precursor homolog (db:pir2.dat) C64224 C64224 Mycoplasma genitalium 2097 -11540281 7500894899 mg220 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75468 pid:1674218 percent) (le:22) (re:330) (di:complement) U39702 U39702 g3844823 Mycoplasma genitalium 2097 -11540281 5000697568 (de:(mg220) (pn:pre-procytotoxin:vaca) (gn:vaca) (gtcfc:12.10) (ec:) (keggfc:11.2) (tigrfc:4.2) (db:gtc-mycoplasma genitalium)) MG220 MG220 Mycoplasma genitalium 2097 10061463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920598	19381	41537	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920603	19382	41538	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920609	19383	41539	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920648	19384	41540	1293	430

Description

6500736424 ffh:mg048 signal recognition particle protein:fifty-four homolog (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium) MG048 MG048 Mycoplasma genitalium 2097 -11540282 99406 ffh:mg048 (de:signal recognition particle protein (fifty-four homolog)) (db:swissprot) SR54_MYCGE P47294 MYCOPLASMA GENITALIUM 2097 -11540282 172664 signal recognition particle protein (cl:signal recognition particle 54k protein) (db:pir2.dat) C64205 C64205 Mycoplasma genitalium 2097 -11540282 7500892047 mg048 signal recognition particle protein ffh (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75054 pid:1673748 percent) (le:7259) (re:8599) (di:complement) U39684 U39684 g1045721 Mycoplasma genitalium 2097 -11540282 5000697561 (de:(mg048) (pn:fifty-four homolog:signal recognition particle protein:ffh) (gn:ffh) (gtcfc:12.10:13.6) (ec:) (sr54_mycge) (keggfc:11.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium)) MG048 MG048 Mycoplasma genitalium 2097 10041264

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920657	19385	41541	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920667	19386	41542	2733	910

Description

GTC ORF with score 465 to: (sr:candida albicans (strain 792-1) dna) (db:genpept-pln1) (de:c. albicans cell division cycle-associated protein (homolog ofs.cerevisiae cdc25) gene, complete cds.) (nt:homologue of s.cerevisiae cdc25 gene) (le:1513) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920679	19387	41543	240	79

Description

6500736425 seca:mg072 preprotein translocase:preprotein translocase subunit (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium) MG072 MG072 Mycoplasma genitalium 2097 -11540283 98295 seca:mg072 (de:preprotein translocase seca subunit) (db:swissprot) SECA_MYCGE P47318 MYCOPLASMA GENITALIUM 2097 -11540283 172600 preprotein translocase seca (cl:preprotein translocase seca:dead/h box helicase homology) (db:pir2.dat) I64207 I64207 Mycoplasma genitalium 2097 -11540283 7500891455 mg072 preprotein translocase seca (db:genpept-bct2) (de:mycoplasma genitalium section 9 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75559 pid:1674324 percent) (le:8429) (re:10849) (di:direct) U39687 U39687 g1045748 Mycoplasma genitalium 2097 -11540283 5000697562 (de:(mg072) (pn:preprotein translocase subunit:preprotein translocase:seca) (gn:seca) (gtcfc:12.10:13.6) (ec:) (seca_mycge) (keggfc:11.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium)) MG072 MG072 Mycoplasma genitalium 2097 10040174

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920680	19388	41544	369	122

Description

6500736426 lepa:mg138 gtp-binding membrane protein:gtp-binding protein (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium) MG138 MG138 Mycoplasma genitalium 2097 -11540284 81891 lepa:mg138 (de:gtp-binding protein lepa) (db:swissprot) LEPA_MYCGE P47384 MYCOPLASMA GENITALIUM 2097 -11540284 154411 gtp-binding membrane protein lepa (cl:gtp-binding membrane protein lepa:translation elongation factor tu homology) (db:pir2.dat) C64215 C64215 Mycoplasma genitalium 2097 -11540284 7500884924 mg138 gtp-binding membrane protein lepa (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75498 pid:1674255 percent) (le:10857) (re:12653) (di:direct) U39693 U39693 g3844728 Mycoplasma genitalium 2097 -11540284 5000697563 (de:(mg138) (pn:gtp-binding protein :gtp-binding membrane protein:lepa) (gn:lepa) (gtcfc:12.10:13.6) (ec:) (lepa_mycge) (keggfc:11.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium)) MG138 MG138 Mycoplasma genitalium 2097 10024125

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920684	19389	41545	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920692	19390	41546	738	245

Description

GTC ORF with score 221 to: (fn:required for cytokinesis) (sr:human) (db:genpept-pri2) (de:homo sapiens protein regulating cytokinesis 1 (prc1) mrna, completecds.) (nt:mitotic spindle-associated cdk substrate) (le:79) (re:1941) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920693	19391	41547	267	88

Description

6500736427 secy:mg170 preprotein translocase secy subunit:preprotein translocase subunit (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium) MG170 MG170 Mycoplasma genitalium 2097 -11540285 98355 secy:mg170 (de:preprotein translocase secy subunit) (db:swissprot) SECY_MYCGE P47416 MYCOPLASMA GENITALIUM 2097 -11540285 172601 preprotein translocase secy (db:pir2.dat) H64218 H64218 Mycoplasma genitalium 2097 -11540285 7500891495 mg170 preprotein translocase secy (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215704 gb:u00089 sp:q59548) (le:11072) (re:12499) (di:direct) U39696 U39696 g3844764 Mycoplasma genitalium 2097 -11540285 5000697564 (de:(mg170) (pn:preprotein translocase subunit:preprotein translocase secy subunit:secy) (gn:secy) (gtcfc:12.10:13.6) (ec:) (secy_mycge) (keggfc:11.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium)) MG170 MG170 Mycoplasma genitalium 2097 10040232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920695	19392	41548	279	92

Description

5000697565 haemolysin secretion atp-binding protein:hlyb:hypothetical abc transporter atp-binding protein mg179 (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium) MG179 MG179 Mycoplasma genitalium 2097 -11540286 108944 mg179 (de:hypothetical abc transporter atp-binding protein mg179) (db:swissprot) Y179_MYCGE P47425 MYCOPLASMA GENITALIUM 2097 -11540286 172368 hemolysin secretion atp-binding protein hlyb homolog (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) H64219 H64219 Mycoplasma genitalium 2097 -11540286 7500894825 mg179 abc transporter atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215695 gb:u00089 sp:q50294) (le:2235) (re:3059) (di:direct) U39697 U39697 g3844775 Mycoplasma genitalium 2097 -11540286 6500736428 haemolysin secretion atp-binding protein:hlyb:hypothetical abc transporter atp-binding protein mg179 (gtcfc:12.10) (keggfc:14.2) (tigrfc:4.5) (db:gtc-mycoplasma genitalium) MG179 MG179 Mycoplasma genitalium 2097 -11540286

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920704	19393	41549	1317	438

Description

6500736429 lsp:mg210 prolipoprotein signal peptidase (gtcfc:10.7:11.1:12.10) (ec:3.4.23.36) (keggfc:14.1) (tigrfc:4.5) (db:gtc-mycoplasma genitalium) MG210 MG210 Mycoplasma genitalium 2097 -11540287 119890 lspa:lsp:mg210 (ec:3.4.23.36) (de:signal peptidase) (signal peptidase ii) (spase ii)) (db:swissprot) LSPA_MYCGE Q49401 MYCOPLASMA GENITALIUM 2097 -11540287 172606 lipoprotein signal peptidase::prolipoprotein signal peptidase lsp homolog (ec:3.4.23.36) (db:pir2.dat) B64223 B64223 Mycoplasma genitalium 2097 -11540287 7500885173 mg210 prolipoprotein signal peptidase lsp (db:genpept-bct2) (de:mycoplasma genitalium section 22 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75484 pid:1674239 percent) (le:9109) (re:9654) (di:complement) U39700 U39700 g3844808 Mycoplasma genitalium 2097 -11540287 5000697566 (de:(mg210) (pn:prolipoprotein signal peptidase:lsp) (gn:lsp) (gtcfc:12.10:13.6) (ec:3.4.23.36) (keggfc:11.1) (tigrfc:4.5) (db:gtc-mycoplasma genitalium)) MG210 MG210 Mycoplasma genitalium 2097 10062622

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920705	19394	41550	327	108

Description

6500736430 pota:mg042 spermidine/putrescine transport atp-binding protein:spermidine/putrescine transport atp-binding protein homolog (gtcfc:12.1:13.11) (keggfc:11.1) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG042 MG042 Mycoplasma genitalium 2097 -11540288 172667 spermidine/putrescine transport atp-binding protein pota homolog (cl:atp-binding cassette homology) (db:pir2.dat) F64204 F64204 Mycoplasma genitalium 2097 -11540288 7500965569 pota spermidine/putrescine transport atp-binding (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium gcp, metx, pota, potb, potc, ptsh, tmpc genesfrom bases 47476 to 56879 (section 5 of 56) of the complete genome.) (nt:identified by sequence similarity;... U39683 U39683 g1045714 Mycoplasma genitalium 2097 -11540288 5000697569 (de:(mg042) (pn:spermidine) (gn:pota) (gtcfc:12.1) (ec:) (pota_mycge) (keggfc:11.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium)) MG042 MG042 Mycoplasma genitalium 2097 10032714

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920718	19395	41551	279	92

Description

6500736431 potb:mg043 spermidine/putrescine transport system permease protein:spermidine/putrescine transport system permease protein homolog (gtcfc:12.1:13.11) (keggfc:11.1) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG043 MG043 Mycoplasma genitalium 2097 -11540289 90596 potb:mg043 (de:spermidine/putrescine transport system permease protein potb homolog) (db:swissprot) POTB_MYCGE P47289 MYCOPLASMA GENITALIUM 2097 -11540289 172668 spermidine/putrescine transport system permease protein potb homolog (cl:spermidine/putrescine transport system permease protein potb) (db:pir2.dat) G64204 G64204 Mycoplasma genitalium 2097 -11540289 7500888284 mg043 spermidine/putrescine abc transporter:permease (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75058 pid:1673753 percent) (le:1814) (re:2671) (di:direct) U39684 U39684 g3844652 Mycoplasma genitalium 2097 -11540289 5000697570 (de:(mg043) (pn:spermidine) (gn:potb) (gtcfc:12.1) (ec:) (potb_mycge) (keggfc:11.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium)) MG043 MG043 Mycoplasma genitalium 2097 10032718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920724	19396	41552	1179	392

Description

6500736432 potc:mg044 spermidine/putrescine transport system permease protein:spermidine/putrescine transport system permease protein homolog (gtcfc:12.1:13.11) (keggfc:11.1) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG044 MG044 Mycoplasma genitalium 2097 -11540290 90599 potc:mg044 (de:spermidine/putrescine transport system permease protein potc homolog) (db:swissprot) POTC_MYCGE P47290 MYCOPLASMA GENITALIUM 2097 -11540290 172669 spermidine/putrescine transport system permease protein potc homolog (cl:spermidine/putrescine transport system permease protein poti) (db:pir2.dat) H64204 H64204 Mycoplasma genitalium 2097 -11540290 7500888287 mg044 spermidine/putrescine abc transporter:permease (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75057 pid:1673752 percent) (le:2655) (re:3509) (di:direct) U39684 U39684 g3844653 Mycoplasma genitalium 2097 -11540290 5000697571 (de:(mg044) (pn:spermidine) (gn:potc) (gtcfc:12.1) (ec:) (potc_mycge) (keggfc:11.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium)) MG044 MG044 Mycoplasma genitalium 2097 10032721

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920777	19397	41553	447	148

Description

6500736433 oppb:mg077 oligopeptide transport system permease protein (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG077 MG077 Mycoplasma genitalium 2097 -11540291 87752 oppb:mg077 (de:oligopeptide transport system permease protein oppb) (db:swissprot) OPPB_MYCGE P47323 MYCOPLASMA GENITALIUM 2097 -11540291 172576 oligopeptide transport system permease protein oppb homolog (db:pir2.dat) E64208 E64208 Mycoplasma genitalium 2097 -11540291 7500887194 mg077 oligopeptide abc transporter:permease protein (db:genpept-bct2) (de:mycoplasma genitalium section 10 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75554 pid:1674318 percent) (le:3764) (re:4987) (di:direct) U39688 U39688 g1045754 Mycoplasma genitalium 2097 -11540291 5000697572 (de:(mg077) (pn:oligopeptide transport system permease protein :oligopeptide transport system permease protein:oppb) (gn:oppb) (gtcfc:12.1) (ec:) (oppb_mycge) (keggfc:11.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium)) MG077 MG077 Mycoplasma genitalium 2097 10029893

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920779	19398	41554	780	259

Description

6500736434 oppc:mg078 oligopeptide transport system permease protein:dciac:oligopeptide transport system permease protein oppc (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG078 MG078 Mycoplasma genitalium 2097 -11540292 87757 oppc:mg078 (de:oligopeptide transport system permease protein oppc) (db:swissprot) OPPC_MYCGE P47324 MYCOPLASMA GENITALIUM 2097 -11540292 172575 oligopeptide transport system permease dciac homolog (db:pir2.dat) F64208 F64208 Mycoplasma genitalium 2097 -11540292 7500887198 mg078 oligopeptide abc transporter:permease protein (db:genpept-bct2) (de:mycoplasma genitalium section 10 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75553 pid:1674317 percent) (le:4980) (re:6110) (di:direct) U39688 U39688 g1045755 Mycoplasma genitalium 2097 -11540292 5000697573 (de:(mg078) (pn:oligopeptide transport system permease protein oppc:oligopeptide transport system permease protein:dciac) (gn:oppc) (gtcfc:12.1) (ec:) (oppc_mycge) (keggfc:11.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium)) MG078 MG078 Mycoplasma genitalium 2097 10029898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920786	19399	41555	501	166

Description

6500736435 oppd:mg079 oligopeptide transport atp-binding protein:amie:oligopeptide transport atp-binding protein oppd (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG079 MG079 Mycoplasma genitalium 2097 -11540293 87763 oppd:mg079 (de:oligopeptide transport atp-binding protein oppd) (db:swissprot) OPPD_MYCGE P47325 MYCOPLASMA GENITALIUM 2097 -11540293 172573 oligopeptide transport atp-binding protein amie (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) G64208 G64208 Mycoplasma genitalium 2097 -11540293 7500887202 mg079 oligopeptide abc transporter:atp-binding (db:genpept-bct2) (de:mycoplasma genitalium section 10 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75552 pid:1674316 percent) (le:6112) (re:7320) (di:direct) U39688 U39688 g1045756 Mycoplasma genitalium 2097 -11540293 5000697574 (de:(mg079) (pn:oligopeptide transport atp-binding protein oppd:oligopeptide transport atp-binding protein:amie) (gn:oppd) (gtcfc:12.1) (ec:) (oppd_mycge) (keggfc:11.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium)) MG079 MG079 Mycoplasma genitalium 2097 10029904

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920809	19400	41556	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920820	19401	41557	969	322

Description

GTC ORF with score 133 to: (sr:epstein-barr virus type 2 misp japanese isolate) (db:genpept-vrl) (de:nuclear antigen-3b {exons berf2a and berf2b} (epstein-barr virus-2ebv-2, misp, japanese isolate, genomic, 3840 nt).) (le:142:577) (re:498:3780) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920822	19402	41558	462	153

Description

6500736436 oppf:mg080 oligopeptide transport atp-binding protein:amif:oligopeptide transport atp-binding protein oppf (gtcfc:12.1:12.6) (keggfc:11.1) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG080 MG080 Mycoplasma genitalium 2097 -11540294 87768 oppf:mg080 (de:oligopeptide transport atp-binding protein oppf) (db:swissprot) OPPF_MYCGE P47326 MYCOPLASMA GENITALIUM 2097 -11540294 172574 oligopeptide transport atp-binding protein amif (cl:atp-binding cassette homology) (db:pir2.dat) H64208 H64208 Mycoplasma genitalium 2097 -11540294 7500887205 mg080 oligopeptide abc transporter:atp-binding (db:genpept-bct2) (de:mycoplasma genitalium section 10 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75551 pid:1674315 percent) (le:7320) (re:9866) (di:direct) U39688 U39688 g1045757 Mycoplasma genitalium 2097 -11540294 5000697575 (de:(mg080) (pn:oligopeptide transport atp-binding protein oppf:oligopeptide transport atp-binding protein:amif) (gn:oppf) (gtcfc:12.1) (ec:) (oppf_mycge) (keggfc:11.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium)) MG080 MG080 Mycoplasma genitalium 2097 10029909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920823	19403	41559	345	114

Description

5000697576 glutamine permease operon protein:glnq:hypothetical abc transporter atp-binding protein mg180 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG180 MG180 Mycoplasma genitalium 2097 -11540295 108948 mg180 (de:hypothetical abc transporter atp-binding protein mg180) (db:swissprot) Y180_MYCGE P47426 MYCOPLASMA GENITALIUM 2097 -11540295 172557 membrane transport protein glnq homolog mg180 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) I64219 I64219 Mycoplasma genitalium 2097 -11540295 7500894827 mg180 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215694 gb:u00089 sp:q50293) (le:3044) (re:3958) (di:direct) U39697 U39697 g3844776 Mycoplasma genitalium 2097 -11540295 6500736437 glutamine permease operon protein:glnq:hypothetical abc transporter atp-binding protein mg180 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG180 MG180 Mycoplasma genitalium 2097 -11540295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920824	19404	41560	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920850	19405	41561	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920854	19406	41562	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920858	19407	41563	378	125

Description

5000697577 aromatic amino acid transport protein:arop:hypothetical protein mg225 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG225 MG225 Mycoplasma genitalium 2097 -11540296 108998 mg225 (de:hypothetical protein mg225) (db:swissprot) Y225_MYCGE P47467 MYCOPLASMA GENITALIUM 2097 -11540296 172413 hypothetical protein homolog mg225 (db:pir2.dat) H64224 H64224 Mycoplasma genitalium 2097 -11540296 7500894914 mg225 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75463 pid:1674213 percent) (le:4352) (re:5821) (di:direct) U39702 U39702 g3844828 Mycoplasma genitalium 2097 -11540296 6500736438 aromatic amino acid transport protein:arop:hypothetical protein mg225 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG225 MG225 Mycoplasma genitalium 2097 -11540296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920871	19408	41564	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920883	19409	41565	651	216

Description

5000697578 aromatic amino acid transport protein:arop:hypothetical protein mg226 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG226 MG226 Mycoplasma genitalium 2097 -11540297 108999 mg226 (de:hypothetical protein mg226) (db:swissprot) Y226_MYCGE P47468 MYCOPLASMA GENITALIUM 2097 -11540297 172292 aromatic amino acid transport protein arop homolog (db:pir2.dat) I64224 I64224 Mycoplasma genitalium 2097 -11540297 7500894916 mg226 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75462 pid:1674212 percent) (le:5886) (re:7265) (di:direct) U39702 U39702 g3844829 Mycoplasma genitalium 2097 -11540297 6500736439 aromatic amino acid transport protein:arop:hypothetical protein mg226 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG226 MG226 Mycoplasma genitalium 2097 -11540297

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920889	19410	41566	705	234

Description

GTC ORF with score 135 to: (sr:aspergillus parasiticus (strain su-1) (library: atcc 56775) dna) (db:genpept-pln1) (de:aspergillus parasticus (aflr) gene, complete cds.) (nt:zinc finger domain basepairs 501-585) (le:418) (re:1551) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920920	19411	41567	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920931	19412	41568	750	249

Description

5000697579 membrane transport protein:glnq:hypothetical abc transporter atp-binding protein mg303 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG303 MG303 Mycoplasma genitalium 2097 -11540298 109064 mg303 (de:hypothetical abc transporter atp-binding protein mg303) (db:swissprot) Y303_MYCGE P47545 MYCOPLASMA GENITALIUM 2097 -11540298 172558 membrane transport protein glnq homolog mg303 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) E64233 E64233 Mycoplasma genitalium 2097 -11540298 7500895094 mg303 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 32 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75356 pid:1674093 percent) (le:8482) (re:9555) (di:complement) U39710 U39710 g3844882 Mycoplasma genitalium 2097 -11540298 6500736440 membrane transport protein:glnq:hypothetical abc transporter atp-binding protein mg303 (gtcfc:12.1) (keggfc:14.2) (tigrfc:13.2) (db:gtc-mycoplasma genitalium) MG303 MG303 Mycoplasma genitalium 2097 -11540298

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920938	19413	41569	249	82

Description

6500736441 thdf:mg008 thiophene and furan oxidizer:tdhf:possible thiophene and furan oxidation protein (gtcfc:12.12) (keggfc:14.2) (tigrfc:4.4) (db:gtc-mycoplasma genitalium) MG008 MG008 Mycoplasma genitalium 2097 -11540299 101287 thdf:mg008 (de:possible thiophene and furan oxidation protein thdf) (db:swissprot) THDF_MYCGE P47254 MYCOPLASMA GENITALIUM 2097 -11540299 172675 thiophene and furan oxidizer tdhf homolog (cl:thiophen / furan oxidation protein:translation elongation factor tu homology) (db:pir2.dat) H64200 H64200 Mycoplasma genitalium 2097 -11540299 7500893025 mg008 thiophene and furan oxidation protein tdhf (db:genpept-bct2) (de:mycoplasma genitalium section 1 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75104 pid:1673806 percent) (le:9924) (re:11252) (di:direct) U39679 U39679 g1045676 Mycoplasma genitalium 2097 -11540299 5000697580 (de:(mg008) (pn:possible thiophene and furan oxidation protein :thiophene and furan oxidizer:tdhf) (gn:thdf) (gtcfc:12.12) (ec:) (thdf_mycge) (keggfc:11.2) (tigrfc:4.4) (db:gtc-mycoplasma genitalium)) MG008 MG008 Mycoplasma genitalium 2097 10043128

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920939	19414	41570	1272	423

Description

6500736442 glpf:mg033 glycerol uptake facilitator:glycerol uptake facilitator protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG033 MG033 Mycoplasma genitalium 2097 -11540300 172360 glycerol uptake facilitator homolog (cl:glycerol facilitator protein) (db:pir2.dat) F64203 F64203 Mycoplasma genitalium 2097 -11540300 7500965551 glpf glycerol uptake facilitator (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium gut2, pbef, adda, asps, glpf, glpk, hiss, tdkgenes from bases 36820 to 47525 (section 4 of 56) of the completegenome.) (nt:identified by sequence simila... U39682 U39682 g1045704 Mycoplasma genitalium 2097 -11540300 5000697589 (de:(mg033) (pn:glycerol uptake facilitator protein:glycerol uptake facilitator:glpf) (gn:glpf) (gtcfc:12.2) (ec:) (glpf_mycge) (keggfc:11.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium)) MG033 MG033 Mycoplasma genitalium 2097 10016561

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920940	19415	41571	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920951	19416	41572	513	170

Description

6500736443 ptsh:mg041 phosphohistidinoprotein-hexose phosphotransferase:phosphocarrier protein hpr:histidine-containing protein (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG041 MG041 Mycoplasma genitalium 2097 -11540301 92323 ptsh:mg041 (de:phosphocarrier protein hpr (histidine-containing protein)) (db:swissprot) PTHP_MYCGE P47287 MYCOPLASMA GENITALIUM 2097 -11540301 172591 phosphotransferase system phosphohistidine-containing protein (cl:phosphotransferase system phosphohistidine-containing protein:phosphotransferase system phosphohistidine-containing protein homology) (db:pir2.dat) E64204 E64204 Mycoplasma genitalium 2097 -11540301 7500888961 mg041 phosphocarrier protein hpr ptsh (db:genpept-bct2) (de:mycoplasma genitalium section 5 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75061 pid:1673757 percent) (le:10355) (re:10621) (di:direct) U39683 U39683 g1045713 Mycoplasma genitalium 2097 -11540301 5000697590 (de:(mg041) (pn:phosphocarrier protein hhistidine-containing protein:phosphohistidinoprotein-hexose phosphotransferase:ptsh) (gn:ptsh) (gtcfc:12.2) (ec:) (ptsh_mycge) (keggfc:11.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium)) MG041 MG041 Mycoplasma genitalium 2097 10034355

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920952	19417	41573	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920960	19418	41574	705	234

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920964	19419	41575	387	128

Description

5000697591 hexosephosphate transport protein:uhpt:hypothetical protein mg061 (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG061 MG061 Mycoplasma genitalium 2097 -11540302 108583 mg061 (de:hypothetical protein mg061) (db:swissprot) Y061_MYCGE P47307 MYCOPLASMA GENITALIUM 2097 -11540302 172378 hexosephosphate transport protein uhpt homolog (db:pir2.dat) G64206 G64206 Mycoplasma genitalium 2097 -11540302 7500894616 mg061 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 7 of 51 of the complete genome.) (nt:similar to gb:u00089 pid:1673733 percent identity:) (le:4008) (re:5393) (di:complement) U39685 U39685 g1045735 Mycoplasma genitalium 2097 -11540302 6500736444 hexosephosphate transport protein:uhpt:hypothetical protein mg061 (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG061 MG061 Mycoplasma genitalium 2097 -11540302

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920975	19420	41576	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920976	19421	41577	1044	347

Description

6500736445 mgla:mg119 methylgalactoside permease atp-binding protein:galactoside transport atp-binding protein homolog (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG119 MG119 Mycoplasma genitalium 2097 -11540303 83639 mgla:mg119 (de:galactoside transport atp-binding protein mgla homolog) (db:swissprot) MGLA_MYCGE P47365 MYCOPLASMA GENITALIUM 2097 -11540303 172562 methylgalactoside permease atp-binding protein homolog (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64213 B64213 Mycoplasma genitalium 2097 -11540303 7500885590 mg119 galactoside abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 14 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75516 pid:1674275 percent) (le:2910) (re:4604) (di:direct) U39692 U39692 g3844709 Mycoplasma genitalium 2097 -11540303 5000697592 (de:(mg119) (pn:galactoside transport atp-binding protein homolog:methylgalactoside permease atp-binding protein:mgla) (gn:mgla) (gtcfc:12.2) (ec:) (mgla_mycge) (keggfc:11.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium)) MG119 MG119 Mycoplasma genitalium 2097 10025853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501920984	19422	41578	1041	346

Description

5000697593 ribose transport system permease protein:rbsc:hypothetical protein mg120 (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG120 MG120 Mycoplasma genitalium 2097 -11540304 108790 mg120 (de:hypothetical protein mg120) (db:swissprot) Y120_MYCGE P47366 MYCOPLASMA GENITALIUM 2097 -11540304 172624 ribose transport system permease homolog (db:pir2.dat) C64213 C64213 Mycoplasma genitalium 2097 -11540304 7500894739 mg120 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 14 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75515 pid:1674274 percent) (le:4611) (re:6173) (di:direct) U39692 U39692 g3844710 Mycoplasma genitalium 2097 -11540304 6500736446 ribose transport system permease protein:rbsc:hypothetical protein mg120 (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG120 MG120 Mycoplasma genitalium 2097 -11540304

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921001	19423	41579	621	206

Description

GTC ORF with score 129 to: (sr:thale cress) (db:genpept-pln1) (de:sequence of bac t1g11 from arabidopsis thaliana chromosome 1,complete sequence.) (nt:contains similarity to daucus glycine-rich cell) (le:31776) (re:32414) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921005	19424	41580	324	107

Description

5000697594 pts glucose-specific permease (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG129 MG129 Mycoplasma genitalium 2097 -11540305 118994 mg129 (de:hypothetical protein mg129) (db:swissprot) Y129_MYCGE Q49397 MYCOPLASMA GENITALIUM 2097 -11540305 172595 phosphotransferase system glucose-specific permease homolog (db:pir2.dat) C64214 C64214 Mycoplasma genitalium 2097 -11540305 7500894753 mg129 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75507 pid:1674265 percent) (le:3489) (re:3842) (di:direct) U39693 U39693 g3844720 Mycoplasma genitalium 2097 -11540305 6500736447 pts glucose-specific permease (gtcfc:12.2) (keggfc:14.2) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG129 MG129 Mycoplasma genitalium 2097 -11540305

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921009	19425	41581	753	250

Description

GTC ORF with score 644 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f57b10.) (nt:similar to phosphoglycerate mutase; coded for by c.) (le:21225:21703:21890:22092) (re:21276:21840:22044:22197) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921010	19426	41582	600	199

Description

GTC ORF with score 611 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f57b10.) (nt:similar to phosphoglycerate mutase; coded for by c.) (le:21225:21703:21890:22092) (re:21276:21840:22044:22197) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921011	19427	41583	270	89

Description

5000697595 membrane protein:msmf:probable abc transporter permease protein mg188 (gtcfc:12.2:12.6) (keggfc:11.1) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG188 MG188 Mycoplasma genitalium 2097 -11540306 108954 mg188 (de:probable abc transporter permease protein mg188) (db:swissprot) Y188_MYCGE P47434 MYCOPLASMA GENITALIUM 2097 -11540306 172556 membrane protein msmf homolog (cl:membrane protein msmf) (db:pir2.dat) H64220 H64220 Mycoplasma genitalium 2097 -11540306 7500894844 mg188 abc transporter:permease protein (db:genpept-bct2) (de:mycoplasma genitalium section 20 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75263 pid:1673666 percent) (le:3769) (re:4758) (di:direct) U39698 U39698 g3844785 Mycoplasma genitalium 2097 -11540306 6500736448 membrane protein:msmf:probable abc transporter permease protein mg188 (gtcfc:12.2:12.6) (keggfc:11.1) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG188 MG188 Mycoplasma genitalium 2097 -11540306

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921013	19428	41584	633	210

Description

5000697596 membrane protein:msmg:probable abc transporter permease protein mg189 (gtcfc:12.2:12.6) (keggfc:11.1) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG189 MG189 Mycoplasma genitalium 2097 -11540307 172555 membrane protein homolog (cl:mycoplasma genitalium probable transport system permease) (db:pir2.dat) I64220 I64220 Mycoplasma genitalium 2097 -11540307 7500965560 mg189 abc transporter:permease protein (db:genpept-bct2) (de:mycoplasma genitalium section 20 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75262 pid:1673665 percent) (le:4682) (re:5686) (di:direct) U39698 U39698 g3844786 Mycoplasma genitalium 2097 -11540307 6500736449 membrane protein:msmg:probable abc transporter permease protein mg189 (gtcfc:12.2:12.6) (keggfc:11.1) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG189 MG189 Mycoplasma genitalium 2097 -11540307

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921034	19429	41585	468	155

Description

6500736450 ptsi:mg429 phosphoenolpyruvate-protein phosphotransferase:phosphotransferase system:enzyme i (gtcfc:12.2) (ec:2.7.3.9) (keggfc:14.1) (tigrfc:13.4) (db:gtc-mycoplasma genitalium) MG429 MG429 Mycoplasma genitalium 2097 -11540308 92091 ptsi:mg429 (ec:2.7.3.9) (de:(phosphotransferase system, enzyme i)) (db:swissprot) PT1_MYCGE P47668 MYCOPLASMA GENITALIUM 2097 -11540308 172594 phosphotransferase system enzyme i::pep-dependent hpr protein kinase phosphoryltransferase ptsi (cl:phosphotransferase system enzyme i:phosphotransferase system enzyme i homology) (ec:2.7.3.9) (db:pir1.dat) D64247 D64247 Mycoplasma genitalium 2097 -11540308 7500888907 mg429 phosphoenolpyruvate-protein phosphotransferase (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75168 pid:1673880 percent) (le:2775) (re:4493) (di:complement) U39725 U39725 g3845022 Mycoplasma genitalium 2097 -11540308 5000697597 (de:(mg429) (pn:phosphotransferase system, enzyme i:phosphoenolpyruvate-protein phosphotransferase) (gn:ptsi) (gtcfc:12.2) (ec:2.7.3.9) (pt1_mycge) (keggfc:11.1) (tigrfc:13.4) (db:gtc-mycoplasma genitalium)) MG429 MG429 Mycoplasma genitalium 2097 10034125

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921035	19430	41586	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921047	19431	41587	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921051	19432	41588	393	130

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921053	19433	41589	471	156

Description

5000697598 atp-binding protein:msmk:hypothetical abc transporter atp-binding protein mg187 (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-mycoplasma genitalium) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) MG187 MG187 Mycoplasma genitalium 2097 -11540309 108953 mg187 (de:hypothetical abc transporter atp-binding protein mg187) (db:swissprot) Y187_MYCGE P47433 MYCOPLASMA GENITALIUM 2097 -11540309 172300 atp-binding protein msmk homolog (cl:atp-binding cassette homology) (db:pir2.dat) G64220 G64220 Mycoplasma genitalium 2097 -11540309 7500894842 mg187 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 20 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75264 pid:1673667 percent) (le:2009) (re:3766) (di:direct) U39698 U39698 g3844784 Mycoplasma genitalium 2097 -11540309 6500736451 atp-binding protein:msmk:hypothetical abc transporter atp-binding protein mg187 (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-mycoplasma genitalium) MG187 MG187 Mycoplasma genitalium 2097 -11540309

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921059	19434	41590	252	83

Description

6500736452 pstb:mg410 phosphate transport system atp-binding protein:phosphate transport atp-binding protein homolog (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-mycoplasma genitalium) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) MG410 MG410 Mycoplasma genitalium 2097 -11540310 92041 pstb:mg410 (de:phosphate transport atp-binding protein pstb homolog) (db:swissprot) PSTB_MYCGE P47650 MYCOPLASMA GENITALIUM 2097 -11540310 172580 peripheral membrane protein b homolog (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) D64245 D64245 Mycoplasma genitalium 2097 -11540310 7500888885 mg410 phosphate abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 45 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75186 pid:1673900 percent) (le:2694) (re:3683) (di:complement) U39723 U39723 g3845003 Mycoplasma genitalium 2097 -11540310 5000697599 (de:(mg410) (pn:phosphate transport atp-binding protein homolog:phosphate transport system atp-binding protein) (gn:pstb) (gtcfc:12.4) (ec:) (pstb_mycge) (keggfc:11.2) (tigrfc:13.3) (db:gtc-mycoplasma genitalium)) MG410 MG410 Mycoplasma genitalium 2097 10034075

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921060	19435	41591	324	107

Description

6500736453 psta:mg411 periplasmic phosphate permease homolog:ag88:phosphate transport system permease protein homolog (gtcfc:12.4:12.6) (keggfc:11.1) (tigrfc:13.3) (db:gtc-mycoplasma genitalium) (gtcfc:cell processes-transport of anions (cl_so4_po4_etc_):cell processes-transporters of unknown specificity (abc_atpases_drug) or metals) MG411 MG411 Mycoplasma genitalium 2097 -11540311 92039 psta:mg411 (de:phosphate transport system permease protein psta homolog) (db:swissprot) PSTA_MYCGE P47651 MYCOPLASMA GENITALIUM 2097 -11540311 172582 periplasmic phosphate permease homolog ag88 homolog (cl:periplasmic phosphate permease ag88) (db:pir2.dat) E64245 E64245 Mycoplasma genitalium 2097 -11540311 7500888879 mg411 phosphate abc transporter:permease protein (db:genpept-bct2) (de:mycoplasma genitalium section 45 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75185 pid:1673899 percent) (le:3668) (re:5632) (di:complement) U39723 U39723 g3845004 Mycoplasma genitalium 2097 -11540311 5000697600 (de:(mg411) (pn:phosphate transport system permease protein homolog:periplasmic phosphate permease homolog:ag88) (gn:psta) (gtcfc:12.4) (ec:) (psta_mycge) (keggfc:11.2) (tigrfc:13.3) (db:gtc-mycoplasma genitalium)) MG411 MG411 Mycoplasma genitalium 2097 10034073

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921065	19436	41592	300	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921066	19437	41593	333	110

Description

5000697601 putative potassium channel protein:hypothetical protein mg323 (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-mycoplasma genitalium) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) MG323 MG323 Mycoplasma genitalium 2097 -11540312 109085 mg323 (de:hypothetical protein mg323) (db:swissprot) Y323_MYCGE P47565 MYCOPLASMA GENITALIUM 2097 -11540312 172424 hypothetical protein homolog mg323 (cl:conserved hypothetical protein mg323) (db:pir2.dat) G64235 G64235 Mycoplasma genitalium 2097 -11540312 7500895127 mg323 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 35 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75322 pid:1674060 percent) (le:6601) (re:7284) (di:direct) U39713 U39713 g3844900 Mycoplasma genitalium 2097 -11540312 6500736454 putative potassium channel protein:hypothetical protein mg323 (gtcfc:12.5) (keggfc:14.2) (tigrfc:13.5) (db:gtc-mycoplasma genitalium) MG323 MG323 Mycoplasma genitalium 2097 -11540312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921069	19438	41594	429	142

Description

5000697699 hypothetical lipoprotein mg045 precursor (gtcfc:12.6) (keggfc:11.1) (db:gtc-mycoplasma genitalium) MG045 MG045 Mycoplasma genitalium 2097 -11540313 108498 mg045 (de:hypothetical lipoprotein mg045 precursor) (db:swissprot) Y045_MYCGE P47291 MYCOPLASMA GENITALIUM 2097 -11540313 172447 hypothetical protein mg045 (db:pir2.dat) I64204 I64204 Mycoplasma genitalium 2097 -11540313 7500894579 mg045 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75056 pid:1673751 percent) (le:3494) (re:4945) (di:direct) U39684 U39684 g3844654 Mycoplasma genitalium 2097 -11540313 6500736455 hypothetical lipoprotein mg045 precursor (gtcfc:12.6) (keggfc:11.1) (db:gtc-mycoplasma genitalium) MG045 MG045 Mycoplasma genitalium 2097 -11540313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921078	19439	41595	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921095	19440	41596	462	153

Description

5000697719 hypothetical lipoprotein mg186 precursor (gtcfc:12.6) (keggfc:11.1) (db:gtc-mycoplasma genitalium) MG186 MG186 Mycoplasma genitalium 2097 -11540314 108952 mg186 (de:hypothetical lipoprotein mg186 precursor) (db:swissprot) Y186_MYCGE P47432 MYCOPLASMA GENITALIUM 2097 -11540314 172469 hypothetical protein mg186 (db:pir2.dat) F64220 F64220 Mycoplasma genitalium 2097 -11540314 7500894840 mg186 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 20 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75265 pid:1673668 percent) (le:1264) (re:2016) (di:direct) U39698 U39698 g3844783 Mycoplasma genitalium 2097 -11540314 6500736456 hypothetical lipoprotein mg186 precursor (gtcfc:12.6) (keggfc:11.1) (db:gtc-mycoplasma genitalium) MG186 MG186 Mycoplasma genitalium 2097 -11540314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921102	19441	41597	414	137

Description

5000697605 atp-binding protein p29:probable abc transporter atp-binding protein p29 (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG290 MG290 Mycoplasma genitalium 2097 -11540315 88090 mg290 (de:probable abc transporter atp-binding protein p29) (db:swissprot) P29_MYCGE P47532 MYCOPLASMA GENITALIUM 2097 -11540315 172301 atp-binding protein p29 homolog (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) A64232 A64232 Mycoplasma genitalium 2097 -11540315 7500887467 mg290 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 31 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75370 pid:1674109 percent) (le:1298) (re:2035) (di:direct) U39709 U39709 g1045987 Mycoplasma genitalium 2097 -11540315 6500736457 atp-binding protein p29:probable abc transporter atp-binding protein p29 (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG290 MG290 Mycoplasma genitalium 2097 -11540315

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921110	19442	41598	330	109

Description

5000697606 p69:transport system permease protein p69 (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG291 MG291 Mycoplasma genitalium 2097 -11540316 88240 mg291 (de:transport system permease protein p69) (db:swissprot) P69_MYCGE P47533 MYCOPLASMA GENITALIUM 2097 -11540316 172694 transport system permease protein p69 homolog mg291 (cl:transport system permease protein p69) (db:pir2.dat) B64232 B64232 Mycoplasma genitalium 2097 -11540316 7500887530 mg291 transport system permease protein p69 (db:genpept-bct2) (de:mycoplasma genitalium section 31 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75369 pid:1674108 percent) (le:2025) (re:3656) (di:direct) U39709 U39709 g1045988 Mycoplasma genitalium 2097 -11540316 6500736458 p69:transport system permease protein p69 (gtcfc:12.6) (keggfc:11.1) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG291 MG291 Mycoplasma genitalium 2097 -11540316

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921114	19443	41599	1128	376

Description

5000697609 abc transporter:hypothetical abc transporter atp-binding protein mg065 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-mycoplasma genitalium) MG065 MG065 Mycoplasma genitalium 2097 -11540317 108588 mg065 (de:hypothetical abc transporter atp-binding protein mg065) (db:swissprot) Y065_MYCGE P47311 MYCOPLASMA GENITALIUM 2097 -11540317 172376 heterocyst maturation protein homolog mg065 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64207 B64207 Mycoplasma genitalium 2097 -11540317 7500894624 mg065 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 8 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75612 pid:1673727 percent) (le:4154) (re:5554) (di:direct) U39686 U39686 g1045740 Mycoplasma genitalium 2097 -11540317 6500736459 abc transporter:hypothetical abc transporter atp-binding protein mg065 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-mycoplasma genitalium) MG065 MG065 Mycoplasma genitalium 2097 -11540317

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921117	19444	41600	1452	483

Description

5000697610 peptide transport system protein sapf:hypothetical abc transporter atp-binding protein mg304 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-mycoplasma genitalium) MG304 MG304 Mycoplasma genitalium 2097 -11540318 109065 mg304 (de:hypothetical abc transporter atp-binding protein mg304) (db:swissprot) Y304_MYCGE P47546 MYCOPLASMA GENITALIUM 2097 -11540318 172553 membrane associated atpase cbio homolog (cl:atp-binding cassette homology) (db:pir2.dat) F64233 F64233 Mycoplasma genitalium 2097 -11540318 7500895095 mg304 abc transporter:atp binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 32 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75355 pid:1674092 percent) (le:9537) (re:10298) (di:complement) U39710 U39710 g3844883 Mycoplasma genitalium 2097 -11540318 6500736460 peptide transport system protein sapf:hypothetical abc transporter atp-binding protein mg304 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-mycoplasma genitalium) MG304 MG304 Mycoplasma genitalium 2097 -11540318

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921119	19445	41601	1149	382

Description

5000697611 sp:p40010:hypothetical gtp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-mycoplasma genitalium) MG442 MG442 Mycoplasma genitalium 2097 -11540319 119125 mg442 (de:hypothetical protein mg442) (db:swissprot) Y442_MYCGE Q49435 MYCOPLASMA GENITALIUM 2097 -11540319 172437 hypothetical protein homolog mg442 (cl:conserved hypothetical protein mg442) (db:pir2.dat) H64248 H64248 Mycoplasma genitalium 2097 -11540319 7500895304 mg442 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75135 pid:1673849 percent) (le:2551) (re:3363) (di:complement) U39726 U39726 g3845035 Mycoplasma genitalium 2097 -11540319 6500736461 sp:p40010:hypothetical gtp-binding protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-mycoplasma genitalium) MG442 MG442 Mycoplasma genitalium 2097 -11540319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921120	19446	41602	513	170

Description

5000697612 abc transporter:hypothetical abc transporter atp-binding protein mg467 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-mycoplasma genitalium) MG467 MG467 Mycoplasma genitalium 2097 -11540320 109188 mg467 (de:hypothetical abc transporter atp-binding protein mg467) (db:swissprot) Y467_MYCGE P47705 MYCOPLASMA GENITALIUM 2097 -11540320 172377 heterocyst maturation protein deva homolog (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F64251 F64251 Mycoplasma genitalium 2097 -11540320 7500895345 mg467 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 50 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75110 pid:1673820 percent) (le:6179) (re:7114) (di:complement) U39728 U39728 g3845062 Mycoplasma genitalium 2097 -11540320 6500736462 abc transporter:hypothetical abc transporter atp-binding protein mg467 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.1) (db:gtc-mycoplasma genitalium) MG467 MG467 Mycoplasma genitalium 2097 -11540320

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921122	19447	41603	306	101

Description

5000697602 transport atp-binding protein:msba:hypothetical abc transporter atp-binding protein mg014 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG014 MG014 Mycoplasma genitalium 2097 -11540321 108371 mg014 (de:hypothetical abc transporter atp-binding protein mg014) (db:swissprot) Y014_MYCGE P47260 MYCOPLASMA GENITALIUM 2097 -11540321 172692 transport atp-binding protein msba homolog mg014 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) E64201 E64201 Mycoplasma genitalium 2097 -11540321 7500894524 mg014 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 2 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75095 pid:1673795 percent) (le:3507) (re:5378) (di:direct) U39680 U39680 g1045683 Mycoplasma genitalium 2097 -11540321 6500736463 transport atp-binding protein:msba:hypothetical abc transporter atp-binding protein mg014 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG014 MG014 Mycoplasma genitalium 2097 -11540321

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921126	19448	41604	1068	355

Description

5000697603 transport atp-binding protein:msba:hypothetical abc transporter atp-binding protein mg015 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG015 MG015 Mycoplasma genitalium 2097 -11540322 108373 mg015 (de:hypothetical abc transporter atp-binding protein mg015) (db:swissprot) Y015_MYCGE P47261 MYCOPLASMA GENITALIUM 2097 -11540322 172693 transport atp-binding protein msba homolog mg015 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F64201 F64201 Mycoplasma genitalium 2097 -11540322 7500894527 mg015 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 2 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75094 pid:1673794 percent) (le:5425) (re:7194) (di:direct) U39680 U39680 g1045684 Mycoplasma genitalium 2097 -11540322 6500736464 transport atp-binding protein:msba:hypothetical abc transporter atp-binding protein mg015 (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG015 MG015 Mycoplasma genitalium 2097 -11540322

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921134	19449	41605	3186	1061

Description

6500736465 p37:mg289 high affinity transport system protein p37:high affinity transport system protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG289 MG289 Mycoplasma genitalium 2097 -11540323 119932 mg289 (de:high affinity transport system protein p37 precursor) (db:swissprot) P37_MYCGE Q49410 MYCOPLASMA GENITALIUM 2097 -11540323 172379 high affinity transport system protein p37 homolog (db:pir2.dat) I64231 I64231 Mycoplasma genitalium 2097 -11540323 7500887513 mg289 high affinity transport system protein p37 (db:genpept-bct2) (de:mycoplasma genitalium section 31 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75371 pid:1674110 percent) (le:202) (re:1308) (di:direct) U39709 U39709 g1045986 Mycoplasma genitalium 2097 -11540323 5000697604 (de:(mg289) (pn:high affinity transport system protein:high affinity transport system protein p37:p37) (gn:p37) (gtcfc:12.6) (ec:) (keggfc:11.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium)) MG289 MG289 Mycoplasma genitalium 2097 10062688

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921139	19450	41606	1296	432

Description

5000697607 atp-dependent transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG390 MG390 Mycoplasma genitalium 2097 -11540324 119105 mg390 (de:hypothetical atp-binding protein mg390) (db:swissprot) Y390_MYCGE Q49430 MYCOPLASMA GENITALIUM 2097 -11540324 172545 lactococcin transport atp-binding protein homolog (cl:atp-binding cassette homology) (db:pir2.dat) B64243 B64243 Mycoplasma genitalium 2097 -11540324 7500895230 mg390 abc transporter:atp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 43 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75207 pid:1673942 percent) (le:489) (re:2471) (di:complement) U39721 U39721 g3844981 Mycoplasma genitalium 2097 -11540324 6500736466 atp-dependent transport protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG390 MG390 Mycoplasma genitalium 2097 -11540324

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921143	19451	41607	471	156

Description

6500736467 p69:mg406 transport system permease protein p69:transport system permease protein (gtcfc:12.6) (keggfc:14.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium) MG406 MG406 Mycoplasma genitalium 2097 -11540325 119108 mg406 (de:hypothetical protein mg406) (db:swissprot) Y406_MYCGE Q49431 MYCOPLASMA GENITALIUM 2097 -11540325 172695 transport system permease protein p69 homolog mg406 (db:pir2.dat) I64244 I64244 Mycoplasma genitalium 2097 -11540325 7500895251 mg406 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to pid:1209759 sp:q50325 percent identity:) (le:8933) (re:9274) (di:complement) U39722 U39722 g3844998 Mycoplasma genitalium 2097 -11540325 5000697608 (de:(mg406) (pn:transport system permease protein:transport system permease protein p69:p69) (gn:p69) (gtcfc:12.6) (ec:) (keggfc:11.2) (tigrfc:13.6) (db:gtc-mycoplasma genitalium)) MG406 MG406 Mycoplasma genitalium 2097 10061553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921170	19452	41608	447	148

Description

5000697613 heat shock protein:dnaj:dnaj-like protein mg002 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG002 MG002 Mycoplasma genitalium 2097 -11540326 68977 mg002 (de:dnaj-like protein mg002) (db:swissprot) DNJL_MYCGE P47248 MYCOPLASMA GENITALIUM 2097 -11540326 172371 heat shock protein dnaj homolog mg002 (cl:dnaj amino-terminal homology) (db:pir2.dat) B64200 B64200 Mycoplasma genitalium 2097 -11540326 7500880509 mg002 dnaj-like protein (db:genpept-bct2) (de:mycoplasma genitalium section 1 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:q50312 pid:1209516) (le:1829) (re:2761) (di:direct) U39679 U39679 g1045670 Mycoplasma genitalium 2097 -11540326 6500736468 heat shock protein:dnaj:dnaj-like protein mg002 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG002 MG002 Mycoplasma genitalium 2097 -11540326

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921195	19453	41609	387	128

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921201	19454	41610	453	150

Description

6500736469 dnaj:mg019 heat shock protein:protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG019 MG019 Mycoplasma genitalium 2097 -11540327 68879 dnaj:mg019 (de:dnaj protein) (db:swissprot) DNAJ_MYCGE P47265 MYCOPLASMA GENITALIUM 2097 -11540327 172370 heat shock protein dnaj (cl:heat shock protein dnaj:dnaj amino-terminal homology) (db:pir2.dat) A64202 A64202 Mycoplasma genitalium 2097 -11540327 7500880428 mg019 heat shock protein dnaj (db:genpept-bct2) (de:mycoplasma genitalium section 3 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78004 pid:1673792 percent) (le:1969) (re:3138) (di:direct) U39681 U39681 g3844628 Mycoplasma genitalium 2097 -11540327 5000697614 (de:(mg019) (pn:protein:heat shock protein:dnaj) (gn:dnaj) (gtcfc:12.7) (ec:) (dnaj_mycge) (keggfc:11.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium)) MG019 MG019 Mycoplasma genitalium 2097 10011464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921202	19455	41611	1206	401

Description

5000697615 rplo:rpl15:mg169 ribosomal protein l15:rplo:50s ribosomal protein l15 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG169 MG169 Mycoplasma genitalium 2097 -11540328 94824 rplo:rpl15:mg169 (de:50s ribosomal protein l15) (db:swissprot) RL15_MYCGE P47415 MYCOPLASMA GENITALIUM 2097 -11540328 172628 ribosomal protein l15 (cl:escherichia coli ribosomal protein l15) (db:pir2.dat) G64218 G64218 Mycoplasma genitalium 2097 -11540328 7500889971 mg169 ribosomal protein l15 rpl15 (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to pid:1215705 gb:u00089 sp:q50300) (le:10620) (re:11072) (di:direct) U39696 U39696 g3844763 Mycoplasma genitalium 2097 -11540328 6500736470 rplo:rpl15 ribosomal protein l15:rplo:50s ribosomal protein l15 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG169 MG169 Mycoplasma genitalium 2097 -11540328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921208	19456	41612	726	241

Description

5000697616 heat shock protein:dnaj:dnaj-like protein mg200 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG200 MG200 Mycoplasma genitalium 2097 -11540329 68978 mg200 (de:dnaj-like protein mg200) (db:swissprot) DNJM_MYCGE P47442 MYCOPLASMA GENITALIUM 2097 -11540329 172372 heat shock protein dnaj homolog mg200 (cl:dnaj amino-terminal homology) (db:pir2.dat) A64222 A64222 Mycoplasma genitalium 2097 -11540329 7500880511 mg200 dnaj-like protein (db:genpept-bct2) (de:mycoplasma genitalium section 21 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75354 pid:1673683 percent) (le:6816) (re:8621) (di:direct) U39699 U39699 g3844797 Mycoplasma genitalium 2097 -11540329 6500736471 heat shock protein:dnaj:dnaj-like protein mg200 (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG200 MG200 Mycoplasma genitalium 2097 -11540329

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921209	19457	41613	507	168

Description

6500736472 grpe:mg201 heat shock protein:protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG201 MG201 Mycoplasma genitalium 2097 -11540330 74559 grpe:mg201 (de:grpe protein) (db:swissprot) GRPE_MYCGE P47443 MYCOPLASMA GENITALIUM 2097 -11540330 172373 heat shock protein grpe (db:pir2.dat) B64222 B64222 Mycoplasma genitalium 2097 -11540330 7500882753 mg201 heat shock protein grpe (db:genpept-bct2) (de:mycoplasma genitalium section 21 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78017 pid:1673682 percent) (le:8633) (re:9286) (di:direct) U39699 U39699 g3844798 Mycoplasma genitalium 2097 -11540330 5000697617 (de:(mg201) (pn:protein:heat shock protein:grpe) (gn:grpe) (gtcfc:12.7) (ec:) (grpe_mycge) (keggfc:11.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium)) MG201 MG201 Mycoplasma genitalium 2097 10017074

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921226	19458	41614	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921229	19459	41615	234	77

Description

5000697618 dnak:hsp70:mg305 heat shock protein 70:dnak:dnak protein:heat shock 70 kd protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG305 MG305 Mycoplasma genitalium 2097 -11540331 68907 dnak:hsp70:mg305 (de:dnak protein (heat shock 70 kd protein) (hsp70)) (db:swissprot) DNAK_MYCGE P47547 MYCOPLASMA GENITALIUM 2097 -11540331 152043 dnak-type molecular chaperone:heat shock protein 70 (cl:heat shock protein 70) (db:pir2.dat) G64233 G64233 Mycoplasma genitalium 2097 -11540331 7500880471 mg305 heat shock protein 70 dnak (db:genpept-bct2) (de:mycoplasma genitalium section 33 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75344 pid:1674090 percent) (le:119) (re:1906) (di:complement) U39711 U39711 g1046004 Mycoplasma genitalium 2097 -11540331 6500736473 dnak:hsp70 heat shock protein 70:dnak:dnak protein:heat shock 70 kd protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG305 MG305 Mycoplasma genitalium 2097 -11540331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921241	19460	41616	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921242	19461	41617	297	98

Description

5000697619 mopa:groel:mg392 heat shock protein:groel:60 kd chaperonin:protein cpn60:groel protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG392 MG392 Mycoplasma genitalium 2097 -11540332 64144 mopa:groel:mg392 (de:60 kd chaperonin (protein cpn60) (groel protein)) (db:swissprot) CH60_MYCGE P47632 MYCOPLASMA GENITALIUM 2097 -11540332 154557 heat shock protein groel (cl:chaperonin groel) (db:pir2.dat) D64243 D64243 Mycoplasma genitalium 2097 -11540332 7500878600 mg392 heat shock protein groel (db:genpept-bct2) (de:mycoplasma genitalium section 43 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78012 pid:1673939 percent) (le:3939) (re:5570) (di:complement) U39721 U39721 g3844983 Mycoplasma genitalium 2097 -11540332 6500736474 mopa:groel heat shock protein:groel:60 kd chaperonin:protein cpn60:groel protein (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG392 MG392 Mycoplasma genitalium 2097 -11540332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921251	19462	41618	372	123

Description

5000697620 mopb:groes:mg393 heat shock protein 60-like protein:pggroes:putative 10 kd chaperonin:protein cpn10:protein groes (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG393 MG393 Mycoplasma genitalium 2097 -11540333 64055 mopb:groes:mg393 (de:putative 10 kd chaperonin (protein cpn10) (protein groes)) (db:swissprot) CH10_MYCGE P47633 MYCOPLASMA GENITALIUM 2097 -11540333 172369 heat shock protein 60-like protein homolog (db:pir2.dat) E64243 E64243 Mycoplasma genitalium 2097 -11540333 7500878588 mg393 heat shock protein groes (db:genpept-bct2) (de:mycoplasma genitalium section 43 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75205 pid:1673938 percent) (le:5583) (re:5915) (di:complement) U39721 U39721 g3844984 Mycoplasma genitalium 2097 -11540333 6500736475 mopb:groes heat shock protein 60-like protein:pggroes:putative 10 kd chaperonin:protein cpn10:protein groes (gtcfc:12.7) (keggfc:14.2) (tigrfc:4.3) (db:gtc-mycoplasma genitalium) MG393 MG393 Mycoplasma genitalium 2097 -11540333

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921254	19463	41619	1149	382

Description

6500736476 ftsz:mg224 cell division protein ftsz:cell division protein homolog (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-mycoplasma genitalium) MG224 MG224 Mycoplasma genitalium 2097 -11540334 72483 ftsz:mg224 (de:cell division protein ftsz) (db:swissprot) FTSZ_MYCGE P47466 MYCOPLASMA GENITALIUM 2097 -11540334 172311 cell division protein ftsz (cl:cell division protein ftsz) (db:pir2.dat) G64224 G64224 Mycoplasma genitalium 2097 -11540334 7500881882 mg224 cell division protein ftsz (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75464 pid:1674214 percent) (le:3197) (re:4306) (di:direct) U39702 U39702 g3844827 Mycoplasma genitalium 2097 -11540334 5000697621 (de:(mg224) (pn:cell division protein homolog:cell division protein ftsz) (gn:ftsz) (gtcfc:12.8) (ec:) (ftsz_mycge) (keggfc:11.2) (tigrfc:4.1) (db:gtc-mycoplasma genitalium)) MG224 MG224 Mycoplasma genitalium 2097 10015034

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921257	19464	41620	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921261	19465	41621	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921262	19466	41622	1287	428

Description

6500736477 tig:mg238 trigger factor:larger protein:tigp2:trigger factor:tf (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-mycoplasma genitalium) MG238 MG238 Mycoplasma genitalium 2097 -11540335 101513 tig:mg238 (de:trigger factor (tf)) (db:swissprot) TIG_MYCGE P47480 MYCOPLASMA GENITALIUM 2097 -11540335 172696 trigger factor homolog (cl:trigger factor) (db:pir2.dat) C64226 C64226 Mycoplasma genitalium 2097 -11540335 7500893185 mg238 trigger factor tig (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:z32656 pid:474090 gb:u00089 sp:p75454) (le:3165) (re:4499) (di:direct) U39703 U39703 g3844842 Mycoplasma genitalium 2097 -11540335 5000697622 (de:(mg238) (pn:trigger factor:tf:trigger factor, larger protein:tigp2) (gn:tig) (gtcfc:12.8) (ec:) (tig_mycge) (keggfc:11.2) (tigrfc:4.1) (db:gtc-mycoplasma genitalium)) MG238 MG238 Mycoplasma genitalium 2097 10043349

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921267	19467	41623	933	310

Description

6500736478 ftsy:mg297 cell division protein:cell division protein homolog (gtcfc:12.8) (keggfc:14.2) (tigrfc:4.1) (db:gtc-mycoplasma genitalium) MG297 MG297 Mycoplasma genitalium 2097 -11540336 72474 ftsy:mg297 (de:cell division protein ftsy homolog) (db:swissprot) FTSY_MYCGE P47539 MYCOPLASMA GENITALIUM 2097 -11540336 172310 cell division protein ftsy (cl:docking protein) (db:pir2.dat) H64232 H64232 Mycoplasma genitalium 2097 -11540336 7500881857 mg297 cell division protein ftsy (db:genpept-bct2) (de:mycoplasma genitalium section 32 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75362 pid:1674100 percent) (le:91) (re:1131) (di:complement) U39710 U39710 g1045995 Mycoplasma genitalium 2097 -11540336 5000697623 (de:(mg297) (pn:cell division protein homolog:cell division protein:ftsy) (gn:ftsy) (gtcfc:12.8) (ec:) (ftsy_mycge) (keggfc:11.2) (tigrfc:4.1) (db:gtc-mycoplasma genitalium)) MG297 MG297 Mycoplasma genitalium 2097 10015025

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921280	19468	41624	336	111

Description

5000697624 pyrh:smba:mg434 uridine 5-monophosphate:pyrh:putative uridylate kinase:uk:uridine monophosphate kinase:ump kinase (gtcfc:12.8) (ec:2.7.4.-) (keggfc:14.1) (tigrfc:4.1) (db:gtc-mycoplasma genitalium) MG434 MG434 Mycoplasma genitalium 2097 -11540337 172566 mukb suppressor protein smba homolog (db:pir2.dat) I64247 I64247 Mycoplasma genitalium 2097 -11540337 7500965561 smba mukb suppressor protein (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium cdsa, frr, hsds, smba, tsf genes from bases539564 to 546816 (section 52 of 56) of the complete genome.) (nt:identified by sequence similarity; similar t... U39730 U39730 g1046151 Mycoplasma genitalium 2097 -11540337 6500736479 pyrh:smba uridine 5-monophosphate:pyrh:putative uridylate kinase:uk:uridine monophosphate kinase:ump kinase (gtcfc:12.8) (ec:2.7.4.-) (keggfc:14.1) (tigrfc:4.1) (db:gtc-mycoplasma genitalium) MG434 MG434 Mycoplasma genitalium 2097 -11540337

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921285	19469	41625	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921317	19470	41626	1320	439

Description

Hypothetical protein

Sequence Listing

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921323	19471	41627	675	224

Description

6500736480 ftsh:mg457 cell division protein:cell division protein homolog (gtcfc:12.8) (ec:3.4.24.-) (keggfc:14.1) (tigrfc:4.1) (db:gtc-mycoplasma genitalium) MG457 MG457 Mycoplasma genitalium 2097 -11540338 72450 ftsh:mg457 (ec:3.4.24.-) (de:cell division protein ftsh homolog,) (db:swissprot) FTSH_MYCGE P47695 MYCOPLASMA GENITALIUM 2097 -11540338 172309 cell division protein ftsh (cl:cell division protein ftsh:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir2.dat) E64250 E64250 Mycoplasma genitalium 2097 -11540338 7500881825 mg457 cell division protein ftsh (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:z32663 pid:474069 gb:u00089 sp:p75120) (le:6176) (re:8284) (di:complement) U39727 U39727 g3845051 Mycoplasma genitalium 2097 -11540338 5000697625 (de:(mg457) (pn:cell division protein homolog:cell division protein:ftsh) (gn:ftsh) (gtcfc:12.8) (ec:3.4.24.-) (ftsh_mycge) (keggfc:11.1) (tigrfc:4.1) (db:gtc-mycoplasma genitalium)) MG457 MG457 Mycoplasma genitalium 2097 10015001

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921327	19472	41628	1551	516

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921334	19473	41629	183	60

Description

5000697626 competence locus e:come3:hypothetical protein mg316 (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-mycoplasma genitalium) MG316 MG316 Mycoplasma genitalium 2097 -11540339 109074 mg316 (de:hypothetical protein mg316) (db:swissprot) Y316_MYCGE P47558 MYCOPLASMA GENITALIUM 2097 -11540339 172313 competence locus e homolog (cl:competence locus e homolog) (db:pir2.dat) I64234 I64234 Mycoplasma genitalium 2097 -11540339 7500895114 mg316 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to pid:639786 gb:u00089 sp:q50361) (le:8050) (re:9159) (di:complement) U39712 U39712 g3844893 Mycoplasma genitalium 2097 -11540339 6500736481 competence locus e:come3:hypothetical protein mg316 (gtcfc:13.12) (keggfc:14.2) (tigrfc:4.6) (db:gtc-mycoplasma genitalium) MG316 MG316 Mycoplasma genitalium 2097 -11540339

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921355	19474	41630	720	239

Description

6500736482 gerbb:mg277 spore germination apparatus protein (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-mycoplasma genitalium) MG277 MG277 Mycoplasma genitalium 2097 -11540340 119045 mg277 (de:hypothetical protein mg277) (db:swissprot) Y277_MYCGE Q49409 MYCOPLASMA GENITALIUM 2097 -11540340 172671 spore germination apparatus protein gerbb homolog (db:pir2.dat) F64230 F64230 Mycoplasma genitalium 2097 -11540340 7500895054 mg277 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 29 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75387 pid:1674129 percent) (le:4333) (re:7245) (di:complement) U39707 U39707 g1045972 Mycoplasma genitalium 2097 -11540340 5000697627 (de:(mg277) (pn:spore germination apparatus protein:gerbb) (gn:gerbb) (gtcfc:13.2) (ec:) (keggfc:11.2) (tigrfc:14.1) (db:gtc-mycoplasma genitalium)) MG277 MG277 Mycoplasma genitalium 2097 10061490

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921356	19475	41631	801	266

Description

5000697628 osmotically inducible protein:osmc:hypothetical protein mg454 (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-mycoplasma genitalium) MG454 MG454 Mycoplasma genitalium 2097 -11540341 109181 mg454 (de:hypothetical protein mg454) (db:swissprot) Y454_MYCGE P47692 MYCOPLASMA GENITALIUM 2097 -11540341 172577 osmotically inducible protein osmc homolog (cl:hypothetical protein ykla) (db:pir2.dat) B64250 B64250 Mycoplasma genitalium 2097 -11540341 7500895326 mg454 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75123 pid:1673836 percent) (le:2985) (re:3452) (di:complement) U39727 U39727 g3845048 Mycoplasma genitalium 2097 -11540341 6500736483 osmotically inducible protein:osmc:hypothetical protein mg454 (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-mycoplasma genitalium) MG454 MG454 Mycoplasma genitalium 2097 -11540341

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921357	19476	41632	1215	404

Description

GTC ORF with score 355 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f7j7 (essaiiproject).) (nt:strong similarity to damage-specific dna binding) (le:12291:12993:13363) (re:12872:13277:13711) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921361	19477	41633	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921362	19478	41634	1881	626

Description

5000697629 soj protein:hypothetical protein mg470 (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-mycoplasma genitalium) MG470 MG470 Mycoplasma genitalium 2097 -11540342 109190 soj:mg470 (de:soj protein homolog) (db:swissprot) SOJ_MYCGE P47706 MYCOPLASMA GENITALIUM 2097 -11540342 172670 spooj regulator homolog (cl:regulatory protein spo0j) (db:pir2.dat) I64251 I64251 Mycoplasma genitalium 2097 -11540342 7500891851 mg470 soj protein soj (db:genpept-bct2) (de:mycoplasma genitalium section 51 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:q50314 pid:1209518) (le:1998) (re:2807) (di:complement) U39729 U39729 g3845067 Mycoplasma genitalium 2097 -11540342 6500736484 soj protein:hypothetical protein mg470 (gtcfc:13.2) (keggfc:14.2) (tigrfc:14.1) (db:gtc-mycoplasma genitalium) MG470 MG470 Mycoplasma genitalium 2097 -11540342

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921363	19479	41635	297	98

Description

5000697695 hypothetical protein mg011 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG011 MG011 Mycoplasma genitalium 2097 -11540343 108366 mg011 (de:hypothetical protein mg011) (db:swissprot) Y011_MYCGE P47257 MYCOPLASMA GENITALIUM 2097 -11540343 172442 hypothetical protein mg011 (db:pir2.dat) B64201 B64201 Mycoplasma genitalium 2097 -11540343 7500894521 mg011 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 2 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75098 pid:1673799 percent) (le:653) (re:1516) (di:complement) U39680 U39680 g3844623 Mycoplasma genitalium 2097 -11540343 6500736485 hypothetical protein mg011 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG011 MG011 Mycoplasma genitalium 2097 -11540343

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921371	19480	41636	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921373	19481	41637	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921379	19482	41638	585	194

Description

GTC ORF with score 189 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f7j7 (essaiiproject).) (nt:strong similarity to damage-specific dna binding) (le:12291:12993:13363) (re:12872:13277:13711) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921388	19483	41639	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921404	19484	41640	591	196

Description

5000697696 hypothetical protein mg017 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG017 MG017 Mycoplasma genitalium 2097 -11540344 108376 mg017 (de:hypothetical protein mg017) (db:swissprot) Y017_MYCGE P47263 MYCOPLASMA GENITALIUM 2097 -11540344 172444 hypothetical protein mg017 (db:pir2.dat) H64201 H64201 Mycoplasma genitalium 2097 -11540344 7500894532 mg017 atp-dependent rna helicase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 2 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75093 pid:1673793 percent) (le:7776) (re:8306) (di:direct) U39680 U39680 g1045686 Mycoplasma genitalium 2097 -11540344 6500736486 hypothetical protein mg017 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG017 MG017 Mycoplasma genitalium 2097 -11540344

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921409	19485	41641	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921411	19486	41642	1224	407

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921424	19487	41643	702	233

Description

5000697697 hypothetical protein mg027 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG027 MG027 Mycoplasma genitalium 2097 -11540345 108422 mg027 (de:hypothetical protein mg027) (db:swissprot) Y027_MYCGE P47273 MYCOPLASMA GENITALIUM 2097 -11540345 172445 hypothetical protein mg027 (db:pir2.dat) I64202 I64202 Mycoplasma genitalium 2097 -11540345 7500894547 mg027 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 4 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75084 pid:1673783 percent) (le:1573) (re:2028) (di:direct) U39682 U39682 g3844637 Mycoplasma genitalium 2097 -11540345 6500736487 hypothetical protein mg027 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG027 MG027 Mycoplasma genitalium 2097 -11540345

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921427	19488	41644	744	247

Description

5000697698 hypothetical protein mg028 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG028 MG028 Mycoplasma genitalium 2097 -11540346 108424 mg028 (de:hypothetical protein mg028) (db:swissprot) Y028_MYCGE P47274 MYCOPLASMA GENITALIUM 2097 -11540346 172446 hypothetical protein mg028 (db:pir2.dat) A64203 A64203 Mycoplasma genitalium 2097 -11540346 7500894552 mg028 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 4 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75083 pid:1673782 percent) (le:2028) (re:2633) (di:direct) U39682 U39682 g3844638 Mycoplasma genitalium 2097 -11540346 6500736488 hypothetical protein mg028 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG028 MG028 Mycoplasma genitalium 2097 -11540346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921442	19489	41645	810	269

Description

5000697700 hypothetical protein mg055 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG055 MG055 Mycoplasma genitalium 2097 -11540347 108539 mg055 (de:hypothetical protein mg055) (db:swissprot) Y055_MYCGE P47301 MYCOPLASMA GENITALIUM 2097 -11540347 172448 hypothetical protein mg055 (db:pir2.dat) A64206 A64206 Mycoplasma genitalium 2097 -11540347 7500894599 mg055 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 6 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75048 pid:1673741 percent) (le:14279) (re:14650) (di:complement) U39684 U39684 g1045728 Mycoplasma genitalium 2097 -11540347 6500736489 hypothetical protein mg055 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG055 MG055 Mycoplasma genitalium 2097 -11540347

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921455	19490	41646	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921456	19491	41647	243	80

Description

GTC ORF with score 170 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c4b4.) (nt:spbc4b4.09, unknown; final exon may be incorrect) (le:21876:22015:22252:22401) (re:21967:22201:22355:22568) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921469	19492	41648	1488	495

Description

GTC ORF with score 1046 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c4b4.) (nt:spbc4b4.09, unknown; final exon may be incorrect) (le:21876:22015:22252:22401) (re:21967:22201:22355:22568) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921472	19493	41649	2010	669

Description

5000697701 hypothetical protein mg064 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG064 MG064 Mycoplasma genitalium 2097 -11540348 108587 mg064 (de:hypothetical protein mg064) (db:swissprot) Y064_MYCGE P47310 MYCOPLASMA GENITALIUM 2097 -11540348 172449 hypothetical protein mg064 (db:pir2.dat) A64207 A64207 Mycoplasma genitalium 2097 -11540348 7500894621 m. genitalium predicted coding region mg064 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium spase, deva_1, fruk, tkta genes from bases72595 to 86160 (section 8 of 56) of the complete genome.) (nt:identified by genemark; putative) (le:1472) (re:... U39686 U39686 g1045739 Mycoplasma genitalium 2097 -11540348 6500736490 hypothetical protein mg064 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG064 MG064 Mycoplasma genitalium 2097 -11540348

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921483	19494	41650	639	212

Description

5000697702 hypothetical lipoprotein mg068 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG068 MG068 Mycoplasma genitalium 2097 -11540349 108595 mg068 (de:hypothetical lipoprotein mg068 precursor) (db:swissprot) Y068_MYCGE P47314 MYCOPLASMA GENITALIUM 2097 -11540349 172450 hypothetical protein mg068 (cl:hypothetical protein mg068) (db:pir2.dat) E64207 E64207 Mycoplasma genitalium 2097 -11540349 7500894630 mg068 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 8 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75609 pid:1673724 percent) (le:9089) (re:10513) (di:direct) U39686 U39686 g1045743 Mycoplasma genitalium 2097 -11540349 6500736491 hypothetical lipoprotein mg068 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG068 MG068 Mycoplasma genitalium 2097 -11540349

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921497	19495	41651	1608	535

Description

5000697703 hypothetical protein mg074 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG074 MG074 Mycoplasma genitalium 2097 -11540350 108630 mg074 (de:hypothetical protein mg074) (db:swissprot) Y074_MYCGE P47320 MYCOPLASMA GENITALIUM 2097 -11540350 172451 hypothetical protein mg074 (cl:hypothetical protein mg074) (db:pir2.dat) B64208 B64208 Mycoplasma genitalium 2097 -11540350 7500894636 mg074 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 9 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75557 pid:1674322) (le:12800) (re:13213) (di:direct) U39687 U39687 g1045750 Mycoplasma genitalium 2097 -11540350 6500736492 hypothetical protein mg074 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG074 MG074 Mycoplasma genitalium 2097 -11540350

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921509	19496	41652	420	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921510	19497	41653	375	124

Description

5000697704 hypothetical protein mg075 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG075 MG075 Mycoplasma genitalium 2097 -11540351 108632 mg075 (de:hypothetical protein mg075) (db:swissprot) Y075_MYCGE P47321 MYCOPLASMA GENITALIUM 2097 -11540351 172452 hypothetical protein mg075 (db:pir2.dat) C64208 C64208 Mycoplasma genitalium 2097 -11540351 7500894642 mg075 116 kda surface antigen (db:genpept-bct2) (de:mycoplasma genitalium section 10 of 51 of the complete genome.) (nt:similar to gp:2222735 percent identity: 50.94;) (le:43) (re:3117) (di:direct) U39688 U39688 g3844665 Mycoplasma genitalium 2097 -11540351 6500736493 hypothetical protein mg075 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG075 MG075 Mycoplasma genitalium 2097 -11540351

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921516	19498	41654	1278	425

Description

5000697705 hypothetical protein mg076 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG076 MG076 Mycoplasma genitalium 2097 -11540352 108634 mg076 (de:hypothetical protein mg076) (db:swissprot) Y076_MYCGE P47322 MYCOPLASMA GENITALIUM 2097 -11540352 172453 hypothetical protein mg076 (db:pir2.dat) D64208 D64208 Mycoplasma genitalium 2097 -11540352 7500894648 mg076 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 10 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75555 pid:1674320 percent) (le:3114) (re:3530) (di:complement) U39688 U39688 g3844666 Mycoplasma genitalium 2097 -11540352 6500736494 hypothetical protein mg076 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG076 MG076 Mycoplasma genitalium 2097 -11540352

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921521	19499	41655	471	156

Description

5000697706 hypothetical lipoprotein mg095 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG095 MG095 Mycoplasma genitalium 2097 -11540353 108710 mg095 (de:hypothetical lipoprotein mg095 precursor) (db:swissprot) Y095_MYCGE P47341 MYCOPLASMA GENITALIUM 2097 -11540353 172454 hypothetical protein mg095 (db:pir2.dat) E64210 E64210 Mycoplasma genitalium 2097 -11540353 7500894673 mg095 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75538 pid:1674300 percent) (le:10968) (re:12164) (di:direct) U39689 U39689 g3844682 Mycoplasma genitalium 2097 -11540353 6500736495 hypothetical lipoprotein mg095 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG095 MG095 Mycoplasma genitalium 2097 -11540353

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921532	19500	41656	192	63

Description

5000697707 hypothetical protein mg096 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG096 MG096 Mycoplasma genitalium 2097 -11540354 108713 mg096 (de:hypothetical protein mg096) (db:swissprot) Y096_MYCGE P47342 MYCOPLASMA GENITALIUM 2097 -11540354 172455 hypothetical protein mg096 (cl:hypothetical protein mg096) (db:pir2.dat) F64210 F64210 Mycoplasma genitalium 2097 -11540354 7500894680 m. genitalium predicted coding region mg096 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium aux2, p48, trxb, ung genes from bases 121638to 131279 (section 11 of 56) of the complete genome.) (nt:identified by genemark; putative) (le:302) (re:188... U39689 U39689 g1045774 Mycoplasma genitalium 2097 -11540354 6500736496 hypothetical protein mg096 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG096 MG096 Mycoplasma genitalium 2097 -11540354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921533	19501	41657	228	75

Description

5000697708 hypothetical protein mg101 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG101 MG101 Mycoplasma genitalium 2097 -11540355 108724 mg101 (de:hypothetical protein mg101) (db:swissprot) Y101_MYCGE P47347 MYCOPLASMA GENITALIUM 2097 -11540355 172456 hypothetical protein mg101 (db:pir2.dat) B64211 B64211 Mycoplasma genitalium 2097 -11540355 7500894701 mg101 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 12 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75532 pid:1674294 percent) (le:7238) (re:7906) (di:direct) U39690 U39690 g3844689 Mycoplasma genitalium 2097 -11540355 6500736497 hypothetical protein mg101 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG101 MG101 Mycoplasma genitalium 2097 -11540355

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921534	19502	41658	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921545	19503	41659	672	223

Description

5000697709 hypothetical protein mg103 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG103 MG103 Mycoplasma genitalium 2097 -11540356 108730 mg103 (de:hypothetical protein mg103) (db:swissprot) Y103_MYCGE P47349 MYCOPLASMA GENITALIUM 2097 -11540356 172457 hypothetical protein mg103 (db:pir2.dat) D64211 D64211 Mycoplasma genitalium 2097 -11540356 7500894705 mg103 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 12 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75530 pid:1674292 percent) (le:8836) (re:9678) (di:direct) U39690 U39690 g3844691 Mycoplasma genitalium 2097 -11540356 6500736498 hypothetical protein mg103 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG103 MG103 Mycoplasma genitalium 2097 -11540356

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921558	19504	41660	771	256

Description

5000697710 hypothetical protein mg105 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG105 MG105 Mycoplasma genitalium 2097 -11540357 108734 mg105 (de:hypothetical protein mg105) (db:swissprot) Y105_MYCGE P47351 MYCOPLASMA GENITALIUM 2097 -11540357 172458 hypothetical protein mg105 (cl:hypothetical protein ybbp) (db:pir2.dat) F64211 F64211 Mycoplasma genitalium 2097 -11540357 7500894711 mg105 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 13 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75528 pid:1674289 percent) (le:2345) (re:2947) (di:direct) U39691 U39691 g3844694 Mycoplasma genitalium 2097 -11540357 6500736499 hypothetical protein mg105 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG105 MG105 Mycoplasma genitalium 2097 -11540357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921562	19505	41661	483	160

Description

5000697711 hypothetical protein mg116 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG116 MG116 Mycoplasma genitalium 2097 -11540358 108769 mg116 (de:hypothetical protein mg116) (db:swissprot) Y116_MYCGE P47362 MYCOPLASMA GENITALIUM 2097 -11540358 172460 hypothetical protein mg116 (db:pir2.dat) H64212 H64212 Mycoplasma genitalium 2097 -11540358 7500894730 mg116 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 14 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75519 pid:1674278 percent) (le:500) (re:1255) (di:direct) U39692 U39692 g3844706 Mycoplasma genitalium 2097 -11540358 6500736500 hypothetical protein mg116 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG116 MG116 Mycoplasma genitalium 2097 -11540358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921571	19506	41662	348	115

Description

5000697712 hypothetical protein mg117 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG117 MG117 Mycoplasma genitalium 2097 -11540359 108773 mg117 (de:hypothetical protein mg117) (db:swissprot) Y117_MYCGE P47363 MYCOPLASMA GENITALIUM 2097 -11540359 172461 hypothetical protein mg117 (cl:hypothetical protein mg117) (db:pir2.dat) I64212 I64212 Mycoplasma genitalium 2097 -11540359 7500894733 mg117 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 14 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75518 pid:1674277 percent) (le:1248) (re:1892) (di:direct) U39692 U39692 g3844707 Mycoplasma genitalium 2097 -11540359 6500736501 hypothetical protein mg117 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG117 MG117 Mycoplasma genitalium 2097 -11540359

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921581	19507	41663	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921583	19508	41664	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921585	19509	41665	762	253

Description

5000697713 hypothetical protein mg133 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG133 MG133 Mycoplasma genitalium 2097 -11540360 172462 hypothetical protein mg133 (db:pir2.dat) G64214 G64214 Mycoplasma genitalium 2097 -11540360 7500965556 mg133 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75503 pid:1674260 percent) (le:6250) (re:6936) (di:complement) U39693 U39693 g3844723 Mycoplasma genitalium 2097 -11540360 6500736502 hypothetical protein mg133 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG133 MG133 Mycoplasma genitalium 2097 -11540360

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921591	19510	41666	444	147

Description

5000697714 hypothetical atp-binding protein mg140 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG140 MG140 Mycoplasma genitalium 2097 -11540361 108865 mg140 (de:hypothetical atp-binding protein mg140) (db:swissprot) Y140_MYCGE P47386 MYCOPLASMA GENITALIUM 2097 -11540361 172463 hypothetical protein mg140 (db:pir2.dat) E64215 E64215 Mycoplasma genitalium 2097 -11540361 7500894774 mg140 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75033 pid:1673646 percent) (le:537) (re:3878) (di:direct) U39695 U39695 g3844733 Mycoplasma genitalium 2097 -11540361 6500736503 hypothetical atp-binding protein mg140 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG140 MG140 Mycoplasma genitalium 2097 -11540361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921601	19511	41667	426	141

Description

5000697715 hypothetical protein mg144 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG144 MG144 Mycoplasma genitalium 2097 -11540362 108871 mg144 (de:hypothetical protein mg144) (db:swissprot) Y144_MYCGE P47390 MYCOPLASMA GENITALIUM 2097 -11540362 172464 hypothetical protein mg144 (db:pir2.dat) I64215 I64215 Mycoplasma genitalium 2097 -11540362 7500894783 mg144 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75588 pid:1674380 percent) (le:7946) (re:8785) (di:direct) U39695 U39695 g3844737 Mycoplasma genitalium 2097 -11540362 6500736504 hypothetical protein mg144 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG144 MG144 Mycoplasma genitalium 2097 -11540362

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921602	19512	41668	546	181

Description

5000697716 hypothetical protein mg147 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG147 MG147 Mycoplasma genitalium 2097 -11540363 108880 mg147 (de:hypothetical protein mg147) (db:swissprot) Y147_MYCGE P47393 MYCOPLASMA GENITALIUM 2097 -11540363 172465 hypothetical protein mg147 (db:pir2.dat) C64216 C64216 Mycoplasma genitalium 2097 -11540363 7500894791 mg147 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75585 pid:1674377 percent) (le:10868) (re:11995) (di:direct) U39695 U39695 g3844740 Mycoplasma genitalium 2097 -11540363 6500736505 hypothetical protein mg147 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG147 MG147 Mycoplasma genitalium 2097 -11540363

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921605	19513	41669	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921606	19514	41670	261	86

Description

5000697717 hypothetical lipoprotein mg149 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG149 MG149 Mycoplasma genitalium 2097 -11540364 108883 mg149 (de:hypothetical lipoprotein mg149 precursor) (db:swissprot) Y149_MYCGE P47395 MYCOPLASMA GENITALIUM 2097 -11540364 172466 hypothetical protein mg149 (db:pir2.dat) E64216 E64216 Mycoplasma genitalium 2097 -11540364 7500894796 mg149 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 18 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75583 pid:1674375 percent) (le:69) (re:914) (di:direct) U39696 U39696 g3844743 Mycoplasma genitalium 2097 -11540364 6500736506 hypothetical lipoprotein mg149 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG149 MG149 Mycoplasma genitalium 2097 -11540364

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921616	19515	41671	423	140

Description

5000697718 hypothetical lipoprotein mg185 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG185 MG185 Mycoplasma genitalium 2097 -11540365 108950 mg185 (de:hypothetical lipoprotein mg185 precursor) (db:swissprot) Y185_MYCGE P47431 MYCOPLASMA GENITALIUM 2097 -11540365 172468 hypothetical protein mg185 (cl:hypothetical protein mg185) (db:pir2.dat) E64220 E64220 Mycoplasma genitalium 2097 -11540365 7500894837 mg185 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215689 gb:u00089 sp:q50289) (le:8807) (re:10912) (di:direct) U39697 U39697 g3844781 Mycoplasma genitalium 2097 -11540365 6500736507 hypothetical lipoprotein mg185 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG185 MG185 Mycoplasma genitalium 2097 -11540365

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921632	19516	41672	936	311

Description

5000697720 hypothetical protein mg199 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG199 MG199 Mycoplasma genitalium 2097 -11540366 108968 mg199 (de:hypothetical protein mg199) (db:swissprot) Y199_MYCGE P47441 MYCOPLASMA GENITALIUM 2097 -11540366 172470 hypothetical protein mg199 (cl:hypothetical protein mg199) (db:pir2.dat) I64221 I64221 Mycoplasma genitalium 2097 -11540366 7500894854 mg199 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 21 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75446 pid:1673685 percent) (le:6061) (re:6564) (di:complement) U39699 U39699 g3844796 Mycoplasma genitalium 2097 -11540366 6500736508 hypothetical protein mg199 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG199 MG199 Mycoplasma genitalium 2097 -11540366

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921637	19517	41673	1113	370

Description

5000697721 hypothetical protein mg202 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG202 MG202 Mycoplasma genitalium 2097 -11540367 108973 mg202 (de:hypothetical protein mg202) (db:swissprot) Y202_MYCGE P47444 MYCOPLASMA GENITALIUM 2097 -11540367 172471 hypothetical protein mg202 (db:pir2.dat) C64222 C64222 Mycoplasma genitalium 2097 -11540367 7500894876 mg202 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 21 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75353 pid:1673681 percent) (le:9296) (re:9664) (di:direct) U39699 U39699 g3844799 Mycoplasma genitalium 2097 -11540367 6500736509 hypothetical protein mg202 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG202 MG202 Mycoplasma genitalium 2097 -11540367

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921642	19518	41674	597	198

Description

5000697722 hypothetical protein mg207 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG207 MG207 Mycoplasma genitalium 2097 -11540368 172472 conserved hypothetical protein mg207 (cl:conserved hypothetical protein mg207:phosphoesterase core homology) (db:pir2.dat) H64222 H64222 Mycoplasma genitalium 2097 -11540368 7500954192 m. genitalium predicted coding region mg207 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium lsp, pfk, plsc, pyk, trna-asp, trna-cys,trna-f-met, trna-ile_2, trna-met, trna-phe, trna-pro, trna-ser_2genes from bases 245836 to 257984 (section 20 of... U39698 U39698 g1045893 Mycoplasma genitalium 2097 -11540368 6500736510 hypothetical protein mg207 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG207 MG207 Mycoplasma genitalium 2097 -11540368

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921645	19519	41675	1560	519

Description

GTC ORF with score 462 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c1a4 left hand region 1-26184 bporiginates from chimeric cosmid.) (nt:spbc1a4.06c, len:383aa, similarity: to ygr046w,) (le:14950:15611:15955) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921654	19520	41676	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921669	19521	41677	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921674	19522	41678	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921680	19523	41679	1260	419

Description

5000697723 hypothetical protein mg208 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG208 MG208 Mycoplasma genitalium 2097 -11540369 108979 mg208 (de:hypothetical protein mg208) (db:swissprot) Y208_MYCGE P47450 MYCOPLASMA GENITALIUM 2097 -11540369 172473 hypothetical protein mg208 (db:pir2.dat) I64222 I64222 Mycoplasma genitalium 2097 -11540369 7500894880 mg208 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 22 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75486 pid:1674241 percent) (le:7609) (re:8199) (di:complement) U39700 U39700 g3844806 Mycoplasma genitalium 2097 -11540369 6500736511 hypothetical protein mg208 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG208 MG208 Mycoplasma genitalium 2097 -11540369

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921688	19524	41680	1839	612

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921689	19525	41681	228	75

Description

5000697724 hypothetical protein mg211 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG211 MG211 Mycoplasma genitalium 2097 -11540370 108983 mg211 (de:hypothetical protein mg211) (db:swissprot) Y211_MYCGE P47453 MYCOPLASMA GENITALIUM 2097 -11540370 172474 hypothetical protein mg211 (db:pir2.dat) C64223 C64223 Mycoplasma genitalium 2097 -11540370 7500894885 mg211 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75481 pid:1674235 percent) (le:126) (re:569) (di:direct) U39701 U39701 g3844811 Mycoplasma genitalium 2097 -11540370 6500736512 hypothetical protein mg211 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG211 MG211 Mycoplasma genitalium 2097 -11540370

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921698	19526	41682	1989	662

Description

5000697725 hypothetical protein mg218 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG218 MG218 Mycoplasma genitalium 2097 -11540371 108989 hmw2:mg218 (de:protein 2)) (db:swissprot) HMW2_MYCGE P47460 MYCOPLASMA GENITALIUM 2097 -11540371 172475 hypothetical protein mg218 (cl:mycoplasma genitalium hypothetical protein mg218) (db:pir2.dat) A64224 A64224 Mycoplasma genitalium 2097 -11540371 7500883440 mg218 cytadherence accessory protein hmw2 (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75471 pid:1674221) (le:8305) (re:13722) (di:direct) U39701 U39701 g3844818 Mycoplasma genitalium 2097 -11540371 6500736513 hypothetical protein mg218 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG218 MG218 Mycoplasma genitalium 2097 -11540371

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921710	19527	41683	402	133

Description

5000697726 hypothetical protein mg223 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG223 MG223 Mycoplasma genitalium 2097 -11540372 108996 mg223 (de:hypothetical protein mg223) (db:swissprot) Y223_MYCGE P47465 MYCOPLASMA GENITALIUM 2097 -11540372 172476 hypothetical protein mg223 (db:pir2.dat) F64224 F64224 Mycoplasma genitalium 2097 -11540372 7500894905 mg223 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75465 pid:1674215 percent) (le:1959) (re:3194) (di:direct) U39702 U39702 g3844826 Mycoplasma genitalium 2097 -11540372 6500736514 hypothetical protein mg223 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG223 MG223 Mycoplasma genitalium 2097 -11540372

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921722	19528	41684	195	64

Description

5000697727 hypothetical protein mg230 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG230 MG230 Mycoplasma genitalium 2097 -11540373 109001 nrdi:mg230 (de:nrdi protein) (db:swissprot) NRDI_MYCGE P47472 MYCOPLASMA GENITALIUM 2097 -11540373 172477 hypothetical protein mg230 (db:pir2.dat) D64225 D64225 Mycoplasma genitalium 2097 -11540373 7500886579 mg230 nrdi protein nrdi (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75460 pid:1674207 percent) (le:10114) (re:10575) (di:direct) U39702 U39702 g3844833 Mycoplasma genitalium 2097 -11540373 6500736515 hypothetical protein mg230 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG230 MG230 Mycoplasma genitalium 2097 -11540373

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921725	19529	41685	462	153

Description

5000697728 hypothetical protein mg236 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG236 MG236 Mycoplasma genitalium 2097 -11540374 109005 mg236 (de:hypothetical protein mg236) (db:swissprot) Y236_MYCGE P47478 MYCOPLASMA GENITALIUM 2097 -11540374 172478 hypothetical protein mg236 (db:pir2.dat) A64226 A64226 Mycoplasma genitalium 2097 -11540374 7500894936 mg236 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75456 pid:1674201 percent) (le:1836) (re:2258) (di:direct) U39703 U39703 g3844840 Mycoplasma genitalium 2097 -11540374 6500736516 hypothetical protein mg236 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG236 MG236 Mycoplasma genitalium 2097 -11540374

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921727	19530	41686	249	82

Description

5000697729 hypothetical protein mg237 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG237 MG237 Mycoplasma genitalium 2097 -11540375 109007 mg237 (de:hypothetical protein mg237) (db:swissprot) Y237_MYCGE P47479 MYCOPLASMA GENITALIUM 2097 -11540375 172479 hypothetical protein mg237 (db:pir2.dat) B64226 B64226 Mycoplasma genitalium 2097 -11540375 7500894938 mg237 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75455 pid:1674200 percent) (le:2251) (re:3135) (di:direct) U39703 U39703 g3844841 Mycoplasma genitalium 2097 -11540375 6500736517 hypothetical protein mg237 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG237 MG237 Mycoplasma genitalium 2097 -11540375

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921739	19531	41687	246	81

Description

5000697730 hypothetical protein mg241 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG241 MG241 Mycoplasma genitalium 2097 -11540376 109010 mg241 (de:hypothetical protein mg241) (db:swissprot) Y241_MYCGE P47483 MYCOPLASMA GENITALIUM 2097 -11540376 172480 hypothetical protein mg241 (cl:mycoplasma genitalium hypothetical protein mg241) (db:pir2.dat) F64226 F64226 Mycoplasma genitalium 2097 -11540376 7500894942 mg241 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75441 pid:1674192 percent) (le:8057) (re:9919) (di:direct) U39703 U39703 g3844845 Mycoplasma genitalium 2097 -11540376 6500736518 hypothetical protein mg241 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG241 MG241 Mycoplasma genitalium 2097 -11540376

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921759	19532	41688	297	98

Description

5000697731 hypothetical protein mg242 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG242 MG242 Mycoplasma genitalium 2097 -11540377 109012 mg242 (de:hypothetical protein mg242) (db:swissprot) Y242_MYCGE P47484 MYCOPLASMA GENITALIUM 2097 -11540377 172481 hypothetical protein mg242 (cl:mycoplasma genitalium hypothetical protein mg241) (db:pir2.dat) G64226 G64226 Mycoplasma genitalium 2097 -11540377 7500894945 mg242 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75440 pid:1674191 percent) (le:9925) (re:11817) (di:direct) U39703 U39703 g3844846 Mycoplasma genitalium 2097 -11540377 6500736519 hypothetical protein mg242 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG242 MG242 Mycoplasma genitalium 2097 -11540377

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921760	19533	41689	999	332

Description

5000697732 hypothetical protein mg243 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG243 MG243 Mycoplasma genitalium 2097 -11540378 109014 mg243 (de:hypothetical protein mg243) (db:swissprot) Y243_MYCGE P47485 MYCOPLASMA GENITALIUM 2097 -11540378 172482 hypothetical protein mg243 (db:pir2.dat) H64226 H64226 Mycoplasma genitalium 2097 -11540378 7500894951 m. genitalium predicted coding region mg243 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium cyss, dnae_2, lig, mutb1, rpod, siga,trna-gly_1 genes from bases 290785 to 306437 (section 25 of 56) ofthe complete genome.) (nt:identified by genemark;... U39703 U39703 g1045934 Mycoplasma genitalium 2097 -11540378 6500736520 hypothetical protein mg243 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG243 MG243 Mycoplasma genitalium 2097 -11540378

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921762	19534	41690	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921768	19535	41691	393	130

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921775	19536	41692	645	214

Description

GTC ORF with score 144 to: (sr:streptomyces hygroscopicus (tissue library: atcc 21705) dna) (db:genpept-bct1) (de:streptomyces hygroscopicus acetyl-hydrolase (bah), thioesterase(orf1 and 2), transport protein (orf3), and regulatory protein(brpa) genes,...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921785	19537	41693	270	89

Description

5000697733 hypothetical protein mg246 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG246 MG246 Mycoplasma genitalium 2097 -11540379 109018 mg246 (de:hypothetical protein mg246) (db:swissprot) Y246_MYCGE P47488 MYCOPLASMA GENITALIUM 2097 -11540379 172483 hypothetical protein mg246 (cl:hypothetical protein ymdb) (db:pir2.dat) B64227 B64227 Mycoplasma genitalium 2097 -11540379 7500894960 mg246 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75429 pid:1674178 percent) (le:15109) (re:15954) (di:direct) U39703 U39703 g1045937 Mycoplasma genitalium 2097 -11540379 6500736521 hypothetical protein mg246 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG246 MG246 Mycoplasma genitalium 2097 -11540379

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921796	19538	41694	741	247

Description

5000697734 hypothetical protein mg255 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG255 MG255 Mycoplasma genitalium 2097 -11540380 109027 mg255 (de:hypothetical protein mg255) (db:swissprot) Y255_MYCGE P47497 MYCOPLASMA GENITALIUM 2097 -11540380 172484 hypothetical protein mg255 (db:pir2.dat) B64228 B64228 Mycoplasma genitalium 2097 -11540380 7500894978 mg255 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75422 pid:1674169 percent) (le:7378) (re:8475) (di:direct) U39704 U39704 g3844853 Mycoplasma genitalium 2097 -11540380 6500736522 hypothetical protein mg255 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG255 MG255 Mycoplasma genitalium 2097 -11540380

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921808	19539	41695	741	246

Description

5000697735 hypothetical protein mg256 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG256 MG256 Mycoplasma genitalium 2097 -11540381 109029 mg256 (de:hypothetical protein mg256) (db:swissprot) Y256_MYCGE P47498 MYCOPLASMA GENITALIUM 2097 -11540381 172485 hypothetical protein mg256 (db:pir2.dat) C64228 C64228 Mycoplasma genitalium 2097 -11540381 7500894981 mg256 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 26 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75421 pid:1674168 percent) (le:9198) (re:9968) (di:direct) U39704 U39704 g1045948 Mycoplasma genitalium 2097 -11540381 6500736523 hypothetical protein mg256 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG256 MG256 Mycoplasma genitalium 2097 -11540381

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921809	19540	41696	645	214

Description

5000697736 hypothetical protein mg267 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG267 MG267 Mycoplasma genitalium 2097 -11540382 109038 mg267 (de:hypothetical protein mg267) (db:swissprot) Y267_MYCGE P47509 MYCOPLASMA GENITALIUM 2097 -11540382 172486 hypothetical protein mg267 (db:pir2.dat) E64229 E64229 Mycoplasma genitalium 2097 -11540382 7500895006 mg267 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75397 pid:1674140 percent) (le:4724) (re:5071) (di:complement) U39706 U39706 g3844863 Mycoplasma genitalium 2097 -11540382 6500736524 hypothetical protein mg267 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG267 MG267 Mycoplasma genitalium 2097 -11540382

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921813	19541	41697	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921815	19542	41698	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921821	19543	41699	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921828	19544	41700	495	164

Description

5000697737 hypothetical protein mg279 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG279 MG279 Mycoplasma genitalium 2097 -11540383 109042 mg279 (de:hypothetical protein mg279) (db:swissprot) Y279_MYCGE P47521 MYCOPLASMA GENITALIUM 2097 -11540383 172487 hypothetical protein mg279 (db:pir2.dat) H64230 H64230 Mycoplasma genitalium 2097 -11540383 7500895057 mg279 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 29 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75385 pid:1674127 percent) (le:9447) (re:10103) (di:complement) U39707 U39707 g1045974 Mycoplasma genitalium 2097 -11540383 6500736525 hypothetical protein mg279 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG279 MG279 Mycoplasma genitalium 2097 -11540383

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921841	19545	41701	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921847	19546	41702	258	85

Description

5000697738 hypothetical protein mg281 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG281 MG281 Mycoplasma genitalium 2097 -11540384 109045 mg281 (de:hypothetical protein mg281) (db:swissprot) Y281_MYCGE P47523 MYCOPLASMA GENITALIUM 2097 -11540384 172488 hypothetical protein mg281 (cl:mycoplasma genitalium hypothetical protein mg281) (db:pir2.dat) A64231 A64231 Mycoplasma genitalium 2097 -11540384 7500895063 mg281 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 30 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75383 pid:1674125 percent) (le:87) (re:1757) (di:complement) U39708 U39708 g1045977 Mycoplasma genitalium 2097 -11540384 6500736526 hypothetical protein mg281 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG281 MG281 Mycoplasma genitalium 2097 -11540384

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921855	19547	41703	702	233

Description

5000697739 hypothetical protein mg284 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG284 MG284 Mycoplasma genitalium 2097 -11540385 109048 mg284 (de:hypothetical protein mg284) (db:swissprot) Y284_MYCGE P47526 MYCOPLASMA GENITALIUM 2097 -11540385 172489 hypothetical protein mg284 (db:pir2.dat) D64231 D64231 Mycoplasma genitalium 2097 -11540385 7500895065 mg284 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 30 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75381 pid:1674121 percent) (le:4908) (re:5306) (di:direct) U39708 U39708 g1045980 Mycoplasma genitalium 2097 -11540385 6500736527 hypothetical protein mg284 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG284 MG284 Mycoplasma genitalium 2097 -11540385

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921861	19548	41704	1500	499

Description

5000697740 hypothetical protein mg285 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG285 MG285 Mycoplasma genitalium 2097 -11540386 109049 mg285 (de:hypothetical protein mg285) (db:swissprot) Y285_MYCGE P47527 MYCOPLASMA GENITALIUM 2097 -11540386 172490 hypothetical protein mg285 (db:pir2.dat) E64231 E64231 Mycoplasma genitalium 2097 -11540386 7500895070 mg285 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 30 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75380 pid:1674120 percent) (le:5269) (re:6312) (di:direct) U39708 U39708 g1045981 Mycoplasma genitalium 2097 -11540386 6500736528 hypothetical protein mg285 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG285 MG285 Mycoplasma genitalium 2097 -11540386

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921865	19549	41705	2490	829

Description

5000697741 hypothetical protein mg286 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG286 MG286 Mycoplasma genitalium 2097 -11540387 109050 mg286 (de:hypothetical protein mg286) (db:swissprot) Y286_MYCGE P47528 MYCOPLASMA GENITALIUM 2097 -11540387 172491 hypothetical protein mg286 (db:pir2.dat) F64231 F64231 Mycoplasma genitalium 2097 -11540387 7500895074 mg286 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 30 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75379 pid:1674119 percent) (le:6315) (re:6905) (di:direct) U39708 U39708 g1045982 Mycoplasma genitalium 2097 -11540387 6500736529 hypothetical protein mg286 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG286 MG286 Mycoplasma genitalium 2097 -11540387

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921869	19550	41706	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921870	19551	41707	834	277

Description

5000697742 hypothetical protein mg296 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG296 MG296 Mycoplasma genitalium 2097 -11540388 109059 mg296 (de:hypothetical protein mg296) (db:swissprot) Y296_MYCGE P47538 MYCOPLASMA GENITALIUM 2097 -11540388 172492 hypothetical protein mg296 (db:pir2.dat) G64232 G64232 Mycoplasma genitalium 2097 -11540388 7500895085 mg296 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 31 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75364 pid:1674102 percent) (le:10204) (re:10593) (di:complement) U39709 U39709 g3844875 Mycoplasma genitalium 2097 -11540388 6500736530 hypothetical protein mg296 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG296 MG296 Mycoplasma genitalium 2097 -11540388

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921872	19552	41708	387	128

Description

5000697743 p115 protein homolog (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG298 MG298 Mycoplasma genitalium 2097 -11540389 88060 mg298 (de:p115 protein homolog) (db:swissprot) P115_MYCGE P47540 MYCOPLASMA GENITALIUM 2097 -11540389 172608 protein p115 homolog (cl:conserved hypothetical p115 protein) (db:pir2.dat) I64232 I64232 Mycoplasma genitalium 2097 -11540389 7500887457 mg298 p115 protein (db:genpept-bct2) (de:mycoplasma genitalium section 32 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75361 pid:1674099 percent) (le:1138) (re:4086) (di:complement) U39710 U39710 g1045996 Mycoplasma genitalium 2097 -11540389 6500736531 p115 protein homolog (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG298 MG298 Mycoplasma genitalium 2097 -11540389

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921879	19553	41709	756	251

Description

5000697744 hypothetical protein mg302 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG302 MG302 Mycoplasma genitalium 2097 -11540390 109063 mg302 (de:hypothetical protein mg302) (db:swissprot) Y302_MYCGE P47544 MYCOPLASMA GENITALIUM 2097 -11540390 172493 hypothetical protein mg302 (db:pir2.dat) D64233 D64233 Mycoplasma genitalium 2097 -11540390 7500895089 mg302 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 32 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75357 pid:1674094 percent) (le:7550) (re:8503) (di:complement) U39710 U39710 g3844881 Mycoplasma genitalium 2097 -11540390 6500736532 hypothetical protein mg302 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG302 MG302 Mycoplasma genitalium 2097 -11540390

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921889	19554	41710	741	246

Description

5000697745 hypothetical protein mg306 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG306 MG306 Mycoplasma genitalium 2097 -11540391 109066 mg306 (de:hypothetical protein mg306) (db:swissprot) Y306_MYCGE P47548 MYCOPLASMA GENITALIUM 2097 -11540391 172494 hypothetical protein mg306 (db:pir2.dat) H64233 H64233 Mycoplasma genitalium 2097 -11540391 7500895098 mg306 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 33 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75343 pid:1674089 percent) (le:1994) (re:3175) (di:complement) U39711 U39711 g3844885 Mycoplasma genitalium 2097 -11540391 6500736533 hypothetical protein mg306 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG306 MG306 Mycoplasma genitalium 2097 -11540391

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921890	19555	41711	489	162

Description

5000697746 hypothetical lipoprotein mg307 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG307 MG307 Mycoplasma genitalium 2097 -11540392 109067 mg307 (de:hypothetical lipoprotein mg307 precursor) (db:swissprot) Y307_MYCGE P47549 MYCOPLASMA GENITALIUM 2097 -11540392 172495 hypothetical protein mg307 (db:pir2.dat) I64233 I64233 Mycoplasma genitalium 2097 -11540392 7500895100 mg307 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 33 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75342 pid:1674088 percent) (le:3175) (re:6708) (di:complement) U39711 U39711 g3844886 Mycoplasma genitalium 2097 -11540392 6500736534 hypothetical lipoprotein mg307 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG307 MG307 Mycoplasma genitalium 2097 -11540392

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921891	19556	41712	333	110

Description

5000697747 hypothetical lipoprotein mg309 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG309 MG309 Mycoplasma genitalium 2097 -11540393 109070 mg309 (de:hypothetical lipoprotein mg309 precursor) (db:swissprot) Y309_MYCGE P47551 MYCOPLASMA GENITALIUM 2097 -11540393 172496 hypothetical protein mg309 (db:pir2.dat) B64234 B64234 Mycoplasma genitalium 2097 -11540393 7500895104 mg309 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 33 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75334 pid:1674079 percent) (le:7932) (re:11609) (di:complement) U39711 U39711 g3844888 Mycoplasma genitalium 2097 -11540393 6500736535 hypothetical lipoprotein mg309 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG309 MG309 Mycoplasma genitalium 2097 -11540393

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921893	19557	41713	252	83

Description

5000697748 hypothetical protein mg319 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG319 MG319 Mycoplasma genitalium 2097 -11540394 109077 mg319 (de:hypothetical protein mg319) (db:swissprot) Y319_MYCGE P47561 MYCOPLASMA GENITALIUM 2097 -11540394 172497 hypothetical protein mg319 (db:pir2.dat) C64235 C64235 Mycoplasma genitalium 2097 -11540394 251984 20.5kda protein (fn:unknown, possibly nuclear targetting) (sr:mycoplasma genitalium (strain g-37) (clone library: puc18 base) (db:genpept-bct1) (de:mycoplasma genitalium 20.5 kda nuclear targetting protein gene, p32adhesin gene, p69 protein gene, complete cds's, and o... MYCADH L43097 g871800 Mycoplasma genitalium 2097 -11540394 7500895117 mg319 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75329 pid:1674068 percent) (le:11873) (re:12409) (di:complement) U39712 U39712 g3844896 Mycoplasma genitalium 2097 -11540394 6500736536 hypothetical protein mg319 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG319 MG319 Mycoplasma genitalium 2097 -11540394

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921897	19558	41714	1158	385

Description

5000697749 hypothetical protein mg320 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG320 MG320 Mycoplasma genitalium 2097 -11540395 109081 mg320 (de:hypothetical protein mg320) (db:swissprot) Y320_MYCGE P47562 MYCOPLASMA GENITALIUM 2097 -11540395 172498 hypothetical protein mg320 (db:pir2.dat) D64235 D64235 Mycoplasma genitalium 2097 -11540395 7500895119 mg320 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 35 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75328 pid:1674067 percent) (le:83) (re:943) (di:complement) U39713 U39713 g1046021 Mycoplasma genitalium 2097 -11540395 6500736537 hypothetical protein mg320 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG320 MG320 Mycoplasma genitalium 2097 -11540395

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921922	19559	41715	1752	583

Description

5000697750 hypothetical lipoprotein mg321 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG321 MG321 Mycoplasma genitalium 2097 -11540396 109082 mg321 (de:hypothetical lipoprotein mg321 precursor) (db:swissprot) Y321_MYCGE P47563 MYCOPLASMA GENITALIUM 2097 -11540396 172499 hypothetical protein mg321 (cl:hypothetical protein mg321) (db:pir2.dat) E64235 E64235 Mycoplasma genitalium 2097 -11540396 7500895122 mg321 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 35 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75327 pid:1674066 percent) (le:1264) (re:4068) (di:complement) U39713 U39713 g3844898 Mycoplasma genitalium 2097 -11540396 6500736538 hypothetical lipoprotein mg321 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG321 MG321 Mycoplasma genitalium 2097 -11540396

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921923	19560	41716	183	60

Description

5000697751 hypothetical protein mg331 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG331 MG331 Mycoplasma genitalium 2097 -11540397 109093 mg331 (de:hypothetical protein mg331) (db:swissprot) Y331_MYCGE P47573 MYCOPLASMA GENITALIUM 2097 -11540397 172500 hypothetical protein mg331 (cl:chondroitin 6-sulfotransferase) (db:pir2.dat) F64236 F64236 Mycoplasma genitalium 2097 -11540397 7500895143 mg331 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75307 pid:1674042 percent) (le:6028) (re:6666) (di:complement) U39714 U39714 g3844911 Mycoplasma genitalium 2097 -11540397 6500736539 hypothetical protein mg331 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG331 MG331 Mycoplasma genitalium 2097 -11540397

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921925	19561	41717	606	201

Description

5000697752 hypothetical protein mg333 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG333 MG333 Mycoplasma genitalium 2097 -11540398 172501 hypothetical protein mg333 (db:pir2.dat) H64236 H64236 Mycoplasma genitalium 2097 -11540398 7500965557 m. genitalium predicted coding region mg333 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium bcho, cmk, fcrv, pepp, rpl33 genes from bases406908 to 416865 (section 37 of 56) of the complete genome.) (nt:identified by genemark; putative) (le:9429... U39715 U39715 g1046036 Mycoplasma genitalium 2097 -11540398 6500736540 hypothetical protein mg333 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG333 MG333 Mycoplasma genitalium 2097 -11540398

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921929	19562	41718	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921935	19563	41719	216	71

Description

5000697753 hypothetical protein mg337 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG337 MG337 Mycoplasma genitalium 2097 -11540399 109097 mg337 (de:hypothetical protein mg337) (db:swissprot) Y337_MYCGE P47579 MYCOPLASMA GENITALIUM 2097 -11540399 172502 hypothetical protein mg337 (cl:hypothetical protein mg337) (db:pir2.dat) C64237 C64237 Mycoplasma genitalium 2097 -11540399 7500895150 mg337 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 37 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75297 pid:1674032 percent) (le:1315) (re:1731) (di:direct) U39715 U39715 g3844919 Mycoplasma genitalium 2097 -11540399 6500736541 hypothetical protein mg337 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG337 MG337 Mycoplasma genitalium 2097 -11540399

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921946	19564	41720	924	307

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921957	19565	41721	528	175

Description

5000697754 hypothetical lipoprotein mg338 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG338 MG338 Mycoplasma genitalium 2097 -11540400 109098 mg338 (de:hypothetical lipoprotein mg338 precursor) (db:swissprot) Y338_MYCGE P47580 MYCOPLASMA GENITALIUM 2097 -11540400 172503 hypothetical protein mg338 (db:pir2.dat) D64237 D64237 Mycoplasma genitalium 2097 -11540400 7500895152 mg338 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 37 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75296 pid:1674030 percent) (le:1718) (re:5533) (di:complement) U39715 U39715 g3844920 Mycoplasma genitalium 2097 -11540400 6500736542 hypothetical lipoprotein mg338 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG338 MG338 Mycoplasma genitalium 2097 -11540400

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921966	19566	41722	240	79

Description

5000697755 hypothetical protein mg342 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG342 MG342 Mycoplasma genitalium 2097 -11540401 109100 mg342 (de:hypothetical protein mg342) (db:swissprot) Y342_MYCGE P47584 MYCOPLASMA GENITALIUM 2097 -11540401 172504 hypothetical protein mg342 (db:pir2.dat) H64237 H64237 Mycoplasma genitalium 2097 -11540401 7500895156 mg342 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75270 pid:1673999 percent) (le:51) (re:557) (di:complement) U39716 U39716 g3844925 Mycoplasma genitalium 2097 -11540401 6500736543 hypothetical protein mg342 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG342 MG342 Mycoplasma genitalium 2097 -11540401

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501921968	19567	41723	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922006	19568	41724	2262	753

Description

5000697756 hypothetical protein mg343 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG343 MG343 Mycoplasma genitalium 2097 -11540402 109101 mg343 (de:hypothetical protein mg343) (db:swissprot) Y343_MYCGE P47585 MYCOPLASMA GENITALIUM 2097 -11540402 172505 hypothetical protein mg343 (db:pir2.dat) I64237 I64237 Mycoplasma genitalium 2097 -11540402 7500895158 mg343 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75269 pid:1673998 percent) (le:636) (re:1676) (di:complement) U39716 U39716 g3844926 Mycoplasma genitalium 2097 -11540402 6500736544 hypothetical protein mg343 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG343 MG343 Mycoplasma genitalium 2097 -11540402

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922008	19569	41725	252	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922013	19570	41726	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922016	19571	41727	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922018	19572	41728	1746	581

Description

5000697757 hypothetical lipoprotein mg348 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG348 MG348 Mycoplasma genitalium 2097 -11540403 109104 mg348 (de:hypothetical lipoprotein mg348 precursor) (db:swissprot) Y348_MYCGE P47590 MYCOPLASMA GENITALIUM 2097 -11540403 172506 hypothetical protein mg348 (db:pir2.dat) E64238 E64238 Mycoplasma genitalium 2097 -11540403 7500895165 mg348 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75255 pid:1673992 percent) (le:6518) (re:7486) (di:complement) U39716 U39716 g3844931 Mycoplasma genitalium 2097 -11540403 6500736545 hypothetical lipoprotein mg348 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG348 MG348 Mycoplasma genitalium 2097 -11540403

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922028	19573	41729	486	161

Description

5000697758 hypothetical protein mg349 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG349 MG349 Mycoplasma genitalium 2097 -11540404 109105 mg349 (de:hypothetical protein mg349) (db:swissprot) Y349_MYCGE P47591 MYCOPLASMA GENITALIUM 2097 -11540404 172507 hypothetical protein mg349 (db:pir2.dat) F64238 F64238 Mycoplasma genitalium 2097 -11540404 7500895167 mg349 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75253 pid:1673990 percent) (le:7897) (re:9111) (di:direct) U39716 U39716 g3844932 Mycoplasma genitalium 2097 -11540404 6500736546 hypothetical protein mg349 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG349 MG349 Mycoplasma genitalium 2097 -11540404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922047	19574	41730	1257	418

Description

5000697759 hypothetical protein mg350 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG350 MG350 Mycoplasma genitalium 2097 -11540405 109107 mg350 (de:hypothetical protein mg350) (db:swissprot) Y350_MYCGE P47592 MYCOPLASMA GENITALIUM 2097 -11540405 172508 hypothetical protein mg350 (cl:hypothetical protein mg350) (db:pir2.dat) G64238 G64238 Mycoplasma genitalium 2097 -11540405 7500895172 mg350 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75252 pid:1673989 percent) (le:9111) (re:10046) (di:direct) U39716 U39716 g3844933 Mycoplasma genitalium 2097 -11540405 6500736547 hypothetical protein mg350 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG350 MG350 Mycoplasma genitalium 2097 -11540405

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922049	19575	41731	1170	389

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922059	19576	41732	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922064	19577	41733	1428	475

Description

GTC ORF with score 279 to: (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae profilin synthetic lethal (psl1) gene,complete cds.) (nt:psl1=sec3; the psl1 product contains a region of) (le:549) (re:4559) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922069	19578	41734	795	264

Description

5000697760 hypothetical protein mg353 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG353 MG353 Mycoplasma genitalium 2097 -11540406 109109 mg353 (de:hypothetical protein mg353) (db:swissprot) Y353_MYCGE P47595 MYCOPLASMA GENITALIUM 2097 -11540406 172509 hypothetical protein mg353 (db:pir2.dat) A64239 A64239 Mycoplasma genitalium 2097 -11540406 7500895176 mg353 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75249 pid:1673985 percent) (le:1848) (re:2177) (di:complement) U39717 U39717 g3844937 Mycoplasma genitalium 2097 -11540406 6500736548 hypothetical protein mg353 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG353 MG353 Mycoplasma genitalium 2097 -11540406

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922083	19579	41735	717	238

Description

5000697761 hypothetical protein mg354 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG354 MG354 Mycoplasma genitalium 2097 -11540407 109111 mg354 (de:hypothetical protein mg354) (db:swissprot) Y354_MYCGE P47596 MYCOPLASMA GENITALIUM 2097 -11540407 172510 hypothetical protein mg354 (db:pir2.dat) B64239 B64239 Mycoplasma genitalium 2097 -11540407 7500895179 mg354 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75248 pid:1673984 percent) (le:2326) (re:2739) (di:direct) U39717 U39717 g3844938 Mycoplasma genitalium 2097 -11540407 6500736549 hypothetical protein mg354 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG354 MG354 Mycoplasma genitalium 2097 -11540407

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922086	19580	41736	495	164

Description

5000697762 hypothetical protein mg366 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG366 MG366 Mycoplasma genitalium 2097 -11540408 109119 mg366 (de:hypothetical protein mg366) (db:swissprot) Y366_MYCGE P47606 MYCOPLASMA GENITALIUM 2097 -11540408 172511 hypothetical protein mg366 (cl:mycoplasma genitalium hypothetical protein mg366) (db:pir2.dat) E64240 E64240 Mycoplasma genitalium 2097 -11540408 7500895195 mg366 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75234 pid:1673969 percent) (le:3095) (re:5098) (di:direct) U39718 U39718 g3844953 Mycoplasma genitalium 2097 -11540408 6500736550 hypothetical protein mg366 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG366 MG366 Mycoplasma genitalium 2097 -11540408

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922095	19581	41737	606	201

Description

5000697763 hypothetical protein mg369 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG369 MG369 Mycoplasma genitalium 2097 -11540409 109120 mg369 (de:hypothetical protein mg369) (db:swissprot) Y369_MYCGE P47609 MYCOPLASMA GENITALIUM 2097 -11540409 172512 hypothetical protein mg369 (cl:mycoplasma genitalium hypothetical protein mg369) (db:pir2.dat) H64240 H64240 Mycoplasma genitalium 2097 -11540409 7500895198 mg369 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75231 pid:1673966 percent) (le:6886) (re:8559) (di:complement) U39718 U39718 g3844956 Mycoplasma genitalium 2097 -11540409 6500736551 hypothetical protein mg369 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG369 MG369 Mycoplasma genitalium 2097 -11540409

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922102	19582	41738	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922114	19583	41739	504	167

Description

5000697764 hypothetical protein mg372 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG372 MG372 Mycoplasma genitalium 2097 -11540410 109124 thii:mg372 (de:probable thiamin biosynthesis protein thii) (db:swissprot) THII_MYCGE P47612 MYCOPLASMA GENITALIUM 2097 -11540410 172513 hypothetical protein mg372 (cl:mycoplasma genitalium hypothetical protein mg372) (db:pir2.dat) B64241 B64241 Mycoplasma genitalium 2097 -11540410 7500895205 mg372 ntp-utilizing enzyme guaa family (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gp:1221579 percent identity: 29.00;) (le:1970) (re:3127) (di:complement) U39719 U39719 g3844960 Mycoplasma genitalium 2097 -11540410 6500736552 hypothetical protein mg372 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG372 MG372 Mycoplasma genitalium 2097 -11540410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922122	19584	41740	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922125	19585	41741	1173	390

Description

5000697765 hypothetical protein mg373 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG373 MG373 Mycoplasma genitalium 2097 -11540411 109125 mg373 (de:hypothetical protein mg373) (db:swissprot) Y373_MYCGE P47613 MYCOPLASMA GENITALIUM 2097 -11540411 172514 hypothetical protein mg373 (db:pir2.dat) C64241 C64241 Mycoplasma genitalium 2097 -11540411 7500895207 mg373 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75227 pid:1673962 percent) (le:3114) (re:3959) (di:complement) U39719 U39719 g3844961 Mycoplasma genitalium 2097 -11540411 6500736553 hypothetical protein mg373 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG373 MG373 Mycoplasma genitalium 2097 -11540411

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922127	19586	41742	243	80

Description

5000697766 hypothetical protein mg374 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG374 MG374 Mycoplasma genitalium 2097 -11540412 109126 mg374 (de:hypothetical protein mg374) (db:swissprot) Y374_MYCGE P47614 MYCOPLASMA GENITALIUM 2097 -11540412 172515 hypothetical protein mg374 (db:pir2.dat) D64241 D64241 Mycoplasma genitalium 2097 -11540412 7500895209 mg374 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75226 pid:1673961 percent) (le:3960) (re:4784) (di:complement) U39719 U39719 g3844962 Mycoplasma genitalium 2097 -11540412 6500736554 hypothetical protein mg374 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG374 MG374 Mycoplasma genitalium 2097 -11540412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922132	19587	41743	1188	395

Description

5000697767 hypothetical protein mg376 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG376 MG376 Mycoplasma genitalium 2097 -11540413 109127 mg376 (de:hypothetical protein mg376) (db:swissprot) Y376_MYCGE P47616 MYCOPLASMA GENITALIUM 2097 -11540413 172516 hypothetical protein mg376 (db:pir2.dat) F64241 F64241 Mycoplasma genitalium 2097 -11540413 7500895211 mg376 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75224 pid:1673959 percent) (le:6471) (re:6785) (di:complement) U39719 U39719 g3844964 Mycoplasma genitalium 2097 -11540413 6500736555 hypothetical protein mg376 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG376 MG376 Mycoplasma genitalium 2097 -11540413

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922135	19588	41744	198	65

Description

5000697768 hypothetical protein mg377 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG377 MG377 Mycoplasma genitalium 2097 -11540414 109128 mg377 (de:hypothetical protein mg377) (db:swissprot) Y377_MYCGE P47617 MYCOPLASMA GENITALIUM 2097 -11540414 172517 hypothetical protein mg377 (db:pir2.dat) G64241 G64241 Mycoplasma genitalium 2097 -11540414 7500895213 mg377 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75223 pid:1673958 percent) (le:6791) (re:7372) (di:complement) U39719 U39719 g3844965 Mycoplasma genitalium 2097 -11540414 6500736556 hypothetical protein mg377 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG377 MG377 Mycoplasma genitalium 2097 -11540414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922159	19589	41745	669	222

Description

5000697769 hypothetical protein mg381 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG381 MG381 Mycoplasma genitalium 2097 -11540415 109131 mg381 (de:hypothetical protein mg381) (db:swissprot) Y381_MYCGE P47621 MYCOPLASMA GENITALIUM 2097 -11540415 172518 hypothetical protein mg381 (db:pir2.dat) B64242 B64242 Mycoplasma genitalium 2097 -11540415 7500895216 mg381 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75219 pid:1673954 percent) (le:11463) (re:12119) (di:direct) U39719 U39719 g3844969 Mycoplasma genitalium 2097 -11540415 6500736557 hypothetical protein mg381 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG381 MG381 Mycoplasma genitalium 2097 -11540415

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922162	19590	41746	537	178

Description

5000697770 hypothetical protein mg385 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG385 MG385 Mycoplasma genitalium 2097 -11540416 109133 mg385 (de:hypothetical protein mg385) (db:swissprot) Y385_MYCGE P47625 MYCOPLASMA GENITALIUM 2097 -11540416 172519 hypothetical protein mg385 (db:pir2.dat) F64242 F64242 Mycoplasma genitalium 2097 -11540416 7500895220 mg385 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 42 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75212 pid:1673947 percent) (le:3517) (re:4227) (di:complement) U39720 U39720 g3844974 Mycoplasma genitalium 2097 -11540416 6500736558 hypothetical protein mg385 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG385 MG385 Mycoplasma genitalium 2097 -11540416

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922165	19591	41747	528	175

Description

5000697771 hypothetical protein mg389 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG389 MG389 Mycoplasma genitalium 2097 -11540417 109137 mg389 (de:hypothetical protein mg389) (db:swissprot) Y389_MYCGE P47629 MYCOPLASMA GENITALIUM 2097 -11540417 172520 hypothetical protein mg389 (db:pir2.dat) A64243 A64243 Mycoplasma genitalium 2097 -11540417 7500895228 mg389 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 43 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75208 pid:1673943 percent) (le:102) (re:485) (di:complement) U39721 U39721 g3844980 Mycoplasma genitalium 2097 -11540417 6500736559 hypothetical protein mg389 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG389 MG389 Mycoplasma genitalium 2097 -11540417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922168	19592	41748	378	125

Description

5000697772 hypothetical lipoprotein mg395 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG395 MG395 Mycoplasma genitalium 2097 -11540418 109142 mg395 (de:hypothetical lipoprotein mg395 precursor) (db:swissprot) Y395_MYCGE P47635 MYCOPLASMA GENITALIUM 2097 -11540418 172521 hypothetical protein mg395 (cl:hypothetical protein mg068) (db:pir2.dat) G64243 G64243 Mycoplasma genitalium 2097 -11540418 7500895239 mg395 putative lipoprotein (db:genpept-bct2) (de:mycoplasma genitalium section 43 of 51 of the complete genome.) (nt:similar to pid:1209775 gb:u00089 pid:1673923) (le:7271) (re:8845) (di:complement) U39721 U39721 g3844986 Mycoplasma genitalium 2097 -11540418 6500736560 hypothetical lipoprotein mg395 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG395 MG395 Mycoplasma genitalium 2097 -11540418

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922178	19593	41749	522	173

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922180	19594	41750	2004	667

Description

5000697773 hypothetical protein mg397 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG397 MG397 Mycoplasma genitalium 2097 -11540419 109144 mg397 (de:hypothetical protein mg397) (db:swissprot) Y397_MYCGE P47637 MYCOPLASMA GENITALIUM 2097 -11540419 172522 hypothetical protein mg397 (cl:mycoplasma genitalium hypothetical protein mg397) (db:pir2.dat) I64243 I64243 Mycoplasma genitalium 2097 -11540419 7500895242 mg397 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 44 of 51 of the complete genome.) (nt:similar to pid:1209768 gb:u00089 sp:q50333) (le:675) (re:2375) (di:complement) U39722 U39722 g3844989 Mycoplasma genitalium 2097 -11540419 6500736561 hypothetical protein mg397 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG397 MG397 Mycoplasma genitalium 2097 -11540419

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922195	19595	41751	3021	1006

Description

5000697774 hypothetical lipoprotein mg412 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG412 MG412 Mycoplasma genitalium 2097 -11540420 109150 mg412 (de:hypothetical lipoprotein mg412 precursor) (db:swissprot) Y412_MYCGE P47652 MYCOPLASMA GENITALIUM 2097 -11540420 172524 hypothetical protein mg412 (db:pir2.dat) F64245 F64245 Mycoplasma genitalium 2097 -11540420 7500895256 mg412 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 45 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75184 pid:1673898 percent) (le:5632) (re:6765) (di:complement) U39723 U39723 g3845005 Mycoplasma genitalium 2097 -11540420 6500736562 hypothetical lipoprotein mg412 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG412 MG412 Mycoplasma genitalium 2097 -11540420

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922196	19596	41752	1209	402

Description

5000697775 hypothetical protein mg414 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG414 MG414 Mycoplasma genitalium 2097 -11540421 109152 mg414 (de:hypothetical protein mg414) (db:swissprot) Y414_MYCGE P47653 MYCOPLASMA GENITALIUM 2097 -11540421 172525 hypothetical protein mg414 (cl:hypothetical protein mg413) (db:pir2.dat) H64245 H64245 Mycoplasma genitalium 2097 -11540421 7500895259 mg414 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 45 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75183 pid:1673897 percent) (le:6886) (re:9996) (di:complement) U39723 U39723 g3845006 Mycoplasma genitalium 2097 -11540421 6500736563 hypothetical protein mg414 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG414 MG414 Mycoplasma genitalium 2097 -11540421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922219	19597	41753	1221	406

Description

5000697776 hypothetical protein mg413 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG413 MG413 Mycoplasma genitalium 2097 -11540422 109151 mg413 (de:hypothetical protein mg413) (db:swissprot) Y413_MYCGE P47654 MYCOPLASMA GENITALIUM 2097 -11540422 172435 hypothetical protein homolog mg413 (cl:hypothetical protein mg413) (db:pir2.dat) G64245 G64245 Mycoplasma genitalium 2097 -11540422 7500895257 hypothetical protein gb:l22432_4 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium rpl13, rps9 genes from bases 516159 to 523312(section 49 of 56) of the complete genome.) (nt:identified by sequence similarity; similar to) (le:87) (re:... U39727 U39727 g1046128 Mycoplasma genitalium 2097 -11540422 6500736564 hypothetical protein mg413 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG413 MG413 Mycoplasma genitalium 2097 -11540422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922221	19598	41754	468	155

Description

5000697777 hypothetical protein mg415 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG415 MG415 Mycoplasma genitalium 2097 -11540423 109153 mg415 (de:hypothetical protein mg415) (db:swissprot) Y415_MYCGE P47655 MYCOPLASMA GENITALIUM 2097 -11540423 172526 hypothetical protein mg415 (cl:hypothetical protein mg415) (db:pir2.dat) I64245 I64245 Mycoplasma genitalium 2097 -11540423 7500895261 mg415 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 45 of 51 of the complete genome.) (nt:similar to gb:u00089 pid:1673896 percent identity:) (le:10061) (re:10879) (di:complement) U39723 U39723 g3845007 Mycoplasma genitalium 2097 -11540423 6500736565 hypothetical protein mg415 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG415 MG415 Mycoplasma genitalium 2097 -11540423

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922227	19599	41755	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922232	19600	41756	270	89

Description

5000697778 hypothetical protein mg419 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG419 MG419 Mycoplasma genitalium 2097 -11540424 109156 mg419 (de:hypothetical protein mg419) (db:swissprot) Y419_MYCGE P47658 MYCOPLASMA GENITALIUM 2097 -11540424 172527 hypothetical protein mg419 (db:pir2.dat) C64246 C64246 Mycoplasma genitalium 2097 -11540424 7500895267 m. genitalium predicted coding region mg419 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium rpl13, rps9 genes from bases 516159 to 523312(section 49 of 56) of the complete genome.) (nt:identified by genemark; putative) (le:6194) (re:7057) (di:c... U39727 U39727 g1046133 Mycoplasma genitalium 2097 -11540424 6500736566 hypothetical protein mg419 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG419 MG419 Mycoplasma genitalium 2097 -11540424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922251	19601	41757	528	175

Description

5000697779 hypothetical protein mg422 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG422 MG422 Mycoplasma genitalium 2097 -11540425 109160 mg422 (de:hypothetical protein mg422) (db:swissprot) Y422_MYCGE P47661 MYCOPLASMA GENITALIUM 2097 -11540425 172528 hypothetical protein mg422 (cl:hypothetical protein mg422) (db:pir2.dat) F64246 F64246 Mycoplasma genitalium 2097 -11540425 7500895273 mg422 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 46 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75175 pid:1673888 percent) (le:6163) (re:8670) (di:complement) U39724 U39724 g3845012 Mycoplasma genitalium 2097 -11540425 6500736567 hypothetical protein mg422 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG422 MG422 Mycoplasma genitalium 2097 -11540425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922261	19602	41758	561	186

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922265	19603	41759	837	278

Description

5000697780 hypothetical protein mg427 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG427 MG427 Mycoplasma genitalium 2097 -11540426 109163 mg427 (de:hypothetical protein mg427) (db:swissprot) Y427_MYCGE P47666 MYCOPLASMA GENITALIUM 2097 -11540426 172530 hypothetical protein mg427 (db:pir2.dat) B64247 B64247 Mycoplasma genitalium 2097 -11540426 7500895279 mg427 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75170 pid:1673883 percent) (le:1727) (re:2152) (di:direct) U39725 U39725 g3845020 Mycoplasma genitalium 2097 -11540426 6500736568 hypothetical protein mg427 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG427 MG427 Mycoplasma genitalium 2097 -11540426

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922297	19604	41760	591	196

Description

5000697781 hypothetical protein mg428 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG428 MG428 Mycoplasma genitalium 2097 -11540427 109164 mg428 (de:hypothetical protein mg428) (db:swissprot) Y428_MYCGE P47667 MYCOPLASMA GENITALIUM 2097 -11540427 172531 hypothetical protein mg428 (db:pir2.dat) C64247 C64247 Mycoplasma genitalium 2097 -11540427 7500895281 mg428 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75169 pid:1673881 percent) (le:2263) (re:2778) (di:direct) U39725 U39725 g3845021 Mycoplasma genitalium 2097 -11540427 6500736569 hypothetical protein mg428 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG428 MG428 Mycoplasma genitalium 2097 -11540427

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922303	19605	41761	6996	2331

Description

5000697782 hypothetical protein mg436 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG436 MG436 Mycoplasma genitalium 2097 -11540428 109165 mg436 (de:hypothetical protein mg436) (db:swissprot) Y436_MYCGE P47674 MYCOPLASMA GENITALIUM 2097 -11540428 172532 hypothetical protein mg436 (db:pir2.dat) B64248 B64248 Mycoplasma genitalium 2097 -11540428 7500895288 m. genitalium predicted coding region mg436 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium cdsa, frr, hsds, smba, tsf genes from bases539564 to 546816 (section 52 of 56) of the complete genome.) (nt:identified by genemark; putative) (le:2173) ... U39730 U39730 g1046153 Mycoplasma genitalium 2097 -11540428 6500736570 hypothetical protein mg436 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG436 MG436 Mycoplasma genitalium 2097 -11540428

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922316	19606	41762	1047	349

Description

5000697783 hypothetical lipoprotein mg439 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG439 MG439 Mycoplasma genitalium 2097 -11540429 109166 mg439 (de:hypothetical lipoprotein mg439 precursor) (db:swissprot) Y439_MYCGE P47677 MYCOPLASMA GENITALIUM 2097 -11540429 172533 hypothetical protein mg439 (db:pir2.dat) E64248 E64248 Mycoplasma genitalium 2097 -11540429 7500895295 mg439 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75150 pid:1673859 percent) (le:233) (re:1051) (di:complement) U39726 U39726 g3845032 Mycoplasma genitalium 2097 -11540429 6500736571 hypothetical lipoprotein mg439 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG439 MG439 Mycoplasma genitalium 2097 -11540429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922350	19607	41763	639	212

Description

5000697784 hypothetical lipoprotein mg440 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG440 MG440 Mycoplasma genitalium 2097 -11540430 172534 hypothetical protein mg440 (cl:hypothetical protein mg440) (db:pir2.dat) F64248 F64248 Mycoplasma genitalium 2097 -11540430 7500965558 mg440 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75154 pid:1673863 percent) (le:1051) (re:1827) (di:complement) U39726 U39726 g3845033 Mycoplasma genitalium 2097 -11540430 6500736572 hypothetical lipoprotein mg440 precursor (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG440 MG440 Mycoplasma genitalium 2097 -11540430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922355	19608	41764	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922358	19609	41765	915	304

Description

GTC ORF with score 180 to: (sr:mice macrophage) (db:genpept-rod) (de:putative transcription regulator {clone t2, repetitive sequence}(mice, macrophage, mrna, 1263 nt).) (nt:method: conceptual translation supplied by author.) (le:55) (re:732) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922359	19610	41766	1059	352

Description

5000697785 hypothetical protein mg441 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG441 MG441 Mycoplasma genitalium 2097 -11540431 109170 mg441 (de:hypothetical protein mg441) (db:swissprot) Y441_MYCGE P47679 MYCOPLASMA GENITALIUM 2097 -11540431 172535 hypothetical protein mg441 (db:pir2.dat) G64248 G64248 Mycoplasma genitalium 2097 -11540431 7500895302 mg441 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75149 pid:1673858 percent) (le:1970) (re:2380) (di:complement) U39726 U39726 g3845034 Mycoplasma genitalium 2097 -11540431 6500736573 hypothetical protein mg441 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG441 MG441 Mycoplasma genitalium 2097 -11540431

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922360	19611	41767	531	176

Description

5000697786 hypothetical protein mg449 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG449 MG449 Mycoplasma genitalium 2097 -11540432 172536 hypothetical protein mg449 (db:pir2.dat) F64249 F64249 Mycoplasma genitalium 2097 -11540432 7500965559 mg449 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75128 pid:1673842 percent) (le:8534) (re:8968) (di:complement) U39726 U39726 g3845042 Mycoplasma genitalium 2097 -11540432 6500736574 hypothetical protein mg449 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG449 MG449 Mycoplasma genitalium 2097 -11540432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922387	19612	41768	3516	1171

Description

GTC ORF with score 310 to: (db:genpept) (de:fusarium solani f. sp. pisi histidine kinase fik (fik) gene,complete cds.) (nt:similar to neurospora nik-1, genbank accession) (le:718:1689:2571:2885) (re:1549:2515:2837:4384) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922401	19613	41769	438	145

Description

GTC ORF with score 121 to: (sr:neurospora crassa strain=74-or23-1va) (db:genpept-pln1) (de:neurospora crassa two-component histidine kinase (nik-1) gene, 5'region and partial cds.) (nt:two-component histidine kinase) (le:1619:2488:3404:3732) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922402	19614	41770	333	110

Description

5000697787 hypothetical protein mg450 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG450 MG450 Mycoplasma genitalium 2097 -11540433 109177 mg450 (de:hypothetical protein mg450) (db:swissprot) Y450_MYCGE P47688 MYCOPLASMA GENITALIUM 2097 -11540433 172537 hypothetical protein mg450 (db:pir2.dat) G64249 G64249 Mycoplasma genitalium 2097 -11540433 7500895319 mg450 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75127 pid:1673841 percent) (le:9229) (re:9942) (di:complement) U39726 U39726 g3845043 Mycoplasma genitalium 2097 -11540433 6500736575 hypothetical protein mg450 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG450 MG450 Mycoplasma genitalium 2097 -11540433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922417	19615	41771	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922418	19616	41772	2214	737

Description

5000697788 hypothetical protein mg452 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG452 MG452 Mycoplasma genitalium 2097 -11540434 109179 mg452 (de:hypothetical protein mg452) (db:swissprot) Y452_MYCGE P47690 MYCOPLASMA GENITALIUM 2097 -11540434 172538 hypothetical protein mg452 (db:pir2.dat) I64249 I64249 Mycoplasma genitalium 2097 -11540434 7500895323 mg452 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75125 pid:1673838 percent) (le:1347) (re:2132) (di:direct) U39727 U39727 g3845046 Mycoplasma genitalium 2097 -11540434 6500736576 hypothetical protein mg452 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG452 MG452 Mycoplasma genitalium 2097 -11540434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922431	19617	41773	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922434	19618	41774	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922461	19619	41775	285	94

Description

5000697789 hypothetical protein mg456 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG456 MG456 Mycoplasma genitalium 2097 -11540435 109182 mg456 (de:hypothetical protein mg456) (db:swissprot) Y456_MYCGE P47694 MYCOPLASMA GENITALIUM 2097 -11540435 172539 hypothetical protein mg456 (db:pir2.dat) D64250 D64250 Mycoplasma genitalium 2097 -11540435 7500895328 mg456 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 49 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75121 pid:1673834 percent) (le:4619) (re:5623) (di:complement) U39727 U39727 g3845050 Mycoplasma genitalium 2097 -11540435 6500736577 hypothetical protein mg456 (gtcfc:14.1:14.2) (keggfc:14.2) (db:gtc-mycoplasma genitalium) MG456 MG456 Mycoplasma genitalium 2097 -11540435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922465	19620	41776	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922472	19621	41777	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922476	19622	41778	906	301

Description

5000697643 hypothetical protein:gb:d26185_102:hypothetical protein mg009 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG009 MG009 Mycoplasma genitalium 2097 -11540436 108343 mg009 (de:hypothetical protein mg009) (db:swissprot) Y009_MYCGE P47255 MYCOPLASMA GENITALIUM 2097 -11540436 172388 hypothetical protein homolog mg009 (db:pir2.dat) I64200 I64200 Mycoplasma genitalium 2097 -11540436 7500894517 mg009 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 1 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p78005 pid:1673805 percent) (le:11252) (re:12040) (di:direct) U39679 U39679 g1045677 Mycoplasma genitalium 2097 -11540436 6500736578 hypothetical protein:gb:d26185_102:hypothetical protein mg009 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG009 MG009 Mycoplasma genitalium 2097 -11540436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922477	19623	41779	210	69

Description

5000697644 hypothetical protein:mj1564:hypothetical protein mg016 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG016 MG016 Mycoplasma genitalium 2097 -11540437 108375 mg016 (de:hypothetical protein mg016) (db:swissprot) Y016_MYCGE P47262 MYCOPLASMA GENITALIUM 2097 -11540437 172443 hypothetical protein mg016 (db:pir2.dat) G64201 G64201 Mycoplasma genitalium 2097 -11540437 7500894529 mg016 atp-dependent rna helicase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 2 of 51 of the complete genome.) (nt:similar to gb:l77117 pid:1500458 percent identity:) (le:7204) (re:7710) (di:direct) U39680 U39680 g1045685 Mycoplasma genitalium 2097 -11540437 6500736579 hypothetical protein:mj1564:hypothetical protein mg016 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG016 MG016 Mycoplasma genitalium 2097 -11540437

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922478	19624	41780	4197	1398

Description

5000697645 4-methyl-5:b-hydroxyethyl-thiazole monophosphate biosynthesis:thij:hypothetical protein mg029 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG029 MG029 Mycoplasma genitalium 2097 -11540438 108427 mg029 (de:hypothetical protein mg029) (db:swissprot) Y029_MYCGE P47275 MYCOPLASMA GENITALIUM 2097 -11540438 172389 hypothetical protein homolog mg029 (db:pir2.dat) B64203 B64203 Mycoplasma genitalium 2097 -11540438 7500894556 mg029 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 4 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75082 pid:1673781 percent) (le:2623) (re:3183) (di:complement) U39682 U39682 g3844639 Mycoplasma genitalium 2097 -11540438 6500736580 4-methyl-5:b-hydroxyethyl-thiazole monophosphate biosynthesis:thij:hypothetical protein mg029 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG029 MG029 Mycoplasma genitalium 2097 -11540438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922479	19625	41781	306	101

Description

5000697646 hypothetical protein:hypothetical protein mg037 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG037 MG037 Mycoplasma genitalium 2097 -11540439 108454 mg037 (de:hypothetical protein mg037) (db:swissprot) Y037_MYCGE P47283 MYCOPLASMA GENITALIUM 2097 -11540439 172599 pre-b cell enhancing factor homolog (cl:pre-b cell enhancing factor) (db:pir2.dat) A64204 A64204 Mycoplasma genitalium 2097 -11540439 7500894565 mg037 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 5 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75067 pid:1673764 percent) (le:4380) (re:5732) (di:direct) U39683 U39683 g3844647 Mycoplasma genitalium 2097 -11540439 6500736581 hypothetical protein:hypothetical protein mg037 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG037 MG037 Mycoplasma genitalium 2097 -11540439

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922485	19626	41782	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922496	19627	41783	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922497	19628	41784	303	101

Description

5000697647 hypothetical protein:gb:d26185_99:hypothetical protein mg056 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG056 MG056 Mycoplasma genitalium 2097 -11540440 108542 mg056 (de:hypothetical protein mg056) (db:swissprot) Y056_MYCGE P47302 MYCOPLASMA GENITALIUM 2097 -11540440 172390 hypothetical protein homolog mg056 (cl:conserved hypothetical protein mg056) (db:pir2.dat) B64206 B64206 Mycoplasma genitalium 2097 -11540440 7500894601 mg056 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 7 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75046 pid:1673738 percent) (le:383) (re:1216) (di:complement) U39685 U39685 g1045730 Mycoplasma genitalium 2097 -11540440 6500736582 hypothetical protein:gb:d26185_99:hypothetical protein mg056 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG056 MG056 Mycoplasma genitalium 2097 -11540440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922519	19629	41785	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922525	19630	41786	1896	631

Description

5000697648 hypothetical protein:gb:d26185_104:hypothetical protein mg057 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG057 MG057 Mycoplasma genitalium 2097 -11540441 108545 mg057 (de:hypothetical protein mg057) (db:swissprot) Y057_MYCGE P47303 MYCOPLASMA GENITALIUM 2097 -11540441 172391 hypothetical protein homolog mg057 (db:pir2.dat) C64206 C64206 Mycoplasma genitalium 2097 -11540441 7500894603 mg057 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 7 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75045 pid:1673737 percent) (le:1198) (re:1734) (di:complement) U39685 U39685 g1045731 Mycoplasma genitalium 2097 -11540441 6500736583 hypothetical protein:gb:d26185_104:hypothetical protein mg057 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG057 MG057 Mycoplasma genitalium 2097 -11540441

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922526	19631	41787	366	121

Description

5000697649 hypothetical protein:hypothetical protein mg084 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG084 MG084 Mycoplasma genitalium 2097 -11540442 108682 mg084 (de:hypothetical protein mg084) (db:swissprot) Y084_MYCGE P47330 MYCOPLASMA GENITALIUM 2097 -11540442 172392 hypothetical protein homolog mg084 (db:pir2.dat) C64209 C64209 Mycoplasma genitalium 2097 -11540442 7500894660 mg084 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 11 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75549 pid:1674311 percent) (le:1694) (re:2566) (di:direct) U39689 U39689 g3844671 Mycoplasma genitalium 2097 -11540442 6500736584 hypothetical protein:hypothetical protein mg084 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG084 MG084 Mycoplasma genitalium 2097 -11540442

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922538	19632	41788	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922554	19633	41789	510	169

Description

5000697650 hypothetical protein:gb:u14003_76:hypothetical protein mg110 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG110 MG110 Mycoplasma genitalium 2097 -11540443 108750 mg110 (de:hypothetical protein mg110) (db:swissprot) Y110_MYCGE P47356 MYCOPLASMA GENITALIUM 2097 -11540443 172459 hypothetical protein mg110 (db:pir2.dat) B64212 B64212 Mycoplasma genitalium 2097 -11540443 7500894718 hypothetical protein gb:u14003_76 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium asns, cfxec, def, gmk, pgib, pgsa, ptc1, vacbgenes from bases 131230 to 142208 (section 12 of 56) of thecomplete genome.) (nt:identified by sequence sim... U39690 U39690 g1045789 Mycoplasma genitalium 2097 -11540443 6500736585 hypothetical protein:gb:u14003_76:hypothetical protein mg110 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG110 MG110 Mycoplasma genitalium 2097 -11540443

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922572	19634	41790	3300	1099

Description

5000697651 hypothetical protein:sp:p31131:hypothetical protein mg115 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG115 MG115 Mycoplasma genitalium 2097 -11540444 108765 mg115 (de:hypothetical protein mg115) (db:swissprot) Y115_MYCGE P47361 MYCOPLASMA GENITALIUM 2097 -11540444 172393 hypothetical protein homolog mg115 (db:pir2.dat) G64212 G64212 Mycoplasma genitalium 2097 -11540444 7500894729 hypothetical protein sp:p31131 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium gale, mgla, rbsc, topa, trps, trx genes frombases 142159 to 158437 (section 13 of 56) of the complete genome.) (nt:identified by sequence similarity; si... U39691 U39691 g1045795 Mycoplasma genitalium 2097 -11540444 6500736586 hypothetical protein:sp:p31131:hypothetical protein mg115 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG115 MG115 Mycoplasma genitalium 2097 -11540444

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922598	19635	41791	1851	616

Description

5000697652 hypothetical protein:sp:p32720:hypothetical protein mg121 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG121 MG121 Mycoplasma genitalium 2097 -11540445 108793 mg121 (de:hypothetical protein mg121) (db:swissprot) Y121_MYCGE P47367 MYCOPLASMA GENITALIUM 2097 -11540445 172394 hypothetical protein homolog mg121 (db:pir2.dat) D64213 D64213 Mycoplasma genitalium 2097 -11540445 7500894741 mg121 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 14 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75514 pid:1674273 percent) (le:6176) (re:7096) (di:direct) U39692 U39692 g3844711 Mycoplasma genitalium 2097 -11540445 6500736587 hypothetical protein:sp:p32720:hypothetical protein mg121 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG121 MG121 Mycoplasma genitalium 2097 -11540445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922601	19636	41792	480	159

Description

5000697653 hypothetical protein:gb:m91593_1:hypothetical protein mg123 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG123 MG123 Mycoplasma genitalium 2097 -11540446 108797 mg123 (de:hypothetical protein mg123) (db:swissprot) Y123_MYCGE P47369 MYCOPLASMA GENITALIUM 2097 -11540446 172395 hypothetical protein homolog mg123 (cl:hypothetical protein mg123) (db:pir2.dat) F64213 F64213 Mycoplasma genitalium 2097 -11540446 7500894743 mg123 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 14 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75513 pid:1674271 percent) (le:9243) (re:10658) (di:direct) U39692 U39692 g3844713 Mycoplasma genitalium 2097 -11540446 6500736588 hypothetical protein:gb:m91593_1:hypothetical protein mg123 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG123 MG123 Mycoplasma genitalium 2097 -11540446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922619	19637	41793	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922625	19638	41794	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922634	19639	41795	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922638	19640	41796	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922654	19641	41797	1269	422

Description

5000697654 hypothetical protein:gb:l10328_61:hypothetical protein mg125 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG125 MG125 Mycoplasma genitalium 2097 -11540447 108800 mg125 (de:hypothetical protein mg125) (db:swissprot) Y125_MYCGE P47371 MYCOPLASMA GENITALIUM 2097 -11540447 172396 hypothetical protein homolog mg125 (db:pir2.dat) H64213 H64213 Mycoplasma genitalium 2097 -11540447 7500894745 mg125 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75511 pid:1674269 percent) (le:348) (re:1205) (di:direct) U39693 U39693 g3844716 Mycoplasma genitalium 2097 -11540447 6500736589 hypothetical protein:gb:l10328_61:hypothetical protein mg125 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG125 MG125 Mycoplasma genitalium 2097 -11540447

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922665	19642	41798	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922674	19643	41799	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922675	19644	41800	399	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922680	19645	41801	975	324

Description

5000697655 yqgz:hypothetical protein mg127 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG127 MG127 Mycoplasma genitalium 2097 -11540448 108803 mg127 (de:hypothetical protein mg127) (db:swissprot) Y127_MYCGE P47373 MYCOPLASMA GENITALIUM 2097 -11540448 172397 hypothetical protein homolog mg127 (cl:hypothetical protein yjbd) (db:pir2.dat) A64214 A64214 Mycoplasma genitalium 2097 -11540448 7500894749 mg127 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75509 pid:1674267 percent) (le:2265) (re:2702) (di:direct) U39693 U39693 g3844718 Mycoplasma genitalium 2097 -11540448 6500736590 yqgz:hypothetical protein mg127 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG127 MG127 Mycoplasma genitalium 2097 -11540448

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922683	19646	41802	807	268

Description

5000697656 hypothetical protein:hi0072:hypothetical protein mg128 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG128 MG128 Mycoplasma genitalium 2097 -11540449 108804 mg128 (de:hypothetical protein mg128) (db:swissprot) Y128_MYCGE P47374 MYCOPLASMA GENITALIUM 2097 -11540449 172398 hypothetical protein homolog mg128 (cl:conserved hypothetical protein hi0072) (db:pir2.dat) B64214 B64214 Mycoplasma genitalium 2097 -11540449 7500894751 mg128 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75508 pid:1674266 percent) (le:2710) (re:3489) (di:direct) U39693 U39693 g3844719 Mycoplasma genitalium 2097 -11540449 6500736591 hypothetical protein:hi0072:hypothetical protein mg128 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG128 MG128 Mycoplasma genitalium 2097 -11540449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922684	19647	41803	1566	521

Description

5000697657 hypothetical protein:gb:m91593_1:hypothetical protein mg130 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG130 MG130 Mycoplasma genitalium 2097 -11540450 108835 mg130 (de:hypothetical protein mg130) (db:swissprot) Y130_MYCGE P47376 MYCOPLASMA GENITALIUM 2097 -11540450 172399 hypothetical protein homolog mg130 (db:pir2.dat) D64214 D64214 Mycoplasma genitalium 2097 -11540450 7500894759 mg130 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75506 pid:1674264 percent) (le:3832) (re:5286) (di:direct) U39693 U39693 g3844721 Mycoplasma genitalium 2097 -11540450 6500736592 hypothetical protein:gb:m91593_1:hypothetical protein mg130 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG130 MG130 Mycoplasma genitalium 2097 -11540450

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922685	19648	41804	408	135

Description

5000697658 hypothetical protein:gb:m38777_3:hypothetical protein mg134 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG134 MG134 Mycoplasma genitalium 2097 -11540451 108842 mg134 (de:hypothetical protein mg134) (db:swissprot) Y134_MYCGE P47380 MYCOPLASMA GENITALIUM 2097 -11540451 172402 hypothetical protein homolog mg134 (db:pir2.dat) H64214 H64214 Mycoplasma genitalium 2097 -11540451 7500894767 mg134 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75502 pid:1674259 percent) (le:7064) (re:7366) (di:direct) U39693 U39693 g3844724 Mycoplasma genitalium 2097 -11540451 6500736593 hypothetical protein:gb:m38777_3:hypothetical protein mg134 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG134 MG134 Mycoplasma genitalium 2097 -11540451

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922688	19649	41805	612	203

Description

5000697659 hypothetical protein 4:gp:z33006_1:hypothetical protein mg135 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG135 MG135 Mycoplasma genitalium 2097 -11540452 108843 mg135 (de:hypothetical protein mg135) (db:swissprot) Y135_MYCGE P47381 MYCOPLASMA GENITALIUM 2097 -11540452 172403 hypothetical protein homolog mg135 4 (db:pir2.dat) I64214 I64214 Mycoplasma genitalium 2097 -11540452 7500894769 mg135 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75501 pid:1674258 percent) (le:7338) (re:8180) (di:complement) U39693 U39693 g3844725 Mycoplasma genitalium 2097 -11540452 6500736594 hypothetical protein 4:gp:z33006_1:hypothetical protein mg135 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG135 MG135 Mycoplasma genitalium 2097 -11540452

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922701	19650	41806	246	82

Description

5000697660 hypothetical protein:gb:l18927_2:hypothetical protein mg139 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG139 MG139 Mycoplasma genitalium 2097 -11540453 108846 mg139 (de:hypothetical protein mg139) (db:swissprot) Y139_MYCGE P47385 MYCOPLASMA GENITALIUM 2097 -11540453 172404 conserved hypothetical protein mg139 (cl:conserved hypothetical protein mg139) (db:pir2.dat) D64215 D64215 Mycoplasma genitalium 2097 -11540453 7500894772 mg139 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 16 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75497 pid:1674253 percent) (le:73) (re:1782) (di:direct) U39694 U39694 g3844731 Mycoplasma genitalium 2097 -11540453 6500736595 hypothetical protein:gb:l18927_2:hypothetical protein mg139 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG139 MG139 Mycoplasma genitalium 2097 -11540453

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922705	19651	41807	603	200

Description

5000697661 hypothetical protein:gb:l18965_6:hypothetical protein mg148 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG148 MG148 Mycoplasma genitalium 2097 -11540454 108881 mg148 (de:hypothetical protein mg148) (db:swissprot) Y148_MYCGE P47394 MYCOPLASMA GENITALIUM 2097 -11540454 172406 hypothetical protein homolog mg148 (cl:hypothetical protein mg148) (db:pir2.dat) D64216 D64216 Mycoplasma genitalium 2097 -11540454 7500894793 mg148 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75584 pid:1674376 percent) (le:12034) (re:13263) (di:direct) U39695 U39695 g3844741 Mycoplasma genitalium 2097 -11540454 6500736596 hypothetical protein:gb:l18965_6:hypothetical protein mg148 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG148 MG148 Mycoplasma genitalium 2097 -11540454

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922713	19652	41808	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922714	19653	41809	1332	443

Description

5000697662 hypothetical protein:hypothetical protein mg181 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG181 MG181 Mycoplasma genitalium 2097 -11540455 108949 mg181 (de:hypothetical protein mg181) (db:swissprot) Y181_MYCGE P47427 MYCOPLASMA GENITALIUM 2097 -11540455 172467 hypothetical protein mg181 (db:pir2.dat) A64220 A64220 Mycoplasma genitalium 2097 -11540455 7500894832 mg181 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 19 of 51 of the complete genome.) (nt:similar to pid:1215693 gb:u00089 sp:q50292) (le:3951) (re:5213) (di:direct) U39697 U39697 g3844777 Mycoplasma genitalium 2097 -11540455 6500736597 hypothetical protein:hypothetical protein mg181 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG181 MG181 Mycoplasma genitalium 2097 -11540455

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922726	19654	41810	1401	466

Description

6500736598 mgpa:mg190 hypothetical protein:protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG190 MG190 Mycoplasma genitalium 2097 -11540456 83655 mgpa:mg190 (de:mgpa protein) (db:swissprot) MGPA_MYCGE P22746 MYCOPLASMA GENITALIUM 2097 -11540456 172564 mgpa operon hypothetical protein mg190 (db:pir2.dat) A64221 A64221 Mycoplasma genitalium 2097 -11540456 7500885596 mg190 mgpa protein mgpa (db:genpept-bct2) (de:mycoplasma genitalium section 20 of 51 of the complete genome.) (nt:similar to pid:1196657 gb:u00089 sp:p75144) (le:5726) (re:6811) (di:direct) U39698 U39698 g3844787 Mycoplasma genitalium 2097 -11540456 5000697663 (de:(mg190) (pn:protein:hypothetical protein) (gn:mgpa) (gtcfc:13.7:14.1) (ec:) (mgpa_mycge) (keggfc:11.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium)) MG190 MG190 Mycoplasma genitalium 2097 10025869

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922727	19655	41811	258	85

Description

6500736599 hrca:mg205 hypothetical protein:gb:m84964_1:heat-inducible transcription repressor homolog (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG205 MG205 Mycoplasma genitalium 2097 -11540457 77607 hrca:mg205 (de:heat-inducible transcription repressor hrca homolog) (db:swissprot) HRCA_MYCGE P47447 MYCOPLASMA GENITALIUM 2097 -11540457 172407 hypothetical protein homolog mg205 (cl:conserved hypothetical protein mg205) (db:pir2.dat) F64222 F64222 Mycoplasma genitalium 2097 -11540457 7500883515 mg205 transcription repressor hrca (db:genpept-bct2) (de:mycoplasma genitalium section 22 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75351 pid:1673678 percent) (le:4272) (re:5303) (di:complement) U39700 U39700 g3844803 Mycoplasma genitalium 2097 -11540457 5000697664 (de:(mg205) (pn:heat-inducible transcription repressor homolog:hypothetical protein:gb:m84964_1) (gn:hrca) (gtcfc:13.7:14.1) (ec:) (hrca_mycge) (keggfc:11.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium)) MG205 MG205 Mycoplasma genitalium 2097 10019967

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922741	19656	41812	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922766	19657	41813	1047	348

Description

5000697665 sfhb:hypothetical protein mg209 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG209 MG209 Mycoplasma genitalium 2097 -11540458 108980 mg209 (de:hypothetical protein mg209) (db:swissprot) Y209_MYCGE P47451 MYCOPLASMA GENITALIUM 2097 -11540458 172408 hypothetical protein homolog mg209 (db:pir2.dat) A64223 A64223 Mycoplasma genitalium 2097 -11540458 7500894882 mg209 sfhb protein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 22 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75485 pid:1674240 percent) (le:8183) (re:9109) (di:complement) U39700 U39700 g3844807 Mycoplasma genitalium 2097 -11540458 6500736600 sfhb:hypothetical protein mg209 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG209 MG209 Mycoplasma genitalium 2097 -11540458

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922786	19658	41814	282	93

Description

GTC ORF with score 142 to: (db:genpept-bct2) (de:pseudomonas fluorescens cyclohexanone monooxygenase homolog gene,partial cds; lactone-specific esterase (estf1) gene, complete cds;and alkane-1 monooxygenase homolog gene, partial cds.) (nt:orf1) (le:<1)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922787	19659	41815	1008	335

Description

GTC ORF with score 262 to: (db:genpept-bct2) (de:pseudomonas fluorescens cyclohexanone monooxygenase homolog gene,partial cds; lactone-specific esterase (estf1) gene, complete cds;and alkane-1 monooxygenase homolog gene, partial cds.) (nt:orf1) (le:<1)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922788	19660	41816	405	134

Description

5000697666 hypothetical protein:gb:l09228_16:hypothetical protein mg213 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG213 MG213 Mycoplasma genitalium 2097 -11540459 108985 mg213 (de:hypothetical protein mg213) (db:swissprot) Y213_MYCGE P47455 MYCOPLASMA GENITALIUM 2097 -11540459 172409 hypothetical protein homolog mg213 (cl:hypothetical protein homolog mg213:type i dihydrofolate reductase homology) (db:pir2.dat) E64223 E64223 Mycoplasma genitalium 2097 -11540459 7500894888 mg213 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75478 pid:1674232 percent) (le:1708) (re:3123) (di:direct) U39701 U39701 g3844813 Mycoplasma genitalium 2097 -11540459 6500736601 hypothetical protein:gb:l09228_16:hypothetical protein mg213 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG213 MG213 Mycoplasma genitalium 2097 -11540459

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922801	19661	41817	297	98

Description

5000697667 hypothetical protein:gb:l09228_17:hypothetical protein mg214 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG214 MG214 Mycoplasma genitalium 2097 -11540460 108986 mg214 (de:hypothetical protein mg214) (db:swissprot) Y214_MYCGE P47456 MYCOPLASMA GENITALIUM 2097 -11540460 172410 hypothetical protein homolog mg214 (db:pir2.dat) F64223 F64223 Mycoplasma genitalium 2097 -11540460 7500894890 mg214 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 23 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75477 pid:1674231 percent) (le:3107) (re:3730) (di:direct) U39701 U39701 g3844814 Mycoplasma genitalium 2097 -11540460 6500736602 hypothetical protein:gb:l09228_17:hypothetical protein mg214 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG214 MG214 Mycoplasma genitalium 2097 -11540460

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922807	19662	41818	1152	383

Description

5000697668 hypothetical protein:sp:p22186:hypothetical protein mg221 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG221 MG221 Mycoplasma genitalium 2097 -11540461 172411 hypothetical protein homolog mg221 (cl:hypothetical protein mg221) (db:pir2.dat) D64224 D64224 Mycoplasma genitalium 2097 -11540461 7500965555 mg221 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75467 pid:1674217 percent) (le:574) (re:1038) (di:direct) U39702 U39702 g3844824 Mycoplasma genitalium 2097 -11540461 6500736603 hypothetical protein:sp:p22186:hypothetical protein mg221 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG221 MG221 Mycoplasma genitalium 2097 -11540461

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922822	19663	41819	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922834	19664	41820	1692	563

Description

5000697669 hypothetical protein:gb:d10483_63:hypothetical protein mg222 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG222 MG222 Mycoplasma genitalium 2097 -11540462 108994 mg222 (de:hypothetical protein mg222) (db:swissprot) Y222_MYCGE P47464 MYCOPLASMA GENITALIUM 2097 -11540462 172412 yabc protein homolog mg222 (cl:escherichia coli yabc protein) (db:pir2.dat) E64224 E64224 Mycoplasma genitalium 2097 -11540462 7500894902 mg222 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 24 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75466 pid:1674216 percent) (le:1028) (re:1957) (di:direct) U39702 U39702 g3844825 Mycoplasma genitalium 2097 -11540462 6500736604 hypothetical protein:gb:d10483_63:hypothetical protein mg222 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG222 MG222 Mycoplasma genitalium 2097 -11540462

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922878	19665	41821	396	131

Description

5000697670 hypothetical protein:gb:m91593_1:hypothetical protein mg240 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG240 MG240 Mycoplasma genitalium 2097 -11540463 109009 mg240 (de:hypothetical protein mg240) (db:swissprot) Y240_MYCGE P47482 MYCOPLASMA GENITALIUM 2097 -11540463 172414 hypothetical protein homolog mg240 (cl:hypothetical protein yqek) (db:pir2.dat) E64226 E64226 Mycoplasma genitalium 2097 -11540463 7500894940 mg240 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75442 pid:1674193 percent) (le:6952) (re:7830) (di:complement) U39703 U39703 g3844844 Mycoplasma genitalium 2097 -11540463 6500736605 hypothetical protein:gb:m91593_1:hypothetical protein mg240 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG240 MG240 Mycoplasma genitalium 2097 -11540463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922882	19666	41822	522	173

Description

5000697671 hypothetical protein:gb:m12965_1:hypothetical protein mg245 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG245 MG245 Mycoplasma genitalium 2097 -11540464 109016 mg245 (de:hypothetical protein mg245) (db:swissprot) Y245_MYCGE P47487 MYCOPLASMA GENITALIUM 2097 -11540464 172415 hypothetical protein homolog mg245 (db:pir2.dat) A64227 A64227 Mycoplasma genitalium 2097 -11540464 7500894953 mg245 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75430 pid:1674179 percent) (le:14619) (re:15116) (di:direct) U39703 U39703 g1045936 Mycoplasma genitalium 2097 -11540464 6500736606 hypothetical protein:gb:m12965_1:hypothetical protein mg245 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG245 MG245 Mycoplasma genitalium 2097 -11540464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922885	19667	41823	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922912	19668	41824	543	180

Description

GTC ORF with score 151 to: (or:Caenorhabditis elegans) (db:genpept-inv) (de:caenorhabditis elegans cosmid f57f5, complete sequence.) (nt:similar to adducin; cdna est embl:d66652 comes from) (le:12680:12943:13416) (re:12807:13192:13727) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922917	19669	41825	879	292

Description

GTC ORF with score 175 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922918	19670	41826	762	253

Description

5000697672 hypothetical protein:sp:p31056:hypothetical protein mg247 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG247 MG247 Mycoplasma genitalium 2097 -11540465 109020 mg247 (de:hypothetical protein mg247) (db:swissprot) Y247_MYCGE P47489 MYCOPLASMA GENITALIUM 2097 -11540465 172416 hypothetical protein homolog mg247 (cl:escherichia coli ygih protein) (db:pir2.dat) C64227 C64227 Mycoplasma genitalium 2097 -11540465 7500894965 mg247 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 25 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75428 pid:1674177 percent) (le:15938) (re:16657) (di:complement) U39703 U39703 g1045938 Mycoplasma genitalium 2097 -11540465 6500736607 hypothetical protein:sp:p31056:hypothetical protein mg247 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG247 MG247 Mycoplasma genitalium 2097 -11540465

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922922	19671	41827	306	101

Description

GTC ORF with score 105 to: (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae oligosaccharyl transferase glycoproteinsubunit 1 (nlt1) and putative orf genes, complete cds.) (nt:orf; putative; method: conceptual translation) (le:3290) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922937	19672	41828	408	135

Description

5000697673 lipoprotein:hypothetical protein mg260 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG260 MG260 Mycoplasma genitalium 2097 -11540466 109033 mg260 (de:hypothetical protein mg260) (db:swissprot) Y260_MYCGE P47502 MYCOPLASMA GENITALIUM 2097 -11540466 172417 hypothetical protein homolog mg260 (cl:hypothetical protein mg185) (db:pir2.dat) G64228 G64228 Mycoplasma genitalium 2097 -11540466 7500894987 mg260 lipoprotein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 27 of 51 of the complete genome.) (nt:similar to gb:u00089 pid:1674249 percent identity:) (le:96) (re:2393) (di:direct) U39705 U39705 g3844856 Mycoplasma genitalium 2097 -11540466 6500736608 lipoprotein:hypothetical protein mg260 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG260 MG260 Mycoplasma genitalium 2097 -11540466

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922939	19673	41829	357	118

Description

5000697674 hypothetical protein:gb:l10328_61:hypothetical protein mg263 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG263 MG263 Mycoplasma genitalium 2097 -11540467 109035 mg263 (de:hypothetical protein mg263) (db:swissprot) Y263_MYCGE P47505 MYCOPLASMA GENITALIUM 2097 -11540467 172418 hypothetical protein homolog mg263 (db:pir2.dat) A64229 A64229 Mycoplasma genitalium 2097 -11540467 7500894996 mg263 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75401 pid:1674144 percent) (le:89) (re:964) (di:direct) U39706 U39706 g3844859 Mycoplasma genitalium 2097 -11540467 6500736609 hypothetical protein:gb:l10328_61:hypothetical protein mg263 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG263 MG263 Mycoplasma genitalium 2097 -11540467

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922940	19674	41830	198	65

Description

5000697675 hypothetical protein:gb:l10328_61:hypothetical protein mg265 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG265 MG265 Mycoplasma genitalium 2097 -11540468 109037 mg265 (de:hypothetical protein mg265) (db:swissprot) Y265_MYCGE P47507 MYCOPLASMA GENITALIUM 2097 -11540468 172419 hypothetical protein homolog mg265 (db:pir2.dat) C64229 C64229 Mycoplasma genitalium 2097 -11540468 7500895004 mg265 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 28 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75399 pid:1674142 percent) (le:1490) (re:2326) (di:complement) U39706 U39706 g3844861 Mycoplasma genitalium 2097 -11540468 6500736610 hypothetical protein:gb:l10328_61:hypothetical protein mg265 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG265 MG265 Mycoplasma genitalium 2097 -11540468

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922953	19675	41831	405	134

Description

5000697676 hypothetical protein:gb:l19201_18:hypothetical protein mg294 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG294 MG294 Mycoplasma genitalium 2097 -11540469 119054 mg294 (de:hypothetical protein mg294) (db:swissprot) Y294_MYCGE Q49411 MYCOPLASMA GENITALIUM 2097 -11540469 172421 hypothetical protein homolog mg294 (cl:hypothetical protein mg294) (db:pir2.dat) E64232 E64232 Mycoplasma genitalium 2097 -11540469 7500895083 mg294 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 31 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75366 pid:1674105 percent) (le:7556) (re:8980) (di:complement) U39709 U39709 g3844873 Mycoplasma genitalium 2097 -11540469 6500736611 hypothetical protein:gb:l19201_18:hypothetical protein mg294 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG294 MG294 Mycoplasma genitalium 2097 -11540469

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922954	19676	41832	645	214

Description

5000697677 hypothetical protein:sp:p25745:hypothetical protein mg295 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG295 MG295 Mycoplasma genitalium 2097 -11540470 109058 trmu:mg295 (ec:2.1.1.61) (de:(ec 2.1.1.61)) (db:swissprot) TRMU_MYCGE P47537 MYCOPLASMA GENITALIUM 2097 -11540470 172422 hypothetical protein homolog mg295 (cl:probable membrane protein ydl033c) (db:pir2.dat) F64232 F64232 Mycoplasma genitalium 2097 -11540470 7500893418 mg295 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 31 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75365 pid:1674103 percent) (le:9098) (re:10201) (di:complement) U39709 U39709 g3844874 Mycoplasma genitalium 2097 -11540470 6500736612 hypothetical protein:sp:p25745:hypothetical protein mg295 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG295 MG295 Mycoplasma genitalium 2097 -11540470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922974	19677	41833	3276	1091

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922975	19678	41834	369	122

Description

5000697678 gp:l38997_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG314 MG314 Mycoplasma genitalium 2097 -11540471 119064 mg314 (de:hypothetical protein mg314) (db:swissprot) Y314_MYCGE Q49415 MYCOPLASMA GENITALIUM 2097 -11540471 172423 hypothetical protein homolog mg314 (db:pir2.dat) G64234 G64234 Mycoplasma genitalium 2097 -11540471 7500895110 mg314 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 34 of 51 of the complete genome.) (nt:similar to pid:639788 gb:u00089 sp:q50363) (le:5878) (re:7209) (di:complement) U39712 U39712 g3844891 Mycoplasma genitalium 2097 -11540471 6500736613 gp:l38997_4:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG314 MG314 Mycoplasma genitalium 2097 -11540471

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922977	19679	41835	717	238

Description

5000697679 hypothetical protein:gb:z18629_1:hypothetical protein mg326 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG326 MG326 Mycoplasma genitalium 2097 -11540472 109088 mg326 (de:hypothetical protein mg326) (db:swissprot) Y326_MYCGE P47568 MYCOPLASMA GENITALIUM 2097 -11540472 172425 hypothetical protein homolog mg326 (db:pir2.dat) A64236 A64236 Mycoplasma genitalium 2097 -11540472 7500895131 mg326 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75312 pid:1674048 percent) (le:14) (re:901) (di:complement) U39714 U39714 g3844906 Mycoplasma genitalium 2097 -11540472 6500736614 hypothetical protein:gb:z18629_1:hypothetical protein mg326 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG326 MG326 Mycoplasma genitalium 2097 -11540472

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922988	19680	41836	885	294

Description

5000697680 hypothetical protein:gb:u00021_5:hypothetical 50 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG329 MG329 Mycoplasma genitalium 2097 -11540473 109089 mg329 (de:hypothetical 50.2 kd gtp-binding protein mg329) (db:swissprot) Y329_MYCGE P47571 MYCOPLASMA GENITALIUM 2097 -11540473 172426 hypothetical protein homolog mg329 (cl:mycobacterium leprae probable gtp-binding protein:translation elongation factor tu homology) (db:pir2.dat) D64236 D64236 Mycoplasma genitalium 2097 -11540473 7500895136 mg329 conserved hypothetical gtp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00021 pid:467147 percent identity:) (le:4016) (re:5362) (di:complement) U39714 U39714 g3844909 Mycoplasma genitalium 2097 -11540473 6500736615 hypothetical protein:gb:u00021_5:hypothetical 50 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG329 MG329 Mycoplasma genitalium 2097 -11540473

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501922997	19681	41837	2415	804

Description

5000697681 hypothetical protein:gb:d10165_3:hypothetical protein mg332 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG332 MG332 Mycoplasma genitalium 2097 -11540474 109094 mg332 (de:hypothetical protein mg332) (db:swissprot) Y332_MYCGE P47574 MYCOPLASMA GENITALIUM 2097 -11540474 172427 hypothetical protein homolog mg332 (cl:hypothetical protein mg332) (db:pir2.dat) G64236 G64236 Mycoplasma genitalium 2097 -11540474 7500895145 mg332 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75306 pid:1674041 percent) (le:6654) (re:7373) (di:complement) U39714 U39714 g3844912 Mycoplasma genitalium 2097 -11540474 6500736616 hypothetical protein:gb:d10165_3:hypothetical protein mg332 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG332 MG332 Mycoplasma genitalium 2097 -11540474

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923005	19682	41838	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923018	19683	41839	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923020	19684	41840	837	278

Description

5000697682 hypothetical protein:sp:p38424:hypothetical gtp-binding protein mg335 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG335 MG335 Mycoplasma genitalium 2097 -11540475 109096 mg335 (de:hypothetical gtp-binding protein mg335) (db:swissprot) Y335_MYCGE P47577 MYCOPLASMA GENITALIUM 2097 -11540475 172428 hypothetical protein homolog mg335 (cl:translation elongation factor tu homology) (db:pir2.dat) A64237 A64237 Mycoplasma genitalium 2097 -11540475 7500895147 mg335 conserved hypothetical gtp-binding protein (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75303 pid:1674038 percent) (le:10514) (re:11089) (di:complement) U39714 U39714 g3844914 Mycoplasma genitalium 2097 -11540475 6500736617 hypothetical protein:sp:p38424:hypothetical gtp-binding protein mg335 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG335 MG335 Mycoplasma genitalium 2097 -11540475

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923021	19685	41841	915	304

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923024	19686	41842	1179	392

Description

5000697683 methylase homolog:cspr:hypothetical rrna methylase mg346 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG346 MG346 Mycoplasma genitalium 2097 -11540476 109102 mg346 (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase mg346,) (db:swissprot) Y346_MYCGE P47588 MYCOPLASMA GENITALIUM 2097 -11540476 172429 hypothetical protein homolog mg346 (db:pir2.dat) C64238 C64238 Mycoplasma genitalium 2097 -11540476 7500895160 mg346 rrna methylase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75257 pid:1673994 percent) (le:5243) (re:5743) (di:direct) U39716 U39716 g3844929 Mycoplasma genitalium 2097 -11540476 6500736618 methylase homolog:cspr:hypothetical rrna methylase mg346 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG346 MG346 Mycoplasma genitalium 2097 -11540476

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923036	19687	41843	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923047	19688	41844	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923088	19689	41845	636	211

Description

5000697684 hypothetical protein:sp:p32049:hypothetical protein mg347 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG347 MG347 Mycoplasma genitalium 2097 -11540477 109103 mg347 (de:hypothetical protein mg347) (db:swissprot) Y347_MYCGE P47589 MYCOPLASMA GENITALIUM 2097 -11540477 172430 hypothetical protein homolog mg347 (cl:hypothetical protein hi0340) (db:pir2.dat) D64238 D64238 Mycoplasma genitalium 2097 -11540477 7500895163 mg347 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 38 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75256 pid:1673993 percent) (le:5734) (re:6366) (di:direct) U39716 U39716 g3844930 Mycoplasma genitalium 2097 -11540477 6500736619 hypothetical protein:sp:p32049:hypothetical protein mg347 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG347 MG347 Mycoplasma genitalium 2097 -11540477

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923092	19690	41846	324	107

Description

GTC ORF with score 91 to: (sr:human) (db:genpept) (de:homo sapiens nadh:ubiquinone oxidoreductase ashi subunit mrna,nuclear gene encoding mitochondrial protein, complete cds.) (nt:complex i subunit; ndufb8 subunit) (le:23) (re:583) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923094	19691	41847	1995	664

Description

6500736620 pona:mg352 penicillin-binding protein (gtcfc:11.4:13.3) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG352 MG352 Mycoplasma genitalium 2097 -11540478 119087 mg352 (de:hypothetical protein mg352) (db:swissprot) Y352_MYCGE Q49422 MYCOPLASMA GENITALIUM 2097 -11540478 172431 hypothetical protein homolog mg352 (db:pir2.dat) I64238 I64238 Mycoplasma genitalium 2097 -11540478 7500895175 mg352 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u11883 sp:p39792 pid:520540) (le:1351) (re:1851) (di:direct) U39717 U39717 g3844936 Mycoplasma genitalium 2097 -11540478 5000697685 (de:(mg352) (pn:penicillin-binding protein:pona) (gn:pona) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium)) MG352 MG352 Mycoplasma genitalium 2097 10061532

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923095	19692	41848	558	185

Description

5000697686 suppressor of ftsh:sfhb:hypothetical protein mg370 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG370 MG370 Mycoplasma genitalium 2097 -11540479 109123 mg370 (de:hypothetical protein mg370) (db:swissprot) Y370_MYCGE P47610 MYCOPLASMA GENITALIUM 2097 -11540479 172432 hypothetical protein homolog mg370 (db:pir2.dat) I64240 I64240 Mycoplasma genitalium 2097 -11540479 7500895201 mg370 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75230 pid:1673965 percent) (le:45) (re:1016) (di:complement) U39719 U39719 g3844958 Mycoplasma genitalium 2097 -11540479 6500736621 suppressor of ftsh:sfhb:hypothetical protein mg370 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG370 MG370 Mycoplasma genitalium 2097 -11540479

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923106	19693	41849	279	92

Description

5000697687 hypothetical protein:gb:d26185_10:hypothetical protein mg371 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG371 MG371 Mycoplasma genitalium 2097 -11540480 119095 mg371 (de:hypothetical protein mg371) (db:swissprot) Y371_MYCGE Q49428 MYCOPLASMA GENITALIUM 2097 -11540480 172433 hypothetical protein homolog mg371 (db:pir2.dat) A64241 A64241 Mycoplasma genitalium 2097 -11540480 7500895203 mg371 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 41 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75229 pid:1673964 percent) (le:1003) (re:1977) (di:complement) U39719 U39719 g3844959 Mycoplasma genitalium 2097 -11540480 6500736622 hypothetical protein:gb:d26185_10:hypothetical protein mg371 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG371 MG371 Mycoplasma genitalium 2097 -11540480

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923110	19694	41850	2274	757

Description

5000697688 hypothetical protein:gb:u00016_19:hypothetical protein mg388 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG388 MG388 Mycoplasma genitalium 2097 -11540481 109135 mg388 (de:hypothetical protein mg388) (db:swissprot) Y388_MYCGE P47628 MYCOPLASMA GENITALIUM 2097 -11540481 172434 hypothetical protein homolog mg388 (db:pir2.dat) I64242 I64242 Mycoplasma genitalium 2097 -11540481 7500895225 mg388 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 42 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75209 pid:1673944 percent) (le:10227) (re:10532) (di:complement) U39720 U39720 g3844977 Mycoplasma genitalium 2097 -11540481 6500736623 hypothetical protein:gb:u00016_19:hypothetical protein mg388 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG388 MG388 Mycoplasma genitalium 2097 -11540481

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923128	19695	41851	1764	587

Description

5000697689 hypothetical protein:hypothetical protein mg423 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG423 MG423 Mycoplasma genitalium 2097 -11540482 109161 mg423 (de:hypothetical protein mg423) (db:swissprot) Y423_MYCGE P47662 MYCOPLASMA GENITALIUM 2097 -11540482 172529 hypothetical protein mg423 (cl:conserved hypothetical protein mg139) (db:pir2.dat) G64246 G64246 Mycoplasma genitalium 2097 -11540482 7500895275 mg423 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 46 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75174 pid:1673887 percent) (le:8708) (re:10393) (di:complement) U39724 U39724 g3845013 Mycoplasma genitalium 2097 -11540482 6500736624 hypothetical protein:hypothetical protein mg423 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG423 MG423 Mycoplasma genitalium 2097 -11540482

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923150	19696	41852	774	257

Description

5000697690 sp:p27712:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG432 MG432 Mycoplasma genitalium 2097 -11540483 119119 mg432 (de:hypothetical protein mg432) (db:swissprot) Y432_MYCGE Q49432 MYCOPLASMA GENITALIUM 2097 -11540483 172436 hypothetical protein homolog mg432 (db:pir2.dat) G64247 G64247 Mycoplasma genitalium 2097 -11540483 7500895283 mg432 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 47 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75166 pid:1673877 percent) (le:6807) (re:8003) (di:complement) U39725 U39725 g3845025 Mycoplasma genitalium 2097 -11540483 6500736625 sp:p27712:hypothetical protein (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG432 MG432 Mycoplasma genitalium 2097 -11540483

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923151	19697	41853	471	156

Description

5000697691 hypothetical protein:gb:d16311_1:hypothetical protein mg443 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG443 MG443 Mycoplasma genitalium 2097 -11540484 109171 mg443 (de:hypothetical protein mg443) (db:swissprot) Y443_MYCGE P47681 MYCOPLASMA GENITALIUM 2097 -11540484 172438 hypothetical protein homolog mg443 (db:pir2.dat) I64248 I64248 Mycoplasma genitalium 2097 -11540484 7500895306 mg443 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75134 pid:1673848 percent) (le:3335) (re:4522) (di:complement) U39726 U39726 g3845036 Mycoplasma genitalium 2097 -11540484 6500736626 hypothetical protein:gb:d16311_1:hypothetical protein mg443 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG443 MG443 Mycoplasma genitalium 2097 -11540484

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923156	19698	41854	561	186

Description

5000697692 hypothetical protein:gb:l08897_1:hypothetical protein mg447 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG447 MG447 Mycoplasma genitalium 2097 -11540485 109173 mg447 (de:hypothetical protein mg447) (db:swissprot) Y447_MYCGE P47685 MYCOPLASMA GENITALIUM 2097 -11540485 172439 hypothetical protein mg447 (cl:mycoplasma genitalium hypothetical protein mg447) (db:pir2.dat) D64249 D64249 Mycoplasma genitalium 2097 -11540485 7500895310 mg447 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 48 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75130 pid:1673844 percent) (le:6474) (re:8117) (di:complement) U39726 U39726 g3845040 Mycoplasma genitalium 2097 -11540485 6500736627 hypothetical protein:gb:l08897_1:hypothetical protein mg447 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG447 MG447 Mycoplasma genitalium 2097 -11540485

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923174	19699	41855	393	130

Description

5000697693 unknown:hypothetical protein mg461 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG461 MG461 Mycoplasma genitalium 2097 -11540486 109184 mg461 (de:hypothetical protein mg461) (db:swissprot) Y461_MYCGE P47699 MYCOPLASMA GENITALIUM 2097 -11540486 172440 hypothetical protein homolog mg461 (db:pir2.dat) I64250 I64250 Mycoplasma genitalium 2097 -11540486 7500895336 mg461 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 50 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75115 pid:1673826 percent) (le:1052) (re:2329) (di:complement) U39728 U39728 g3845056 Mycoplasma genitalium 2097 -11540486 6500736628 unknown:hypothetical protein mg461 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG461 MG461 Mycoplasma genitalium 2097 -11540486

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923181	19700	41856	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923190	19701	41857	618	205

Description

5000697694 hypothetical protein:gb:d14982_3:hypothetical protein mg464 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG464 MG464 Mycoplasma genitalium 2097 -11540487 109186 mg464 (de:hypothetical protein mg464) (db:swissprot) Y464_MYCGE P47702 MYCOPLASMA GENITALIUM 2097 -11540487 172441 hypothetical protein homolog mg464 (db:pir2.dat) C64251 C64251 Mycoplasma genitalium 2097 -11540487 7500895342 mg464 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 50 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75112 pid:1673823 percent) (le:4523) (re:5680) (di:complement) U39728 U39728 g3845059 Mycoplasma genitalium 2097 -11540487 6500736629 hypothetical protein:gb:d14982_3:hypothetical protein mg464 (gtcfc:14.1) (keggfc:14.2) (tigrfc:15.1) (db:gtc-mycoplasma genitalium) MG464 MG464 Mycoplasma genitalium 2097 -11540487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923196	19702	41858	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923199	19703	41859	1605	534

Description

6500736630 smpb:mg059 small protein:small protein b homolog (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG059 MG059 Mycoplasma genitalium 2097 -11540488 98688 smpb:mg059 (de:small protein b homolog) (db:swissprot) SMPB_MYCGE P47305 MYCOPLASMA GENITALIUM 2097 -11540488 172666 small protein smpb homolog (cl:small protein smpb) (db:pir2.dat) E64206 E64206 Mycoplasma genitalium 2097 -11540488 7500891750 mg059 small protein smpb (db:genpept-bct2) (de:mycoplasma genitalium section 7 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75043 pid:1673735 percent) (le:2692) (re:3129) (di:complement) U39685 U39685 g1045733 Mycoplasma genitalium 2097 -11540488 5000697630 (de:(mg059) (pn:small protein b homolog:small protein:smpb) (gn:smpb) (gtcfc:13.7) (ec:) (smpb_mycge) (keggfc:11.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium)) MG059 MG059 Mycoplasma genitalium 2097 10040563

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923220	19704	41860	522	173

Description

5000697631 orf3:hypothetical protein mg098 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG098 MG098 Mycoplasma genitalium 2097 -11540489 108717 mg098 (de:hypothetical protein mg098) (db:swissprot) Y098_MYCGE P47344 MYCOPLASMA GENITALIUM 2097 -11540489 172344 eggshell protein p48 homolog (db:pir2.dat) H64210 H64210 Mycoplasma genitalium 2097 -11540489 7500894681 mg098 glu-trna amidotransferase subunit gatc-related (db:genpept-bct2) (de:mycoplasma genitalium section 12 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75535 pid:1674297 percent) (le:2968) (re:4401) (di:direct) U39690 U39690 g3844686 Mycoplasma genitalium 2097 -11540489 6500736631 orf3:hypothetical protein mg098 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG098 MG098 Mycoplasma genitalium 2097 -11540489

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923241	19705	41861	438	145

Description

5000697632 hypothetical protein:gb:m31161_3:hypothetical protein mg131 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG131 MG131 Mycoplasma genitalium 2097 -11540490 108837 mg131 (de:hypothetical protein mg131) (db:swissprot) Y131_MYCGE P47377 MYCOPLASMA GENITALIUM 2097 -11540490 172400 hypothetical protein homolog mg131 (db:pir2.dat) E64214 E64214 Mycoplasma genitalium 2097 -11540490 7500894762 mg131 m. genitalium predicted coding region mg131 (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:hypothetical protein; identified by genemark;) (le:5289) (re:5513) (di:direct) U39693 U39693 g3844729 Mycoplasma genitalium 2097 -11540490 6500736632 hypothetical protein:gb:m31161_3:hypothetical protein mg131 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG131 MG131 Mycoplasma genitalium 2097 -11540490

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923242	19706	41862	429	142

Description

5000697633 hit protein:member of the hit-family:hypothetical 15 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG132 MG132 Mycoplasma genitalium 2097 -11540491 112882 mg132 (de:hypothetical hit-like protein mg132) (db:swissprot) YHIT_MYCGE P47378 MYCOPLASMA GENITALIUM 2097 -11540491 172401 histidine triad protein mg132 (cl:protein kinase c inhibitor:histidine triad homology) (db:pir2.dat) F64214 F64214 Mycoplasma genitalium 2097 -11540491 7500937001 mg132 hit protein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 15 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75504 pid:1674261 percent) (le:5847) (re:6272) (di:complement) U39693 U39693 g3844722 Mycoplasma genitalium 2097 -11540491 6500736633 hit protein:member of the hit-family:hypothetical 15 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG132 MG132 Mycoplasma genitalium 2097 -11540491

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923249	19707	41863	597	198

Description

5000697634 protein x:hypothetical protein mg145 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG145 MG145 Mycoplasma genitalium 2097 -11540492 108874 ribf:mg145 (ec:2.7.1.26:2.7.7.2) (de:synthetase)) (db:swissprot) RIBF_MYCGE P47391 MYCOPLASMA GENITALIUM 2097 -11540492 172612 protein x homolog (cl:conserved hypothetical protein hi0963) (db:pir2.dat) A64216 A64216 Mycoplasma genitalium 2097 -11540492 7500889773 mg145 riboflavin kinase/ fmn adenylyltransferase (db:genpept-bct2) (de:mycoplasma genitalium section 17 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75587 pid:1674379 percent) (le:8785) (re:9594) (di:direct) U39695 U39695 g3844738 Mycoplasma genitalium 2097 -11540492 6500736634 protein x:hypothetical protein mg145 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG145 MG145 Mycoplasma genitalium 2097 -11540492

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923253	19708	41864	1386	461

Description

5000697635 sensory rhodopsin ii transducer:htrii:hypothetical protein mg280 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG280 MG280 Mycoplasma genitalium 2097 -11540493 172661 sensory rhodopsin ii transducer homolog (db:pir2.dat) I64230 I64230 Mycoplasma genitalium 2097 -11540493 7500965568 mg280 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 29 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75384 pid:1674126 percent) (le:10096) (re:10842) (di:complement) U39707 U39707 g1045975 Mycoplasma genitalium 2097 -11540493 6500736635 sensory rhodopsin ii transducer:htrii:hypothetical protein mg280 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG280 MG280 Mycoplasma genitalium 2097 -11540493

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923256	19709	41865	606	201

Description

5000697636 nodulation protein f:nodf:acyl carrier protein homolog:acp (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG287 MG287 Mycoplasma genitalium 2097 -11540494 58257 mg287 (de:acyl carrier protein homolog (acp)) (db:swissprot) ACPH_MYCGE P47529 MYCOPLASMA GENITALIUM 2097 -11540494 172571 nodulation protein nodf homolog (cl:acyl carrier protein:acyl carrier protein homology) (db:pir2.dat) G64231 G64231 Mycoplasma genitalium 2097 -11540494 7500876353 mg287 acyl carrier protein:putative (db:genpept-bct2) (de:mycoplasma genitalium section 30 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75378 pid:1674118 percent) (le:6937) (re:7191) (di:direct) U39708 U39708 g1045983 Mycoplasma genitalium 2097 -11540494 6500736636 nodulation protein f:nodf:acyl carrier protein homolog:acp (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG287 MG287 Mycoplasma genitalium 2097 -11540494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923258	19710	41866	405	134

Description

5000697637 protein 1:hypothetical protein mg288 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG288 MG288 Mycoplasma genitalium 2097 -11540495 109051 mg288 (de:hypothetical protein mg288) (db:swissprot) Y288_MYCGE P47530 MYCOPLASMA GENITALIUM 2097 -11540495 172607 protein 1 homolog (cl:hypothetical protein mg096) (db:pir2.dat) H64231 H64231 Mycoplasma genitalium 2097 -11540495 7500895078 protein 1 (sr:mycoplasma genitalium (individual_isolate g37) dna) (db:genpept-bct1) (de:mycoplasma genitalium p37, p69_1 genes from bases 350467 to 357707(section 31 of 56) of the complete genome.) (nt:identified by sequence similarity; similar to) (le:1324) (re... U39709 U39709 g1045985 Mycoplasma genitalium 2097 -11540495 6500736637 protein 1:hypothetical protein mg288 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG288 MG288 Mycoplasma genitalium 2097 -11540495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923260	19711	41867	639	212

Description

6500736638 bcho:mg327 magnesium-chelatase 30 kda subunit (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG327 MG327 Mycoplasma genitalium 2097 -11540496 118146 mg327 (ec:3.1.-.-) (de:putative esterase/lipase 2,) (db:swissprot) ESL2_MYCGE Q49418 MYCOPLASMA GENITALIUM 2097 -11540496 172551 protoporphyrin ix magnesium chelatase:bcho homolog (cl:triacylglycerol lipase 1) (ec:4.99.1.-) (db:pir2.dat) B64236 B64236 Mycoplasma genitalium 2097 -11540496 7500881167 mg327 lipase/esterase:putative (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75311 pid:1674047 percent) (le:914) (re:1720) (di:complement) U39714 U39714 g3844907 Mycoplasma genitalium 2097 -11540496 5000697638 (de:(mg327) (pn:magnesium-chelatase 30 kda subunit:bcho) (gn:bcho) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium)) MG327 MG327 Mycoplasma genitalium 2097 10060206

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923273	19712	41868	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923288	19713	41869	900	299

Description

6500736639 fcrv:mg328 protein v (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG328 MG328 Mycoplasma genitalium 2097 -11540497 119075 mg328 (de:hypothetical protein mg328) (db:swissprot) Y328_MYCGE Q49419 MYCOPLASMA GENITALIUM 2097 -11540497 172611 protein v fcrv homolog (db:pir2.dat) C64236 C64236 Mycoplasma genitalium 2097 -11540497 7500895133 mg328 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 36 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75310 pid:1674046 percent) (le:1707) (re:3977) (di:complement) U39714 U39714 g3844908 Mycoplasma genitalium 2097 -11540497 5000697639 (de:(mg328) (pn:protein v:fcrv) (gn:fcrv) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium)) MG328 MG328 Mycoplasma genitalium 2097 10061520

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923321	19714	41870	615	204

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923323	19715	41871	987	328

Description

6500736640 nifs:mg336 nitrogen fixation protein (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG336 MG336 Mycoplasma genitalium 2097 -11540498 500684767 mg336 (de:nifs-like protein) (db:swissprot) NISH_MYCGE Q49420 MYCOPLASMA GENITALIUM 2097 -11540498 172570 nitrogen fixation protein nifs homolog (db:pir2.dat) B64237 B64237 Mycoplasma genitalium 2097 -11540498 7500886482 mg336 nitrogen fixation protein nifs (db:genpept-bct2) (de:mycoplasma genitalium section 37 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75298 pid:1674033 percent) (le:85) (re:1311) (di:direct) U39715 U39715 g3844918 Mycoplasma genitalium 2097 -11540498 5000697640 (de:(mg336) (pn:nitrogen fixation protein:nifs) (gn:nifs) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium)) MG336 MG336 Mycoplasma genitalium 2097 10059274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923352	19716	41872	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923359	19717	41873	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923361	19718	41874	441	146

Description

6500736641 mucb:mg360 uv protection protein (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG360 MG360 Mycoplasma genitalium 2097 -11540499 121769 mg360 (de:hypothetical protein mg360) (db:swissprot) Y360_MYCGE Q49426 MYCOPLASMA GENITALIUM 2097 -11540499 172708 uv protection protein mucb homolog (db:pir2.dat) H64239 H64239 Mycoplasma genitalium 2097 -11540499 7500895190 mg360 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 39 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75241 pid:1673977 percent) (le:9389) (re:10624) (di:complement) U39717 U39717 g3844944 Mycoplasma genitalium 2097 -11540499 5000697641 (de:(mg360) (pn:uv protection protein:mucb) (gn:mucb) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium)) MG360 MG360 Mycoplasma genitalium 2097 10065244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923364	19719	41875	870	289

Description

5000697642 mobilization protein:mob13:hypothetical protein mg364 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG364 MG364 Mycoplasma genitalium 2097 -11540500 109117 mg364 (de:hypothetical protein mg364) (db:swissprot) Y364_MYCGE P47604 MYCOPLASMA GENITALIUM 2097 -11540500 172565 mobilization protein mob13 homolog (db:pir2.dat) C64240 C64240 Mycoplasma genitalium 2097 -11540500 7500895192 mg364 conserved hypothetical protein (db:genpept-bct2) (de:mycoplasma genitalium section 40 of 51 of the complete genome.) (nt:similar to gb:u00089 sp:p75236 pid:1673971 percent) (le:1491) (re:2165) (di:direct) U39718 U39718 g3844951 Mycoplasma genitalium 2097 -11540500 6500736642 mobilization protein:mob13:hypothetical protein mg364 (gtcfc:14.3) (keggfc:14.2) (tigrfc:14.2) (db:gtc-mycoplasma genitalium) MG364 MG364 Mycoplasma genitalium 2097 -11540500

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923378	19720	41876	444	147

Description

6500736643 succ:mj0210 succinyl-coa synthetase:beta subunit:succinyl-coa synthetase beta chain:scs-beta (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (keggfc:1.2:1.10:1.12:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-c... MJ0210 MJ0210 Methanococcus jannaschii 2190 -11540501 121483 succ:mj0210 (ec:6.2.1.5) (de:succinyl-coa synthetase beta chain, (scs-beta)) (db:swissprot) SUCC_METJA Q57663 METHANOCOCCUS JANNASCHII 2190 -11540501 174554 succinyl-coa synthetase:beta subunit (cl:succinate--coa ligase (adp-forming) beta chain) (db:pir2.dat) (mp:for201043-202137) C64326 C64326 Methanococcus jannaschii 2190 -11540501 246645 mj0210 succinyl-coa synthetase:beta subunit (db:genpept-bct1) (de:methanococcus jannaschii section 19 of 150 of the complete genome.) (nt:similar to sp:p25126 pid:48177 percent identity:) (le:69) (re:1163) (di:direct) U67477 U67477 g1590950 Methanococcus jannaschii 2190 -11540501 5000697802 (de:(mj0210) (pn:succinyl-coa synthetase beta chain:scs-beta:succinyl-coa synthetase, beta subunit) (gn:succ) (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (succ_metja) (keggfc:1.2:1.10:1.12:2.4) (tigrfc:6.12) (db:gtc-methanococcus jan) MJ0210 MJ0210 Methanococcus jannaschii 2190 10064844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923383	19721	41877	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923398	19722	41878	723	240

Description

GTC ORF with score 353 to: (db:genpept) (de:pseuodmonas stutzeri transposase-like protein tnpa3 (tnpa3),salicylate hydroxylase (nahw), transposase-like protein (tnpa2) andregulatory protein (nahr) genes; and naphthalene degradationlower-pathway gene ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923399	19723	41879	216	71

Description

GTC ORF with score 106 to: (db:genpept) (de:pseuodmonas stutzeri transposase-like protein tnpa3 (tnpa3),salicylate hydroxylase (nahw), transposase-like protein (tnpa2) andregulatory protein (nahr) genes; and naphthalene degradationlower-pathway gene ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923409	19724	41880	1224	407

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923416	19725	41881	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923426	19726	41882	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923427	19727	41883	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923463	19728	41884	699	232

Description

6500736644 pyruvate ferredoxin oxidoreductase:subunit beta:porb:ferredoxin oxidoreductase:beta subunit (gtcfc:1.10:1.11:1.8:2.2:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-pyruvate and ... MJ0266 MJ0266 Methanococcus jannaschii 2190 -11540502 173098 probable pyruvate synthase:beta chain (cl:pyruvate synthase beta chain) (ec:1.2.7.1) (db:pir2.dat) (mp:rev253867-252971) C64333 C64333 Methanococcus jannaschii 2190 -11540502 246701 mj0266 pyruvate ferredoxin oxidoreductase:subunit beta (db:genpept-bct1) (de:methanococcus jannaschii section 24 of 150 of the complete genome.) (nt:similar to pid:1197364 percent identity: 58.89;) (le:1191) (re:2087) (di:complement) U67482 U67482 g1590994 Methanococcus jannaschii 2190 -11540502 5000697803 (de:(mj0266) (pn:ferredoxin oxidoreductase, beta subunit) (gtcfc:1.10:1.11:1.8:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ0266 MJ0266 Methanococcus jannaschii 2190 10091492

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923464	19729	41885	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923466	19730	41886	909	302

Description

6500736645 pyruvate ferredoxin oxidoreductase:subunit alpha:pora:ferredoxin oxidoreductase:alpha subunit (gtcfc:1.10:1.11:1.8:2.2:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-pyruvate and ... MJ0267 MJ0267 Methanococcus jannaschii 2190 -11540503 173099 pyruvate synthase:alpha chain (cl:pyruvate synthase alpha chain) (ec:1.2.7.1) (db:pir2.dat) (mp:rev255064-253895) D64333 D64333 Methanococcus jannaschii 2190 -11540503 246702 mj0267 pyruvate ferredoxin oxidoreductase:subunit (db:genpept-bct1) (de:methanococcus jannaschii section 24 of 150 of the complete genome.) (nt:similar to pid:1197363 percent identity: 57.33;) (le:2115) (re:3284) (di:complement) U67482 U67482 g1590995 Methanococcus jannaschii 2190 -11540503 5000697804 (de:(mj0267) (pn:ferredoxin oxidoreductase, alpha subunit) (gtcfc:1.10:1.11:1.8:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ0267 MJ0267 Methanococcus jannaschii 2190 10091493

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923467	19731	41887	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923475	19732	41888	255	84

Description

6500736646 pyruvate ferredoxin oxidoreductase:subunit delta:pord:ferredoxin oxidoreductase:delta subunit (gtcfc:1.10:1.11:1.8:2.2:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-pyruvate and ... MJ0268 MJ0268 Methanococcus jannaschii 2190 -11540504 173101 ferredoxin 2 4fe-4s mj0268:ferredoxin oxidoreductase delta subunit) (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:rev255346-255086) E64333 E64333 Methanococcus jannaschii 2190 -11540504 246703 mj0268 pyruvate ferredoxin oxidoreductase:subunit (db:genpept-bct1) (de:methanococcus jannaschii section 24 of 150 of the complete genome.) (nt:similar to gp:1197362 percent identity: 58.82;) (le:3306) (re:3566) (di:complement) U67482 U67482 g1499049 Methanococcus jannaschii 2190 -11540504 5000697805 (de:(mj0268) (pn:ferredoxin oxidoreductase, delta subunit) (gtcfc:1.10:1.11:1.8:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ0268 MJ0268 Methanococcus jannaschii 2190 10091495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923476	19733	41889	327	108

Description

6500736647 pyruvate ferredoxin oxidoreductase:subunit gamma:porg:ferredoxin oxidoreductase:gamma subunit (gtcfc:1.10:1.11:1.8:2.2:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-pyruvate and ... MJ0269 MJ0269 Methanococcus jannaschii 2190 -11540505 173102 probable pyruvate synthase:gamma chain (ec:1.2.7.1) (db:pir2.dat) (mp:rev255901-255365) F64333 F64333 Methanococcus jannaschii 2190 -11540505 246704 mj0269 pyruvate ferredoxin oxidoreductase:subunit (db:genpept-bct1) (de:methanococcus jannaschii section 24 of 150 of the complete genome.) (nt:similar to pid:1197358 percent identity: 63.22;) (le:3585) (re:4121) (di:complement) U67482 U67482 g1590996 Methanococcus jannaschii 2190 -11540505 5000697806 (de:(mj0269) (pn:ferredoxin oxidoreductase, gamma subunit) (gtcfc:1.10:1.11:1.8:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ0269 MJ0269 Methanococcus jannaschii 2190 10091496

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923477	19734	41890	228	75

Description

6500736648 2-ketoglutarate ferredoxin oxidoreductase:subunit alpha:kora:ferredoxin oxidoreductase:alpha subunit (gtcfc:1.10:1.11:1.8:2.2:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-pyruvate and ... MJ0276 MJ0276 Methanococcus jannaschii 2190 -11540506 7500895051 mj0276 (de:hypothetical protein mj0276) (db:swissprot) Y276_METJA Q57724 METHANOCOCCUS JANNASCHII 2190 -11540506 173100 2-oxoacid--ferredoxin oxidoreductase:alpha chain:2-oxoacid:ferredoxin oxidoreductase coa-acetylating (cl:helicobacter pylori 2-oxoacid ferredoxin oxidoreductase:2-oxoacid ferredoxin oxidoreductase homology) (ec:1.2.7.-) (db:pir2.dat) (mp:rev262731-261631) E64334 E64334 Methanococcus jannaschii 2190 -11540506 7500895053 mj0276 2-ketoglutarate ferredoxin oxidoreductase (db:genpept-bct1) (de:methanococcus jannaschii section 25 of 150 of the complete genome.) (nt:similar to gb:x64521 pid:43498 percent ident:) (le:58) (re:1158) (di:complement) U67483 U67483 g1592279 Methanococcus jannaschii 2190 -11540506 246711 mju67483 (le:261631) (re:262731) (di:direct) (de:or:methanococcus jannaschii pn:ferredoxin oxidoreductase, alpha subunit gn:mj0276 le:277 re:1377 di:complement nt:similar to x64521_1 percent identity: 44.2;) U67483 U67483 g1592279 Methanococcus jannaschii 2190 -11540506 5000697807 (de:(mj0276) (pn:ferredoxin oxidoreductase, alpha subunit) (gtcfc:1.10:1.11:1.8:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ0276 MJ0276 Methanococcus jannaschii 2190 10091494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923488	19735	41891	1383	460

Description

6500736649 ldh:mj0490 l-lactate dehydrogenase egad (gtcfc:1.1:1.8:2.8) (ec:1.1.1.27) (keggfc:1.1:1.8:1.10:5.5:5.12:5.13) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ0490 MJ0490 Methanococcus jannaschii 2190 -11540507 119884 ldh:mj0490 (ec:1.1.1.27) (de:l-lactate dehydrogenase,) (db:swissprot) LDH_METJA Q60176 METHANOCOCCUS JANNASCHII 2190 -11540507 174307 l-lactate dehydrogenase (cl:l-lactate dehydrogenase) (ec:1.1.1.27) (db:pir2.dat) (mp:for433728-434669) B64361 B64361 Methanococcus jannaschii 2190 -11540507 246924 mj0490 l-lactate dehydrogenase egad|7256|705 (db:genpept-bct1) (de:methanococcus jannaschii section 41 of 150 of the complete genome.) (nt:similar to sp:p16115 gb:x74302 pid:396281 percent) (le:2965) (re:3906) (di:direct) U67499 U67499 g1591194 Methanococcus jannaschii 2190 -11540507 5000697794 (de:(mj0490) (pn:l-lactate dehydrogenase:lactate dehydrogenase) (gn:ldh) (gtcfc:1.1:1.10:1.8:5.12:5.13) (ec:1.1.1.27) (ldh_metja) (keggfc:1.1:1.8:1.10:5.12:5.13) (tigrfc:6.8) (db:gtc-methanococcus jannaschii)) MJ0490 MJ0490 Methanococcus jannaschii 2190 10062614

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923490	19736	41892	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923506	19737	41893	555	184

Description

6500736650 2-ketoglutarate ferredoxin oxidoreductase:subunit gamma:korg:ferredoxin oxidoreductase:gamma subunit (gtcfc:1.10:1.11:1.8:2.2:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-pyruvate and ... MJ0536 MJ0536 Methanococcus jannaschii 2190 -11540508 173103 probable 2-oxoglutarate synthase:gamma chain (cl:pyruvate synthase gamma chain) (ec:1.2.7.3) (db:pir2.dat) (mp:rev472943-472380) H64366 H64366 Methanococcus jannaschii 2190 -11540508 246970 mj0536 2-ketoglutarate ferredoxin oxidoreductase (db:genpept-bct1) (de:methanococcus jannaschii section 45 of 150 of the complete genome.) (nt:similar to pid:1197358 percent identity: 32.00;) (le:535) (re:1098) (di:complement) U67503 U67503 g1591240 Methanococcus jannaschii 2190 -11540508 5000697808 (de:(mj0536) (pn:ferredoxin oxidoreductase, gamma subunit) (gtcfc:1.10:1.11:1.8:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ0536 MJ0536 Methanococcus jannaschii 2190 10091497

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923508	19738	41894	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923521	19739	41895	402	133

Description

6500736651 2-ketoglutarate ferredoxin oxidoreductase:subunit beta:korb:ferredoxin oxidoreductase:beta subunit (gtcfc:1.10:1.11:1.8:2.2:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-pyruvate and ... MJ0537 MJ0537 Methanococcus jannaschii 2190 -11540509 174459 pyruvate synthase:beta chain:ferredoxin oxidoreductase:beta subunit (cl:pyruvate synthase beta chain) (ec:1.2.7.1) (db:pir2.dat) (mp:rev473748-472936) A64367 A64367 Methanococcus jannaschii 2190 -11540509 246971 mj0537 2-ketoglutarate ferredoxin oxidoreductase (db:genpept-bct1) (de:methanococcus jannaschii section 45 of 150 of the complete genome.) (nt:similar to gb:x64521 pid:43499 percent identity:) (le:1091) (re:1903) (di:complement) U67503 U67503 g1591241 Methanococcus jannaschii 2190 -11540509 5000697809 (de:(mj0537) (pn:ferredoxin oxidoreductase, beta subunit) (gtcfc:1.10:1.11:1.8:2.5) (ec:1.2.7.1) (keggfc:1.8:1.10:1.11:2.4) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ0537 MJ0537 Methanococcus jannaschii 2190 10092455

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923527	19740	41896	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923528	19741	41897	633	210

Description

GTC ORF with score 372 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c17d11.) (nt:spbc17d11.09, len:435aa, similarity: to s.) (le:19897:20255:20529:20835) (re:20139:20488:20770:21392) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923529	19742	41898	573	190

Description

6500736652 accc:mj1229 biotin carboxylase:a subunit of acetyl-coa carboxylase:acc (gtcfc:1.10:1.8:3.1:3.2) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ1229 MJ1229 Methanococcus jannaschii 2190 -11540510 117610 accc:mj1229 (ec:6.3.4.14:6.4.1.2) (de:carboxylase,) (acc)) (db:swissprot) ACCC_METJA Q58626 METHANOCOCCUS JANNASCHII 2190 -11540510 172984 biotin carboxylase (cl:biotin carboxylase:biotin carboxylase homology) (ec:6.3.4.14) (db:pir2.dat) (mp:rev1173221-1171716) D64453 D64453 Methanococcus jannaschii 2190 -11540510 247662 mj1229 biotin carboxylase accc (db:genpept-bct1) (de:methanococcus jannaschii section 105 of 150 of the complete genome.) (nt:similar to gb:l14862 sp:q06862 pid:289133 percent) (le:9518) (re:11023) (di:complement) U67563 U67563 g1591860 Methanococcus jannaschii 2190 -11540510 5000697810 (de:(mj1229) (pn:a subunit of acetyl-coa carboxylase :acc:biotin carboxylase) (gn:accc) (gtcfc:1.10:1.8:3.1) (ec:6.3.4.14) (accc_metja) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-methanococcus jannaschii)) MJ1229 MJ1229 Methanococcus jannaschii 2190 10059503

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923543	19743	41899	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923561	19744	41900	7401	2467

Description

6500736653 sucd:mj1246 succinyl-coa synthetase:alpha subunit:succinyl-coa synthetase alpha chain:scs-alpha (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (keggfc:1.2:1.10:1.12:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-c... MJ1246 MJ1246 Methanococcus jannaschii 2190 -11540511 121482 sucd:mj1246 (ec:6.2.1.5) (de:succinyl-coa synthetase alpha chain, (scs-alpha)) (db:swissprot) SUCD_METJA Q58643 METHANOCOCCUS JANNASCHII 2190 -11540511 174553 succinyl-coa synthetase:alpha subunit (cl:succinate--coa ligase (adp-forming) alpha chain) (ec:6.2.1.-) (db:pir2.dat) (mp:rev1189795-1188911) E64455 E64455 Methanococcus jannaschii 2190 -11540511 247679 mj1246 succinyl-coa synthetase:alpha subunit sucd (db:genpept-bct1) (de:methanococcus jannaschii section 107 of 150 of the complete genome.) (nt:similar to gb:j01619 sp:p07459 pid:146204) (le:2996) (re:3880) (di:complement) U67565 U67565 g1591879 Methanococcus jannaschii 2190 -11540511 5000697811 (de:(mj1246) (pn:succinyl-coa synthetase alpha chain:scs-alpha:succinyl-coa synthetase, alpha subunit) (gn:sucd) (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (sucd_metja) (keggfc:1.2:1.10:1.12:2.4) (tigrfc:6.12) (db:gtc-methanococcus) MJ1246 MJ1246 Methanococcus jannaschii 2190 10064842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923576	19745	41901	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923629	19746	41902	2235	744

Description

6500736654 pyruvate kinase:pk (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (keggfc:1.1:1.8:2.3) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ0108 MJ0108 Methanococcus jannaschii 2190 -11540512 119844 mj0108 (ec:2.7.1.40) (de:pyruvate kinase, (pk)) (db:swissprot) KPYK_METJA Q57572 METHANOCOCCUS JANNASCHII 2190 -11540512 174458 pyruvate kinase (ec:2.7.1.40) (db:pir2.dat) (mp:for104305-105648) D64313 D64313 Methanococcus jannaschii 2190 -11540512 246542 mj0108 pyruvate kinase (db:genpept-bct1) (de:methanococcus jannaschii section 10 of 150 of the complete genome.) (nt:similar to gb:d13095 sp:q02499 gb:x57859 pid:285623) (le:2565) (re:3908) (di:direct) U67468 U67468 g1590885 Methanococcus jannaschii 2190 -11540512 5000697792 (de:(mj0108) (pn:pk:pyruvate kinase) (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (kpyk_metja) (keggfc:1.1:1.8:2.3) (tigrfc:6.8) (db:gtc-methanococcus jannaschii)) MJ0108 MJ0108 Methanococcus jannaschii 2190 10062572

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923644	19747	41903	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923647	19748	41904	351	116

Description

6500736655 eno:mj0232 enolase:lase:2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase (gtcfc:1.1) (ec:4.2.1.11) (keggfc:1.1) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ0232 MJ0232 Methanococcus jannaschii 2190 -11540513 118134 eno:mj0232 (ec:4.2.1.11) (de:glycerate hydro-lyase)) (db:swissprot) ENO_METJA Q60173 METHANOCOCCUS JANNASCHII 2190 -11540513 174418 phosphopyruvate hydratase::enolase (cl:enolase) (ec:4.2.1.11) (db:pir2.dat) (mp:rev224209-222926) A64329 A64329 Methanococcus jannaschii 2190 -11540513 246667 mj0232 enolase eno (db:genpept-bct1) (de:methanococcus jannaschii section 21 of 150 of the complete genome.) (nt:similar to gb:l29475 sp:p37869 pid:460259) (le:1477) (re:2760) (di:complement) U67479 U67479 g1590967 Methanococcus jannaschii 2190 -11540513 5000697793 (de:(mj0232) (pn:lase:2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase:enolase) (gn:eno) (gtcfc:1.1) (ec:4.2.1.11) (eno_metja) (keggfc:1.1) (tigrfc:6.8) (db:gtc-methanococcus jannaschii)) MJ0232 MJ0232 Methanococcus jannaschii 2190 10060193

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923665	19749	41905	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923694	19750	41906	654	217

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923740	19751	41907	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923743	19752	41908	5112	1703

Description

6500736656 dihydrolipoamide dehydrogenase (gtcfc:1.1:1.8) (ec:1.8.1.4) (keggfc:1.1:1.2:1.8:5.3) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0636 MJ0636 Methanococcus jannaschii 2190 -11540514 4000708384 mj0636 (de:hypothetical protein mj0636) (db:swissprot) Y636_METJA Q58053 METHANOCOCCUS JANNASCHII 2190 -11540514 173053 dihydrolipoamide dehydrogenase (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (ec:1.8.1.4) (db:pir2.dat) (mp:for565881-567074) D64379 D64379 Methanococcus jannaschii 2190 -11540514 247070 mj0636 dihydrolipoamide dehydrogenase (db:genpept-bct1) (de:methanococcus jannaschii section 53 of 150 of the complete genome.) (nt:similar to percent identity: 28.88; identified by) (le:6452) (re:7645) (di:direct) U67511 U67511 g1591348 Methanococcus jannaschii 2190 -11540514 5000697795 (de:(mj0636) (pn:dihydrolipoamide dehydrogenase) (gtcfc:1.1:1.2:5.3) (ec:1.8.1.4) (keggfc:1.1:1.2:5.3) (tigrfc:6.10) (db:gtc-methanococcus jannaschii)) MJ0636 MJ0636 Methanococcus jannaschii 2190 10091471

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923774	19753	41909	366	121

Description

6500736657 pgk:mj0641 phosphoglycerate kinase (gtcfc:1.1:2.4) (ec:2.7.2.3) (keggfc:1.1:2.3) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ0641 MJ0641 Methanococcus jannaschii 2190 -11540515 4000709395 pgk:mj0641 (ec:2.7.2.3) (de:phosphoglycerate kinase,) (db:swissprot) PGK_METJA Q58058 METHANOCOCCUS JANNASCHII 2190 -11540515 174413 phosphoglycerate kinase (cl:phosphoglycerate kinase) (ec:2.7.2.3) (db:pir2.dat) (mp:rev571288-570035) A64380 A64380 Methanococcus jannaschii 2190 -11540515 247075 mj0641 phosphoglycerate kinase pgk (db:genpept-bct1) (de:methanococcus jannaschii section 54 of 150 of the complete genome.) (nt:similar to gb:m55529 sp:p20971 pid:149808 percent) (le:105) (re:1358) (di:complement) U67512 U67512 g1592299 Methanococcus jannaschii 2190 -11540515 5000697796 (de:(mj0641) (pn:3-phosphoglycerate kinase) (gtcfc:1.1:2.4) (ec:2.7.2.3) (keggfc:1.1:2.3) (tigrfc:6.8) (db:gtc-methanococcus jannaschii)) MJ0641 MJ0641 Methanococcus jannaschii 2190 10071019

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923781	19754	41910	2301	766

Description

6500736658 glyceraldehyde 3-phosphate dehydrogenase (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ1146 MJ1146 Methanococcus jannaschii 2190 -11540516 7500881974 gap:mj1146 (ec:1.2.1.12) (de:glyceraldehyde 3-phosphate dehydrogenase, (gapdh)) (db:swissprot) G3P_METJA Q58546 METHANOCOCCUS JANNASCHII 2190 -11540516 173149 glyceraldehyde-3-phosphate dehydrogenase (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir2.dat) (mp:rev1086336-1085305) A64443 A64443 Methanococcus jannaschii 2190 -11540516 7500881976 mj1146 glyceraldehyde 3-phosphate dehydrogenase (db:genpept-bct1) (de:methanococcus jannaschii section 99 of 150 of the complete genome.) (nt:similar to sp:p10618 pid:149792 percent ident:) (le:583) (re:1614) (di:complement) U67557 U67557 g1591778 Methanococcus jannaschii 2190 -11540516 247579 mju67557 (le:1085305) (re:1086336) (di:direct) (de:or:methanococcus jannaschii pn:glyceraldehyde 3-phosphate dehydrogenase gn:mj1146 le:583 re:1614 di:complement nt:similar to p10618 percent identity: 60.0;) U67557 U67557 g1591778 Methanococcus jannaschii 2190 -11540516 5000697797 (de:(mj1146) (pn:glyceraldehyde 3-phosphate dehydrogenase) (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (tigrfc:6.8) (db:gtc-methanococcus jannaschii)) MJ1146 MJ1146 Methanococcus jannaschii 2190 10069487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923782	19755	41911	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923783	19756	41912	366	121

Description

6500736659 tpia:mj1528 triosephosphate isomerase:putative triosephosphate isomerase:tim (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (keggfc:1.1:1.5:2.3:8.1) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ1528 MJ1528 Methanococcus jannaschii 2190 -11540517 121636 tpia:mj1528 (ec:5.3.1.1) (de:putative triosephosphate isomerase, (tim)) (db:swissprot) TPIS_METJA Q58923 METHANOCOCCUS JANNASCHII 2190 -11540517 174590 triose-phosphate isomerase (ec:5.3.1.1) (db:pir2.dat) (mp:rev1506406-1505747) G64490 G64490 Methanococcus jannaschii 2190 -11540517 247961 mj1528 triosephosphate isomerase (db:genpept-bct1) (de:methanococcus jannaschii section 135 of 150 of the complete genome.) (nt:similar to gp:1695188 percent identity: 66.83;) (le:13790) (re:14449) (di:complement) U67593 U67593 g1592158 Methanococcus jannaschii 2190 -11540517 5000697798 (de:(mj1528) (pn:putative triosephosphate isomerase:tim:triosephosphate isomerase) (gn:tpia) (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (tpis_metja) (keggfc:1.1:1.5:2.3:8.1) (tigrfc:6.8) (db:gtc-methanococcus jannaschii)) MJ1528 MJ1528 Methanococcus jannaschii 2190 10065065

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923791	19757	41913	507	168

Description

6500736660 glucose-6-phosphate isomerase (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (keggfc:1.1:1.3:7.1) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ1605 MJ1605 Methanococcus jannaschii 2190 -11540518 173140 glucose-6-phosphate isomerase (ec:5.3.1.9) (db:pir2.dat) (mp:rev1579943-1578738) D64500 D64500 Methanococcus jannaschii 2190 -11540518 248038 mj1605 glucose-6-phosphate isomerase (db:genpept-bct1) (de:methanococcus jannaschii section 142 of 150 of the complete genome.) (nt:similar to sp:p13376 gb:x16640 pid:40048 percent) (le:8331) (re:9536) (di:complement) U67600 U67600 g1500502 Methanococcus jannaschii 2190 -11540518 5000697799 (de:(mj1605) (pn:glucose-6-phosphate isomerase) (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (keggfc:1.1:1.3:7.1) (tigrfc:6.8) (db:gtc-methanococcus jannaschii)) MJ1605 MJ1605 Methanococcus jannaschii 2190 10091525

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923799	19758	41914	312	103

Description

6500736661 ppsa:mj0542 phosphoenolpyruvate synthase:probable phosphoenolpyruvate synthase:pyruvate:water dikinase:pep synthase (gtcfc:1.1:1.8:2.5) (ec:2.7.9.2) (keggfc:1.8:2.4) (tigrfc:6.7) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-glycolysis--gluconeogenesis:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:energy metabolism-reductive carboxyla... MJ0542 MJ0542 Methanococcus jannaschii 2190 -11540519 4000709383 ppsa:mj0542 (ec:2.7.9.2) (de:dikinase) (pep synthase)) (db:swissprot) PPSA_METJA Q57962 METHANOCOCCUS JANNASCHII 2190 -11540519 174460 pyruvate:water dikinase:intein-containing:phosphoenolpyruvate synthase (ec:2.7.9.2) (db:pir2.dat) (mp:rev481132-477566) F64367 F64367 Methanococcus jannaschii 2190 -11540519 246976 mj0542 phosphoenolpyruvate synthase (db:genpept-bct1) (de:methanococcus jannaschii section 45 of 150 of the complete genome.) (nt:similar to sp:p46893 percent identity: 48.46;) (le:5721) (re:9287) (di:complement) U67503 U67503 g1591246 Methanococcus jannaschii 2190 -11540519 5000697837 (de:(mj0542) (pn:phosphoenolpyruvate synthase) (gtcfc:1.8:2.5) (ec:2.7.9.2) (keggfc:1.8:2.4) (tigrfc:6.7) (db:gtc-methanococcus jannaschii)) MJ0542 MJ0542 Methanococcus jannaschii 2190 10092456

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923800	19759	41915	444	147

Description

6500736662 glyceraldehyde-3-phosphate dehydrogenase:nadp-dependent:gapn:nadp-dependent glyceraldehyde-3-phosphate dehydrogenase (gtcfc:1.1) (ec:1.2.1.9) (keggfc:14.1) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ1411 MJ1411 Methanococcus jannaschii 2190 -11540520 174377 nadp-dependent glyceraldehyde-3-phosphate dehydrogenase (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (ec:1.2.1.-) (db:pir2.dat) (mp:for1371808-1373199) B64476 B64476 Methanococcus jannaschii 2190 -11540520 247844 mju67581 (le:1371808) (re:1373199) (di:direct) (de:or:methanococcus jannaschii pn:nadp-dependent glyceraldehyde-3-phosphate gn:mj1411 le:5883 re:7274 di:direct nt:similar to 138521_1 percent identity: 39.2;) U67581 U67581 g1592060 Methanococcus jannaschii 2190 -11540520 5000697800 (de:(mj1411) (pn:nadp-dependent glyceraldehyde-3-phosphate dehydrogenase) (gtcfc:1.1) (ec:1.2.1.9) (keggfc:11.1) (tigrfc:6.8) (db:gtc-methanococcus jannaschii)) MJ1411 MJ1411 Methanococcus jannaschii 2190 10092412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923802	19760	41916	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923812	19761	41917	318	105

Description

5000697801 2pgk:2-phosphoglycerate kinase (gtcfc:1.1) (keggfc:14.2) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ1482 MJ1482 Methanococcus jannaschii 2190 -11540521 172913 2-phosphoglycerate kinase (cl:2-phosphoglycerate kinase) (ec:2.7.2.-) (db:pir2.dat) (mp:for1453393-1454322) A64485 A64485 Methanococcus jannaschii 2190 -11540521 247915 mj1482 2-phosphoglycerate kinase 2pgk (db:genpept-bct1) (de:methanococcus jannaschii section 131 of 150 of the complete genome.) (nt:similar to gb:x70785 pid:467751 percent identity:) (le:3836) (re:4765) (di:direct) U67589 U67589 g1592120 Methanococcus jannaschii 2190 -11540521 6500736663 2pgk:2-phosphoglycerate kinase (gtcfc:1.1) (keggfc:14.2) (tigrfc:6.8) (db:gtc-methanococcus jannaschii) MJ1482 MJ1482 Methanococcus jannaschii 2190 -11540521

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923819	19762	41918	423	140

Description

5000697812 succinate dehydrogenase:flavoprotein subunit:sdha:hypothetical fad flavoprotein oxidase (gtcfc:2.8:9.5) (keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii) (keggfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-butanoate metabolism:energy metabolism-oxidative phosphorylation:energy metaboli... MJ0033 MJ0033 Methanococcus jannaschii 2190 -11540522 118737 mj0033 (de:hypothetical fad flavoprotein oxidase mj0033) (db:swissprot) Y033_METJA Q60356 METHANOCOCCUS JANNASCHII 2190 -11540522 174552 succinate dehydrogenase:flavoprotein (cl:fumarate reductase flavoprotein:3-oxosteroid 1-dehydrogenase homology:fumarate reductase flavoprotein homology) (ec:1.3.99.1) (db:pir2.dat) (mp:for33629-35248) A64304 A64304 Methanococcus jannaschii 2190 -11540522 246467 mj0033 succinate dehydrogenase:flavoprotein subunit (db:genpept-bct1) (de:methanococcus jannaschii section 4 of 150 of the complete genome.) (nt:similar to gp:1524302 percent identity: 41.63;) (le:153) (re:1772) (di:direct) U67462 U67462 g1592258 Methanococcus jannaschii 2190 -11540522 6500736664 succinate dehydrogenase:flavoprotein subunit:sdha:hypothetical fad flavoprotein oxidase (gtcfc:2.8:9.5) (keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii) MJ0033 MJ0033 Methanococcus jannaschii 2190 -11540522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923827	19763	41919	411	136

Description

6500736665 group ii decarboxylase:glutamate decarboxylase (gtcfc:1.11:1.8:5.1:5.2:6.1) (ec:4.1.1.15) (keggfc:1.11:5.1:5.2:6.1:6.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ0050 MJ0050 Methanococcus jannaschii 2190 -11540523 118750 mj0050 (de:hypothetical protein mj0050) (db:swissprot) Y050_METJA Q60358 METHANOCOCCUS JANNASCHII 2190 -11540523 173311 hypothetical protein mj0050 (cl:escherichia coli glutamate decarboxylase) (db:pir2.dat) (mp:rev52237-51047) B64306 B64306 Methanococcus jannaschii 2190 -11540523 246484 mj0050 group ii decarboxylase (db:genpept-bct1) (de:methanococcus jannaschii section 5 of 150 of the complete genome.) (nt:similar to gp:1226312 percent identity: 30.62;) (le:2335) (re:3525) (di:complement) U67463 U67463 g1498811 Methanococcus jannaschii 2190 -11540523 5000698002 (de:(mj0050) (pn:hypothetical protein mj0050:l-2,4-diaminobutyrate decarboxylase) (gtcfc:5.1) (ec:) (y050_metja) (keggfc:11.2) (tigrfc:1.3) (db:gtc-methanococcus jannaschii)) MJ0050 MJ0050 Methanococcus jannaschii 2190 10061112

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923837	19764	41920	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923845	19765	41921	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923858	19766	41922	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923880	19767	41923	360	119

Description

6500736666 heterodisulfide reductase:subunit d:hdrd:putative iron-sulfur protein (gtcfc:1.11:1.2:2.1:2.2:2.5) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-oxidative phosp... MJ0092 MJ0092 Methanococcus jannaschii 2190 -11540524 118259 mj0092 (de:putative iron-sulfur protein mj0092) (db:swissprot) Y092_METJA Q57557 METHANOCOCCUS JANNASCHII 2190 -11540524 173135 fumarate reductase (cl:methanococcus fumarate reductase) (ec:1.3.99.1) (db:pir2.dat) (mp:for86613-88082) D64311 D64311 Methanococcus jannaschii 2190 -11540524 246526 mj0092 heterodisulfide reductase:subunit d hdrd (db:genpept-bct1) (de:methanococcus jannaschii section 8 of 150 of the complete genome.) (nt:similar to gp:1890198 percent identity: 31.87;) (le:7076) (re:8545) (di:direct) U67466 U67466 g1498856 Methanococcus jannaschii 2190 -11540524 5000699462 (de:(mj0092) (pn:putative iron-sulfur protein mj0092:fumarate reductase) (gtcfc:13.7) (ec:) (y092_metja) (keggfc:11.2) (tigrfc:6.3) (db:gtc-methanococcus jannaschii)) MJ0092 MJ0092 Methanococcus jannaschii 2190 10060387

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923881	19768	41924	252	83

Description

6500736667 ilvn:mj0161 acetolactate synthase small subunit:probable acetolactate synthase small subunit:ahas:acetohydroxy-acid synthase small subunit:als (gtcfc:1.11:1.12:5.2:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabolis... MJ0161 MJ0161 Methanococcus jannaschii 2190 -11540525 121641 ilvn:mj0161 (ec:4.1.3.18) (de:(acetohydroxy-acid synthase small subunit) (als)) (db:swissprot) ILVN_METJA Q57625 METHANOCOCCUS JANNASCHII 2190 -11540525 172932 acetolactate synthase::small subunit (cl:acetolactate synthase small chain) (ec:4.1.3.18) (db:pir2.dat) (mp:rev165174-164656) B64320 B64320 Methanococcus jannaschii 2190 -11540525 246596 mj0161 acetolactate synthase small subunit ilvn (db:genpept-bct1) (de:methanococcus jannaschii section 15 of 150 of the complete genome.) (nt:similar to gb:l03181 sp:p37252 pid:143092) (le:6957) (re:7475) (di:complement) U67473 U67473 g1590918 Methanococcus jannaschii 2190 -11540525 5000697813 (de:(mj0161) (pn:probable acetolactate synthase small subunit:ahas:acetohydroxy-acid synthase small subunit:als:acetolactate synthase, small subunit) (gn:ilvn) (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (ilvn_metja) (keggfc:1.11:1.1) MJ0161 MJ0161 Methanococcus jannaschii 2190 10065070

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923882	19769	41925	534	177

Description

6500736668 ilvb:mj0277 acetolactate synthase large subunit:probable acetolactate synthase large subunit:ahas:acetohydroxy-acid synthase large subunit:als (gtcfc:1.11:1.12:5.2:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabolis... MJ0277 MJ0277 Methanococcus jannaschii 2190 -11540526 121640 ilvb:mj0277 (ec:4.1.3.18) (de:(acetohydroxy-acid synthase large subunit) (als)) (db:swissprot) ILVB_METJA Q57725 METHANOCOCCUS JANNASCHII 2190 -11540526 172930 acetolactate synthase:large subunit (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (ec:4.1.3.18) (db:pir2.dat) (mp:rev264626-262851) F64334 F64334 Methanococcus jannaschii 2190 -11540526 246712 mj0277 acetolactate synthase large subunit ilvb (db:genpept-bct1) (de:methanococcus jannaschii section 25 of 150 of the complete genome.) (nt:similar to gb:l03181 sp:p37251 pid:143091 percent) (le:1278) (re:3053) (di:complement) U67483 U67483 g1591003 Methanococcus jannaschii 2190 -11540526 5000697814 (de:(mj0277) (pn:probable acetolactate synthase large subunit:ahas:acetohydroxy-acid synthase large subunit:als:acetolactate synthase, large subunit) (gn:ilvb) (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (ilvb_metja) (keggfc:1.11:1.1) MJ0277 MJ0277 Methanococcus jannaschii 2190 10065069

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923886	19770	41926	429	143

Description

GTC ORF with score 171 to: (or:Emericella nidulans) (db:genpept-pln1) (ec:3.2.1.28) (de:emericella nidulans acid trehalase precursor (trea) gene, completecds.) (nt:alpha, alpha-trehalose glucohydrolase) (le:769:837:2620) (re:780:2570:4038) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923889	19771	41927	789	262

Description

6500736669 acetolactate synthase large subunit:ilvb:acetolactate synthase:large subunit homolog (gtcfc:1.11:1.12:5.2:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabolis... MJ0663 MJ0663 Methanococcus jannaschii 2190 -11540527 500685352 mj0663 (de:hypothetical protein mj0663) (db:swissprot) Y663_METJA Q58077 METHANOCOCCUS JANNASCHII 2190 -11540527 172931 acetolactate synthase:large subunit (ec:4.1.3.18) (db:pir2.dat) (mp:for587753-589237) G64382 G64382 Methanococcus jannaschii 2190 -11540527 247097 mj0663 acetolactate synthase large subunit ilvb (db:genpept-bct1) (de:methanococcus jannaschii section 55 of 150 of the complete genome.) (nt:similar to gb:l10328 sp:p08142 gb:j01633 gb:x02541) (le:6851) (re:8335) (di:direct) U67513 U67513 g1591376 Methanococcus jannaschii 2190 -11540527 5000698069 (de:(mj0663) (pn:hypothetical protein mj0663:acetolactate synthase, large subunit) (gtcfc:5.7) (ec:) (y663_metja) (keggfc:11.2) (tigrfc:1.4) (db:gtc-methanococcus jannaschii)) MJ0663 MJ0663 Methanococcus jannaschii 2190 10065071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923890	19772	41928	522	173

Description

6500736670 ribosomal protein s18 alanine acetyltransferase:n-terminal acetyltransferase complex:subunit ard1 (gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1:10.7) (ec:2.3.1.-) (keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (tigrfc:12.3) (db:gtc-methanococcus jannaschii) MJ1530 MJ1530 Methanococcus jannaschii 2190 -11540528 174360 n-terminal acetyltransferase complex:subunit ard1 homolog (cl:escherichia coli peptide n-acetyltransferase rimi) (db:pir2.dat) (mp:for1507108-1507578) A64491 A64491 Methanococcus jannaschii 2190 -11540528 247963 mj1530 ribosomal protein s18 alanine acetyltransferase (db:genpept-bct1) (de:methanococcus jannaschii section 136 of 150 of the complete genome.) (nt:similar to gp:1707812 percent identity: 36.11;) (le:115) (re:585) (di:direct) U67594 U67594 g1592161 Methanococcus jannaschii 2190 -11540528 5000698251 (de:(mj1530) (pn:n-terminal acetyltransferase complex, subunit ard1) (gtcfc:10.5) (ec:) (keggfc:11.2) (tigrfc:12.4) (db:gtc-methanococcus jannaschii)) MJ1530 MJ1530 Methanococcus jannaschii 2190 10092404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923894	19773	41929	1860	619

Description

GTC ORF with score 2324 to: (db:genpept-pln1) (ec:3.2.1.28) (de:emericella nidulans acid trehalase precursor (trea) gene, completecds.) (nt:alpha, alpha-trehalose glucohydrolase) (le:769:837:2620) (re:780:2570:4038) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923898	19774	41930	207	68

Description

6500736671 3-isopropylmalate dehydratase:leuc:aconitase (gtcfc:1.2:1.9:2.5:5.2) (ec:4.2.1.3) (keggfc:1.2:1.9:2.4) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-glyoxylate and dicarboxylate metabolism:energy metabolism-reductiv... MJ0499 MJ0499 Methanococcus jannaschii 2190 -11540529 7500884866 mj0499 (ec:4.2.1.33) (de:(isopropylmalate isomerase) (alpha-ipm isomerase) (ipmi)) (db:swissprot) LE22_METJA P81291 METHANOCOCCUS JANNASCHII 2190 -11540529 172937 aconitate hydratase::aconitase (cl:aconitate hydratase) (ec:4.2.1.3) (db:pir2.dat) (mp:rev441104-439830) C64362 C64362 Methanococcus jannaschii 2190 -11540529 7500884868 mj0499 3-isopropylmalate dehydratase leuc (db:genpept-bct1) (de:methanococcus jannaschii section 41 of 150 of the complete genome.) (nt:similar to gb:d10483 sp:p30127 gb:d17631 gb:d17632) (le:9067) (re:10341) (di:complement) U67499 U67499 g1591201 Methanococcus jannaschii 2190 -11540529 246933 mju67499 (le:439830) (re:441104) (di:direct) (de:or:methanococcus jannaschii pn:aconitase gn:mj0499 le:9067 re:10341 di:complement nt:similar to p19414 percent identity: 29.6;) U67499 U67499 g1591201 Methanococcus jannaschii 2190 -11540529 5000697815 (de:(mj0499) (pn:aconitase) (gtcfc:1.2:1.9:2.5) (ec:4.2.1.3) (keggfc:1.2:1.9:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii)) MJ0499 MJ0499 Methanococcus jannaschii 2190 10091404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923900	19775	41931	438	145

Description

6500736672 tartrate dehydratse:subunit beta:ttdb:putative fumarate hydratase beta subunit:fumarase (gtcfc:1.2:2.1:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (tigrfc:6.1) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-oxidative phosphorylation:energy metabolism-reductive carboxylate cycle (co2 fix... MJ0617 MJ0617 Methanococcus jannaschii 2190 -11540530 4000707965 mj0617 (ec:4.2.1.2) (de:putative fumarate hydratase beta subunit, (fumarase)) (db:swissprot) FUMB_METJA Q58034 METHANOCOCCUS JANNASCHII 2190 -11540530 173133 fumarate hydratase (cl:iron-dependent tartrate dehydratase beta chain:iron-dependent tartrate dehydratase beta chain homology) (ec:4.2.1.2) (db:pir2.dat) (mp:for547001-547588) A64377 A64377 Methanococcus jannaschii 2190 -11540530 247051 mj0617 tartrate dehydratse:subunit beta ttdb (db:genpept-bct1) (de:methanococcus jannaschii section 52 of 150 of the complete genome.) (nt:similar to pid:882585 gb:u00096 pid:1789443 percent) (le:1452) (re:2039) (di:direct) U67510 U67510 g1591328 Methanococcus jannaschii 2190 -11540530 5000697816 (de:(mj0617) (pn:fumarate hydratase, class i "") (gtcfc:1.2:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii)) MJ0617 MJ0617 Methanococcus jannaschii 2190 10091520

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923913	19776	41932	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923930	19777	41933	447	148

Description

6500736673 nadp:mj0720 3-isopropylmalate dehydrogenase 1:leub1:isocitrate dehydrogenase (gtcfc:1.2:2.5:5.2:6.16) (ec:1.1.1.42) (keggfc:1.2:2.4:6.9) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation):l-amino acid metabolism-ala... MJ0720 MJ0720 Methanococcus jannaschii 2190 -11540531 174299 isocitrate dehydrogenase nadp+ (cl:3-isopropylmalate dehydrogenase) (ec:1.1.1.42) (db:pir2.dat) (mp:rev654942-653929) H64389 H64389 Methanococcus jannaschii 2190 -11540531 5500686364 mj0720 (de:hypothetical protein mj0720) (db:swissprot) Y720_METJA Q58130 METHANOCOCCUS JANNASCHII 2190 -11540531 247154 mju67519 (le:653929) (re:654942) (di:direct) (de:or:methanococcus jannaschii pn:isocitrate dehydrogenase (nadp) gn:mj0720 le:53 re:1066 di:complement nt:similar to p33197 percent identity: 47.9;) U67519 U67519 g1592302 Methanococcus jannaschii 2190 -11540531 5000697817 (de:(mj0720) (pn:isocitrate dehydrogenase:nadp) (gtcfc:1.2:2.5:6.16) (ec:1.1.1.42) (keggfc:1.2:2.4:6.9) (tigrfc:6.12) (db:gtc-methanococcus jannaschii)) MJ0720 MJ0720 Methanococcus jannaschii 2190 10092358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923945	19778	41934	393	130

Description

6500736674 tartrate dehydratase:subunit alpha:ttda:putative fumarate hydratase alpha subunit:fumarase (gtcfc:1.2:2.1:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (tigrfc:6.1) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-oxidative phosphorylation:energy metabolism-reductive carboxylate cycle (co2 fix... MJ1294 MJ1294 Methanococcus jannaschii 2190 -11540532 4000707964 mj1294 (ec:4.2.1.2) (de:putative fumarate hydratase alpha subunit, (fumarase)) (db:swissprot) FUMA_METJA Q58690 METHANOCOCCUS JANNASCHII 2190 -11540532 173134 fumarate hydratase::class i (cl:iron-dependent tartrate dehydratase alpha chain:iron-dependent tartrate dehydratase alpha chain homology) (ec:4.2.1.2) (db:pir2.dat) (mp:rev1242836-1241979) E64461 E64461 Methanococcus jannaschii 2190 -11540532 247727 mj1294 tartrate dehydratase:subunit alpha ttda (db:genpept-bct1) (de:methanococcus jannaschii section 112 of 150 of the complete genome.) (nt:similar to gb:l14781 sp:p05847 pid:347084) (le:3445) (re:4302) (di:complement) U67570 U67570 g1591932 Methanococcus jannaschii 2190 -11540532 5000697818 (de:(mj1294) (pn:fumarate hydratase, class i ") (gtcfc:1.2:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii)) MJ1294 MJ1294 Methanococcus jannaschii 2190 10091521

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923953	19779	41935	462	153

Description

6500736675 mdh:mj1425 malate dehydrogenase (gtcfc:1.2:1.8:1.9:2.4:2.5) (keggfc:1.2:1.8:1.9:2.3:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-pyruvate and acetyl-coa metabolism:carbohydrate metabolism-glyoxyl... MJ1425 MJ1425 Methanococcus jannaschii 2190 -11540533 119984 mdh:mj1425 (ec:1.1.1.37:1.1.1.82) (de:malate dehydrogenase,,) (db:swissprot) MDH_METJA Q58820 METHANOCOCCUS JANNASCHII 2190 -11540533 174314 malate dehydrogenase (cl:malate dehydrogenase ylbc) (ec:1.1.1.37) (db:pir2.dat) (mp:for1395033-1396067) H64477 H64477 Methanococcus jannaschii 2190 -11540533 247858 mj1425 malate dehydrogenase (db:genpept-bct1) (de:methanococcus jannaschii section 125 of 150 of the complete genome.) (nt:similar to sp:p16142 gb:x51714 gb:x51840 pid:44278) (le:9129) (re:10163) (di:direct) U67583 U67583 g1592075 Methanococcus jannaschii 2190 -11540533 5000697819 (de:(mj1425) (pn:malate dehydrogenase) (gn:mdh) (gtcfc:1.2:1.8:1.9:2.4:2.5) (ec:1.1.1.37) (mdh_metja) (keggfc:1.2:1.8:1.9:2.3:2.4) (tigrfc:6.12) (db:gtc-methanococcus jannaschii)) MJ1425 MJ1425 Methanococcus jannaschii 2190 10062760

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923954	19780	41936	300	99

Description

6500736676 icd:mj1596 3-isopropylmalate dehydrogenase 2:leub2:isocitrate dehydrogenase:nadp:oxalosuccinate decarboxylase:idh:nadp+-specific icdh:idp (gtcfc:1.2:2.5:5.2:6.16) (ec:1.1.1.42) (keggfc:1.2:2.4:6.9) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation):l-amino acid metabolism-ala... MJ1596 MJ1596 Methanococcus jannaschii 2190 -11540534 174298 isocitrate dehydrogenase (cl:3-isopropylmalate dehydrogenase) (ec:1.1.1.-) (db:pir2.dat) (mp:rev1568452-1567337) C64499 C64499 Methanococcus jannaschii 2190 -11540534 119689 icd:mj1596 (ec:1.1.1.42) (de:decarboxylase) (idh) (nadp+-specific icdh) (idp)) (db:swissprot) IDH_METJA Q58991 METHANOCOCCUS JANNASCHII 2190 -11540534 248029 mju67599 (le:1567337) (re:1568452) (di:direct) (de:or:methanococcus jannaschii pn:isocitrate dehydrogenase gn:mj1596 le:6637 re:7752 di:complement nt:similar to p33197 percent identity: 42.9;) U67599 U67599 g1592206 Methanococcus jannaschii 2190 -11540534 5000697820 (de:(mj1596) (pn:oxalosuccinate decarboxylase:idh:nadp:isocitrate dehydrogenase) (gn:icd) (gtcfc:1.2:2.5:6.16) (ec:1.1.1.42) (idh_metja) (keggfc:1.2:2.4:6.9) (tigrfc:6.12) (db:gtc-methanococcus jannaschii)) MJ1596 MJ1596 Methanococcus jannaschii 2190 10062354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923955	19781	41937	435	144

Description

6500736677 ribokinase:rbsk:hypothetical sugar kinase (gtcfc:1.3:7.1) (ec:2.7.1.15) (keggfc:1.3) (tigrfc:6.11) (db:gtc-methanococcus jannaschii) MJ0406 MJ0406 Methanococcus jannaschii 2190 -11540535 4000707673 mj0406 (de:hypothetical sugar kinase mj0406) (db:swissprot) Y406_METJA Q57849 METHANOCOCCUS JANNASCHII 2190 -11540535 174471 ribokinase (ec:2.7.1.15) (db:pir2.dat) (mp:for365549-366457) F64350 F64350 Methanococcus jannaschii 2190 -11540535 246840 mj0406 ribokinase rbsk (db:genpept-bct1) (de:methanococcus jannaschii section 35 of 150 of the complete genome.) (nt:similar to gb:l10328 sp:p05054 gb:m13169 pid:147516) (le:103) (re:1011) (di:direct) U67493 U67493 g1592288 Methanococcus jannaschii 2190 -11540535 5000697821 (de:(mj0406) (pn:ribokinase) (gtcfc:1.3) (ec:2.7.1.15) (keggfc:1.3) (tigrfc:5.9) (db:gtc-methanococcus jannaschii)) MJ0406 MJ0406 Methanococcus jannaschii 2190 10092464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923962	19782	41938	390	129

Description

6500736678 transketolase (gtcfc:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (tigrfc:6.9) (db:gtc-methanococcus jannaschii) MJ0679 MJ0679 Methanococcus jannaschii 2190 -11540536 5500686068 mj0679 (ec:2.2.1.1) (de:putative transketolase c-terminal section, (tk)) (db:swissprot) TKTC_METJA Q58092 METHANOCOCCUS JANNASCHII 2190 -11540536 174580 transketolase (ec:2.2.1.1) (db:pir2.dat) (mp:rev606237-605287) G64384 G64384 Methanococcus jannaschii 2190 -11540536 247113 mj0679 transketolase (db:genpept-bct1) (de:methanococcus jannaschii section 57 of 150 of the complete genome.) (nt:similar to gb:m86521 sp:p29401 percent identity:) (le:3307) (re:4257) (di:complement) U67515 U67515 g1591394 Methanococcus jannaschii 2190 -11540536 5000697822 (de:(mj0679) (pn:transketolase"") (gtcfc:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (tigrfc:6.9) (db:gtc-methanococcus jannaschii)) MJ0679 MJ0679 Methanococcus jannaschii 2190 10092496

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923978	19783	41939	597	198

Description

GTC ORF with score 548 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1038.) (nt:similar to saccharomyces cerevisiae hypothetical) (le:<1) (re:1010) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923979	19784	41940	360	119

Description

6500736679 pentose-5-phosphate-3-epimerase (gtcfc:1.3:1.4:2.4) (ec:5.1.3.1) (keggfc:1.3:1.4:2.3) (tigrfc:6.9) (db:gtc-methanococcus jannaschii) MJ0680 MJ0680 Methanococcus jannaschii 2190 -11540537 5500685903 rpe:mj0680 (ec:5.1.3.1) (de:epimerase) (ppe) (r5p3e)) (db:swissprot) RPE_METJA Q58093 METHANOCOCCUS JANNASCHII 2190 -11540537 174398 pentose-5-phosphate-3-epimerase (cl:yeast ribulose-5-phosphate-epimerase) (ec:5.1.3.-) (db:pir2.dat) (mp:rev606981-606277) H64384 H64384 Methanococcus jannaschii 2190 -11540537 247114 mj0680 pentose-5-phosphate-3-epimerase (db:genpept-bct1) (de:methanococcus jannaschii section 57 of 150 of the complete genome.) (nt:similar to pid:606320 pid:1789788 percent identity:) (le:4297) (re:5001) (di:complement) U67515 U67515 g1591395 Methanococcus jannaschii 2190 -11540537 5000697823 (de:(mj0680) (pn:pentose-5-phosphate-3-epimerase) (gtcfc:1.3:1.4:2.4) (ec:5.1.3.1) (keggfc:1.3:1.4:2.3) (tigrfc:6.9) (db:gtc-methanococcus jannaschii)) MJ0680 MJ0680 Methanococcus jannaschii 2190 10092425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923980	19785	41941	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501923998	19786	41942	1299	432

Description

6500736680 transketolase (gtcfc:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (tigrfc:6.9) (db:gtc-methanococcus jannaschii) MJ0681 MJ0681 Methanococcus jannaschii 2190 -11540538 5500686069 mj0681 (ec:2.2.1.1) (de:putative transketolase n-terminal section, (tk)) (db:swissprot) TKTN_METJA Q58094 METHANOCOCCUS JANNASCHII 2190 -11540538 174579 transketolase (cl:ferredoxin 2(4fe-4s)-related protein:ferredoxin 2(4fe-4s) homology) (ec:2.2.1.1) (db:pir2.dat) (mp:rev607829-607005) A64385 A64385 Methanococcus jannaschii 2190 -11540538 247115 mj0681 transketolase (db:genpept-bct1) (de:methanococcus jannaschii section 57 of 150 of the complete genome.) (nt:similar to gb:m86521 sp:p29401 percent identity:) (le:5025) (re:5849) (di:complement) U67515 U67515 g1591396 Methanococcus jannaschii 2190 -11540538 5000697824 (de:(mj0681) (pn:transketolase") (gtcfc:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (tigrfc:6.9) (db:gtc-methanococcus jannaschii)) MJ0681 MJ0681 Methanococcus jannaschii 2190 10092495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924000	19787	41943	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924001	19788	41944	1239	412

Description

6500736681 ribose-phosphate pyrophosphokinase::prsa:ribose-phosphate pyrophosphokinase (gtcfc:1.3:4.1) (ec:2.7.6.1) (keggfc:1.3:4.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ1366 MJ1366 Methanococcus jannaschii 2190 -11540539 174475 ribose-phosphate pyrophosphokinase (cl:ribose-phosphate pyrophosphokinase catalytic chain) (ec:2.7.6.1) (db:pir2.dat) (mp:rev1316804-1315929) E64470 E64470 Methanococcus jannaschii 2190 -11540539 247799 mj1366 ribose-phosphate pyrophosphokinase:prsa (db:genpept-bct1) (de:methanococcus jannaschii section 118 of 150 of the complete genome.) (nt:similar to gb:m13174 sp:p08330 pid:147379 gb:u00096) (le:7468) (re:8343) (di:complement) U67576 U67576 g1592010 Methanococcus jannaschii 2190 -11540539 5000697825 (de:(mj1366) (pn:ribose-phosphate pyrophosphokinase) (gtcfc:1.3:4.1) (ec:2.7.6.1) (keggfc:1.3:4.1) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ1366 MJ1366 Methanococcus jannaschii 2190 10092466

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924002	19789	41945	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924010	19790	41946	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924018	19791	41947	441	146

Description

6500736682 ribose 5-phosphate isomerase (gtcfc:1.3:2.4) (ec:5.3.1.6) (keggfc:1.3:2.3) (tigrfc:6.9) (db:gtc-methanococcus jannaschii) MJ1603 MJ1603 Methanococcus jannaschii 2190 -11540540 174474 ribose-5-phosphate isomerase (cl:haemophilus influenzae ribose-5-phosphate isomerase) (ec:5.3.1.6) (db:pir2.dat) (mp:for1576614-1577294) B64500 B64500 Methanococcus jannaschii 2190 -11540540 248036 mj1603 ribose 5-phosphate isomerase (db:genpept-bct1) (de:methanococcus jannaschii section 142 of 150 of the complete genome.) (nt:similar to pid:1001613 pid:1001678 percent) (le:6207) (re:6887) (di:direct) U67600 U67600 g1500500 Methanococcus jannaschii 2190 -11540540 5000697826 (de:(mj1603) (pn:ribose 5-phosphate isomerase) (gtcfc:1.3:2.4) (ec:5.3.1.6) (keggfc:1.3:2.3) (tigrfc:6.9) (db:gtc-methanococcus jannaschii)) MJ1603 MJ1603 Methanococcus jannaschii 2190 10092465

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924019	19792	41948	819	272

Description

6500736683 transaldolase (gtcfc:1.3) (ec:2.2.1.-) (keggfc:14.1) (tigrfc:6.9) (db:gtc-methanococcus jannaschii) MJ0960 MJ0960 Methanococcus jannaschii 2190 -11540541 7500892746 tal:mj0960 (ec:2.2.1.-) (de:transaldolase-like protein,) (db:swissprot) TAL_METJA Q58370 METHANOCOCCUS JANNASCHII 2190 -11540541 174570 transaldolase (cl:bacillus subtilis 23k phosphoprotein orfu) (ec:2.2.1.2) (db:pir2.dat) (mp:rev892437-891784) H64419 H64419 Methanococcus jannaschii 2190 -11540541 7500892748 mj0960 transaldolase (db:genpept-bct1) (de:methanococcus jannaschii section 81 of 150 of the complete genome.) (nt:similar to sp:p19669 pid:853766 gb:al009126 percent) (le:7990) (re:8643) (di:complement) U67539 U67539 g1591624 Methanococcus jannaschii 2190 -11540541 247394 mju67539 (le:891784) (re:892437) (di:direct) (de:or:methanococcus jannaschii pn:transaldolase gn:mj0960 le:7990 re:8643 di:complement nt:similar to p19669 percent identity: 59.0;) U67539 U67539 g1591624 Methanococcus jannaschii 2190 -11540541 5000697827 (de:(mj0960) (pn:transaldolase) (gtcfc:1.3) (ec:2.2.1.-) (keggfc:11.1) (tigrfc:6.9) (db:gtc-methanococcus jannaschii)) MJ0960 MJ0960 Methanococcus jannaschii 2190 10081201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924020	19793	41949	1872	623

Description

6500736684 gtab:putative utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp:alpha-d-glucosyl-1-phosphate uridylyltransferase:uridine diphosphoglucose pyrophosphorylase (gtcfc:1.4:1.6:1.8:4.3:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ1334 MJ1334 Methanococcus jannaschii 2190 -11540542 121705 mj1334 (ec:2.7.7.9) (de:uridylyltransferase) (uridine diphosphoglucose pyrophosphorylase)) (db:swissprot) YD34_METJA Q58730 METHANOCOCCUS JANNASCHII 2190 -11540542 174615 utp--glucose-1-phosphate uridylyltransferase::udp-glucose pyrophosphorylase (cl:escherichia coli utp--glucose-1-phosphate uridylyltransferase) (ec:2.7.7.9) (db:pir1.dat) (mp:rev1284127-1283276) E64466 E64466 Methanococcus jannaschii 2190 -11540542 247767 mj1334 udp-glucose pyrophosphorylase gtab (db:genpept-bct1) (de:methanococcus jannaschii section 115 of 150 of the complete genome.) (nt:similar to gb:u02258 gb:l43967 sp:p47691 pid:406922) (le:7941) (re:8792) (di:complement) U67573 U67573 g1591975 Methanococcus jannaschii 2190 -11540542 5000697828 (de:(mj1334) (pn:putative utp--glucose-1-phosphate uridylyltransferase:udpalpha-d-glucosyl-1-phosphate uridylyltransferase:uridine diphosphoglucose pyrophosphorylase:udp-glucose pyrophosphorylase) (gtcfc:1.4:1.6:4.3:7.2) (ec:2.7.7) MJ1334 MJ1334 Methanococcus jannaschii 2190 10065172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924028	19794	41950	390	129

Description

6500736685 manb:mj0399 phosphomannomutase:pmma:probable phosphomannomutase:pmm (gtcfc:1.5:11.2) (ec:5.4.2.8) (keggfc:1.5) (tigrfc:3.3) (db:gtc-methanococcus jannaschii) MJ0399 MJ0399 Methanococcus jannaschii 2190 -11540543 4000709396 manb:mj0399 (ec:5.4.2.8) (de:probable phosphomannomutase, (pmm)) (db:swissprot) MANB_METJA Q57842 METHANOCOCCUS JANNASCHII 2190 -11540543 174414 phosphomannomutase (ec:5.4.2.8) (db:pir2.dat) (mp:rev361503-360154) G64349 G64349 Methanococcus jannaschii 2190 -11540543 246833 mj0399 phosphomannomutase pmma (db:genpept-bct1) (de:methanococcus jannaschii section 34 of 150 of the complete genome.) (nt:similar to sp:p37742 gb:l11721 sp:p24175 gb:m77127) (le:4431) (re:5780) (di:complement) U67492 U67492 g1591104 Methanococcus jannaschii 2190 -11540543 5000697832 (de:(mj0399) (pn:phosphomannomutase) (gtcfc:1.5) (ec:5.4.2.8) (keggfc:1.5) (tigrfc:3.3) (db:gtc-methanococcus jannaschii)) MJ0399 MJ0399 Methanococcus jannaschii 2190 10092433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924036	19795	41951	321	106

Description

6500736686 n-acetylglucosamine-1-phosphate transferase (gtcfc:1.5:7.1:8.5:11.2:11.3:11.4) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5) (tigrfc:3.3) (db:gtc-methanococcus jannaschii) MJ1113 MJ1113 Methanococcus jannaschii 2190 -11540544 174355 udp-n-acetylglucosamine--dolichyl-phosphate n-acetylglucosaminephosphotransferase (cl:n-acetylglucosamine-1-phosphate transferase) (ec:2.7.8.15) (db:pir2.dat) (mp:rev1054913-1054008) H64438 H64438 Methanococcus jannaschii 2190 -11540544 247546 mj1113 n-acetylglucosamine-1-phosphate transferase (db:genpept-bct1) (de:methanococcus jannaschii section 96 of 150 of the complete genome.) (nt:similar to gb:d28748 sp:p39465 pid:506372 percent) (le:3699) (re:4604) (di:complement) U67554 U67554 g1591753 Methanococcus jannaschii 2190 -11540544 5000698325 (de:(mj1113) (pn:n-acetylglucosamine-1-phosphate transferase) (gtcfc:11.2) (ec:) (keggfc:11.2) (tigrfc:3.3) (db:gtc-methanococcus jannaschii)) MJ1113 MJ1113 Methanococcus jannaschii 2190 10092399

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924061	19796	41952	675	224

Description

6500736687 udp-glucose 4-epimerase:gale:putative udp-glucose 4-epimerase:galactowaldenase:udp-galactose 4-epimerase (gtcfc:1.6:4.3:11.2) (ec:5.1.3.2) (keggfc:1.6:4.3) (tigrfc:3.3) (db:gtc-methanococcus jannaschii) MJ0211 MJ0211 Methanococcus jannaschii 2190 -11540545 500684893 mj0211 (ec:5.1.3.2) (de:galactose 4-epimerase)) (db:swissprot) GALE_METJA Q57664 METHANOCOCCUS JANNASCHII 2190 -11540545 174607 udpglucose 4-epimerase (cl:escherichia coli udpglucose 4-epimerase:udpglucose 4-epimerase homology) (ec:5.1.3.2) (db:pir2.dat) (mp:for202715-203632) D64326 D64326 Methanococcus jannaschii 2190 -11540545 246646 mj0211 udp-glucose 4-epimerase gale (db:genpept-bct1) (de:methanococcus jannaschii section 19 of 150 of the complete genome.) (nt:similar to gb:m38175 sp:p21977 pid:153749 percent) (le:1741) (re:2658) (di:direct) U67477 U67477 g1590951 Methanococcus jannaschii 2190 -11540545 5000697833 (de:(mj0211) (pn:udp-glucose 4-epimerase) (gtcfc:1.6:4.3) (ec:5.1.3.2) (keggfc:1.6:4.3) (tigrfc:3.3) (db:gtc-methanococcus jannaschii)) MJ0211 MJ0211 Methanococcus jannaschii 2190 10060410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924072	19797	41953	531	176

Description

6500736688 phenylacrylic acid decarboxylase (gtcfc:1.7:1.8:5.10:5.12:5.13:5.14:9.12:9.3:13.3) (ec:4.1.1.-) (keggfc:1.7:1.8:5.10:5.12:5.13:5.14:9.3:9.13) (tigrfc:14.3) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-ascorbate and aldarate metabolism:carbohydrate metabolism-pyruva... MJ0102 MJ0102 Methanococcus jannaschii 2190 -11540546 118783 mj0102 (de:hypothetical protein mj0102) (db:swissprot) Y102_METJA Q57566 METHANOCOCCUS JANNASCHII 2190 -11540546 174403 phenylacrylic acid decarboxylase homolog (cl:dedf protein) (db:pir2.dat) (mp:rev97053-96499) F64312 F64312 Methanococcus jannaschii 2190 -11540546 246536 mj0102 phenylacrylic acid decarboxylase (db:genpept-bct1) (de:methanococcus jannaschii section 9 of 150 of the complete genome.) (nt:similar to sp:p33751 pid:1165293 pid:393285 percent) (le:6995) (re:7549) (di:complement) U67467 U67467 g1590879 Methanococcus jannaschii 2190 -11540546 5000698438 (de:(mj0102) (pn:hypothetical protein mj0102:phenylacrylic acid decarboxylase) (gtcfc:13.3) (ec:) (y102_metja) (keggfc:11.2) (tigrfc:14.3) (db:gtc-methanococcus jannaschii)) MJ0102 MJ0102 Methanococcus jannaschii 2190 10061145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924081	19798	41954	696	231

Description

5000697835 hpce:2-hydroxyhepta-2:4-diene-1:7-dioate isomerase (gtcfc:1.7:1.8:5.10:5.12:5.13:5.14:9.12:9.3:14.3) (keggfc:1.7:1.8:5.10:5.12:5.13:5.14:9.3:9.13) (tigrfc:5.9) (db:gtc-methanococcus jannaschii) (gtcfc:carbohydrate metabolism-ascorbate and aldarate metabolism:carbohydrate metabolism-pyruvate and acetyl-... MJ1656 MJ1656 Methanococcus jannaschii 2190 -11540547 172909 2-hydroxyhepta-2:4-diene-1:7-dioate isomerase homolog (cl:2-hydroxyhepta-2,4-diene-1,7-dioate isomerase) (db:pir2.dat) (mp:for1638663-1639376) F64506 F64506 Methanococcus jannaschii 2190 -11540547 248088 mj1656 2-hydroxyhepta-2:4-diene-1:7-dioate isomerase (db:genpept-bct1) (de:methanococcus jannaschii section 148 of 150 of the complete genome.) (nt:similar to sp:p37352 gb:x75028 gb:z37980 pid:402576) (le:1701) (re:2414) (di:direct) U67606 U67606 g1500558 Methanococcus jannaschii 2190 -11540547 6500736689 hpce:2-hydroxyhepta-2:4-diene-1:7-dioate isomerase (gtcfc:1.7:1.8:5.10:5.12:5.13:5.14:9.12:9.3:14.3) (keggfc:1.7:1.8:5.10:5.12:5.13:5.14:9.3:9.13) (tigrfc:5.9) (db:gtc-methanococcus jannaschii) MJ1656 MJ1656 Methanococcus jannaschii 2190 -11540547

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924082	19799	41955	588	195

Description

GTC ORF with score 170 to: (sr:burkholderia pickettii (strain:dtp0602) dna) (db:genpept-bct1) (de:burkholderia pickettii dna for hydroxyquinol-1, 2-dioxygenase andchlorophenol-4-hydroxylase,complete cds.) (le:2659) (re:3606) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924092	19800	41956	546	181

Description

5000697836 2-isopropylmalate synthase:leua:putative 2-isopropylmalate/homocitrate synthase (gtcfc:1.8:5.15:5.2:5.7:5.8:5.9:9.12) (keggfc:1.8:5.7:5.8:5.9:5.15:9.13) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) MJ0503 MJ0503 Methanococcus jannaschii 2190 -11540548 117420 mj0503 (ec:4.1.3.-) (de:putative 2-isopropylmalate/homocitrate synthase mj0503,) (db:swissprot) Y503_METJA Q57926 METHANOCOCCUS JANNASCHII 2190 -11540548 172911 2-isopropylmalate synthase (ec:4.1.3.12) (db:pir2.dat) (mp:for444536-445756) G64362 G64362 Methanococcus jannaschii 2190 -11540548 246937 mj0503 2-isopropylmalate synthase leua (db:genpept-bct1) (de:methanococcus jannaschii section 42 of 150 of the complete genome.) (nt:similar to gb:d10483 sp:p09151 pid:216492 gb:u00096) (le:3241) (re:4461) (di:direct) U67500 U67500 g1591206 Methanococcus jannaschii 2190 -11540548 6500736690 2-isopropylmalate synthase:leua:putative 2-isopropylmalate/homocitrate synthase (gtcfc:1.8:5.15:5.2:5.7:5.8:5.9:9.12) (keggfc:1.8:5.7:5.8:5.9:5.15:9.13) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) MJ0503 MJ0503 Methanococcus jannaschii 2190 -11540548

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924095	19801	41957	414	137

Description

5000697838 2-isopropylmalate synthase:leua:putative 2-isopropylmalate/homocitrate synthase (gtcfc:1.8:5.15:5.2:5.7:5.8:5.9:9.12) (keggfc:1.8:5.7:5.8:5.9:5.15:9.13) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) MJ1195 MJ1195 Methanococcus jannaschii 2190 -11540549 117421 mj1195 (ec:4.1.3.-) (de:putative 2-isopropylmalate/homocitrate synthase mj1195,) (db:swissprot) YB95_METJA Q58595 METHANOCOCCUS JANNASCHII 2190 -11540549 172910 2-isopropylmalate synthase (cl:2-isopropylmalate synthase leua) (ec:4.1.3.12) (db:pir2.dat) (mp:rev1138913-1137357) B64449 B64449 Methanococcus jannaschii 2190 -11540549 247628 mj1195 2-isopropylmalate synthase leua (db:genpept-bct1) (de:methanococcus jannaschii section 103 of 150 of the complete genome.) (nt:similar to gb:d10483 sp:p09151 pid:216492 gb:u00096) (le:102) (re:1658) (di:complement) U67561 U67561 g1591824 Methanococcus jannaschii 2190 -11540549 6500736691 2-isopropylmalate synthase:leua:putative 2-isopropylmalate/homocitrate synthase (gtcfc:1.8:5.15:5.2:5.7:5.8:5.9:9.12) (keggfc:1.8:5.7:5.8:5.9:5.15:9.13) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) MJ1195 MJ1195 Methanococcus jannaschii 2190 -11540549

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924102	19802	41958	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924105	19803	41959	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924111	19804	41960	186	61

Description

6500736692 oxaloacetate decarboxylase alpha chain:oada:oxaloacetate decarboxylase:alpha subunit (gtcfc:1.8:5.10:12.2) (ec:4.1.1.3) (keggfc:1.8:5.10) (tigrfc:13.4) (db:gtc-methanococcus jannaschii) MJ1231 MJ1231 Methanococcus jannaschii 2190 -11540550 174395 oxaloacetate decarboxylase:alpha subunit (cl:klebsiella pneumoniae oxaloacetate decarboxylase alpha chain:lipoyl/biotin-binding homology) (ec:4.1.1.3) (db:pir2.dat) (mp:rev1175190-1173487) F64453 F64453 Methanococcus jannaschii 2190 -11540550 247664 mj1231 oxaloacetate decarboxylase alpha chain oada (db:genpept-bct1) (de:methanococcus jannaschii section 105 of 150 of the complete genome.) (nt:similar to gb:m96434 sp:q03030 gb:x52093 pid:408892) (le:11289) (re:12992) (di:complement) U67563 U67563 g1591862 Methanococcus jannaschii 2190 -11540550 5000697839 (de:(mj1231) (pn:oxaloacetate decarboxylase, alpha subunit) (gtcfc:1.8:5.10) (ec:4.1.1.3) (keggfc:1.8:5.10) (tigrfc:13.5) (db:gtc-methanococcus jannaschii)) MJ1231 MJ1231 Methanococcus jannaschii 2190 10092422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924112	19805	41961	429	142

Description

5000697840 2-isopropylmalate synthase:leua:putative 2-isopropylmalate/homocitrate synthase (gtcfc:1.8:5.15:5.2:5.7:5.8:5.9:9.12) (keggfc:1.8:5.7:5.8:5.9:5.15:9.13) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) MJ1392 MJ1392 Methanococcus jannaschii 2190 -11540551 117422 mj1392 (ec:4.1.3.-) (de:putative 2-isopropylmalate/homocitrate synthase mj1392,) (db:swissprot) YD92_METJA Q58787 METHANOCOCCUS JANNASCHII 2190 -11540551 172912 2-isopropylmalate synthase (cl:2-isopropylmalate synthase leua) (ec:4.1.3.12) (db:pir2.dat) (mp:for1340258-1341733) G64473 G64473 Methanococcus jannaschii 2190 -11540551 247825 mj1392 2-isopropylmalate synthase leua (db:genpept-bct1) (de:methanococcus jannaschii section 121 of 150 of the complete genome.) (nt:similar to gb:d10483 sp:p09151 pid:216492 gb:u00096) (le:1850) (re:3325) (di:direct) U67579 U67579 g1592039 Methanococcus jannaschii 2190 -11540551 6500736693 2-isopropylmalate synthase:leua:putative 2-isopropylmalate/homocitrate synthase (gtcfc:1.8:5.15:5.2:5.7:5.8:5.9:9.12) (keggfc:1.8:5.7:5.8:5.9:5.15:9.13) (tigrfc:1.5) (db:gtc-methanococcus jannaschii) MJ1392 MJ1392 Methanococcus jannaschii 2190 -11540551

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924113	19806	41962	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924116	19807	41963	468	155

Description

GTC ORF with score 162 to: (db:genpept-bct2) (de:pseudomonas fluorescens cyclohexanone monooxygenase homolog gene,partial cds; lactone-specific esterase (estf1) gene, complete cds;and alkane-1 monooxygenase homolog gene, partial cds.) (nt:estf1) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924127	19808	41964	243	80

Description

GTC ORF with score 124 to: (sr:schizosaccharomyces pombe (strain:972h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:fission yeast dna for isp4, peptidyl-prolyl cis-trans isomerase,atf1, chromosome ii cosmid 1228 sequence.) (nt:probable reductase, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924129	19809	41965	372	123

Description

GTC ORF with score 112 to: (db:genpept-bct2) (ec:3.1.1.24:4.1.1.44) (de:rhodococcus opacus succinyl coa:3-oxoadipate coa transferasesubunit homolog (pcai') gene, partial cds, protocatechuatedioxygenase beta subunit (pcah), protocatechuate dioxygenase ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924134	19810	41966	399	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924139	19811	41967	813	270

Description

GTC ORF with score 135 to: (or:Homo sapiens) (sr:human) (db:genpept-pri3) (de:homo sapiens pitslre protein kinase alpha sv5 isoform (cdc2l1)mrna, complete cds.) (nt:corresponding genomic sequence deposited as genbank) (le:261) (re:2474) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924149	19812	41968	3294	1097

Description

6500736694 fuca:fuculose-1-phosphate aldolase (gtcfc:1.8:7.1) (ec:4.1.2.17) (keggfc:1.8) (tigrfc:6.11) (db:gtc-methanococcus jannaschii) MJ1418 MJ1418 Methanococcus jannaschii 2190 -11540552 5500686552 mj1418 (de:hypothetical protein mj1418) (db:swissprot) YE18_METJA Q58813 METHANOCOCCUS JANNASCHII 2190 -11540552 173132 fuculose-1-phosphate aldolase (cl:methanococcus jannaschii fuculose-1-phosphate aldolase) (ec:4.1.2.-) (db:pir2.dat) (mp:for1381152-1381697) A64477 A64477 Methanococcus jannaschii 2190 -11540552 247851 mj1418 fuculose-1-phosphate aldolase fuca (db:genpept-bct1) (de:methanococcus jannaschii section 124 of 150 of the complete genome.) (nt:similar to gb:l42023 pid:1006225 pid:1221126) (le:5326) (re:5871) (di:direct) U67582 U67582 g1592067 Methanococcus jannaschii 2190 -11540552 5000698466 (de:(mj1418) (pn:fuculose-1-phosphate aldolase) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:6.11) (db:gtc-methanococcus jannaschii)) MJ1418 MJ1418 Methanococcus jannaschii 2190 10091519

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924151	19813	41969	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924156	19814	41970	2814	937

Description

6500736695 acetyl-coa decarbonylase/synthase:subunit gamma:cdhe:corrinoid/iron-sulfur protein:large subunit (gtcfc:1.8) (keggfc:14.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0112 MJ0112 Methanococcus jannaschii 2190 -11540553 123218 corrinoid/iron-sulfur protein large chain:c/fe-sp large chain (cl:corrinoid/iron-sulfur protein large chain) (db:pir1.dat) (mp:rev110157-108691) H64313 H64313 Methanococcus jannaschii 2190 -11540553 246546 mj0112 acetyl-coa decarbonylase/synthase:subunit gamma (db:genpept-bct1) (de:methanococcus jannaschii section 10 of 150 of the complete genome.) (nt:similar to pid:1002692 sp:q50539 percent identity:) (le:6951) (re:8417) (di:complement) U67468 U67468 g1590888 Methanococcus jannaschii 2190 -11540553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924164	19815	41971	228	75

Description

6500736696 acetyl-coa decarbonylase/synthase:subunit delta:cdhd:corrinoid/iron-sulfur protein:small subunit (gtcfc:1.8) (keggfc:14.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0113 MJ0113 Methanococcus jannaschii 2190 -11540554 123220 corrinoid/iron-sulfur protein small chain:c/fe-sp small chain (cl:corrinoid/iron-sulfur protein small chain) (db:pir1.dat) (mp:rev111545-110328) A64314 A64314 Methanococcus jannaschii 2190 -11540554 246547 mj0113 acetyl-coa decarbonylase/synthase:subunit delta (db:genpept-bct1) (de:methanococcus jannaschii section 10 of 150 of the complete genome.) (nt:similar to pid:1002691 sp:q50538 pid:1575542) (le:8588) (re:9805) (di:complement) U67468 U67468 g1590889 Methanococcus jannaschii 2190 -11540554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924169	19816	41972	234	78

Description

6500736697 carbon monoxide dehydrogenase:subunit alpha:carbon monoxide dehydrogenase:alpha subunit (gtcfc:1.8:2.2) (ec:1.2.99.2) (keggfc:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0152 MJ0152 Methanococcus jannaschii 2190 -11540555 172997 carbon-monoxide dehydrogenase:alpha chain (ec:1.2.99.2) (db:pir2.dat) (mp:for147298-149544) A64319 A64319 Methanococcus jannaschii 2190 -11540555 246587 mj0152 carbon monoxide dehydrogenase:subunit alpha (db:genpept-bct1) (de:methanococcus jannaschii section 14 of 150 of the complete genome.) (nt:similar to gb:m62727 sp:p27988 pid:144786 percent) (le:3770) (re:6016) (di:direct) U67472 U67472 g1590910 Methanococcus jannaschii 2190 -11540555

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924200	19817	41973	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924204	19818	41974	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924210	19819	41975	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924211	19820	41976	687	229

Description

6500736698 cdha:mj0153 acetyl-coa decarbonylase/synthase:subunit alpha:carbon monoxide dehydrogenase alpha subunit (gtcfc:1.8:2.2) (ec:1.2.99.2) (keggfc:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0153 MJ0153 Methanococcus jannaschii 2190 -11540556 172998 carbon-monoxide dehydrogenase:alpha subunit (ec:1.2.99.2) (db:pir2.dat) (mp:for149781-152108) B64319 B64319 Methanococcus jannaschii 2190 -11540556 500684885 cdha:mj0153 (ec:1.2.99.2) (de:carbon monoxide dehydrogenase alpha subunit,) (db:swissprot) DCMA_METJA Q57617 METHANOCOCCUS JANNASCHII 2190 -11540556 246588 mju67472 (le:149781) (re:152108) (di:direct) (de:or:methanococcus jannaschii pn:carbon monoxide dehydrogenase, alpha subunit gn:mj0153 le:6253 re:8580 di:direct nt:similar to p26692 percent identity: 47.9;) U67472 U67472 g1590911 Methanococcus jannaschii 2190 10060242

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924217	19821	41977	681	226

Description

6500736699 acetyl-coa decarbonylase/synthase:subunit epsilon:cdhb:carbon monoxide dehydrogenase:beta subunit (gtcfc:1.8:2.2) (ec:1.2.99.2) (keggfc:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0154 MJ0154 Methanococcus jannaschii 2190 -11540557 173370 hypothetical protein mj0154 (db:pir2.dat) (mp:for152140-152592) C64319 C64319 Methanococcus jannaschii 2190 -11540557 246589 mju67472 (le:152140) (re:152592) (di:direct) (de:or:methanococcus jannaschii pn:m. jannaschii predicted coding region mj0154 gn:mj0154 le:8612 re:9064 di:direct nt:identified by genemark; putative) U67472 U67472 g1590912 Methanococcus jannaschii 2190 -11540557 5000698547 (de:(mj0154) (pn:hypothetical protein mj0154:hypothetical protein) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (tigrfc:15.1) (db:gtc-methanococcus jannaschii)) MJ0154 MJ0154 Methanococcus jannaschii 2190 10091619

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924219	19822	41978	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924220	19823	41979	1551	517

Description

6500736700 acetyl-coa decarbonylase/synthase:subunit beta:cdhc:carbon monoxide dehydrogenase:alpha subunit (gtcfc:1.8:2.2) (ec:1.2.99.2) (keggfc:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0156 MJ0156 Methanococcus jannaschii 2190 -11540558 172999 carbon-monoxide dehydrogenase:alpha subunit (ec:1.2.99.2) (db:pir2.dat) (mp:for153072-154481) E64319 E64319 Methanococcus jannaschii 2190 -11540558 246591 mj0156 acetyl-coa decarbonylase/synthase:subunit beta (db:genpept-bct1) (de:methanococcus jannaschii section 14 of 150 of the complete genome.) (nt:similar to gb:m62727 sp:p27988 pid:144786 percent) (le:9544) (re:10953) (di:direct) U67472 U67472 g1590913 Methanococcus jannaschii 2190 -11540558

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924221	19824	41980	312	103

Description

6500736701 carbon monoxide dehydrogenase:iron sulfur subunit coof-1:coof1:formate hydrogenlyase:iron-sulfur subunit 2 (gtcfc:1.8:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0264 MJ0264 Methanococcus jannaschii 2190 -11540559 500684889 mj0264 (de:hypothetical protein mj0264) (db:swissprot) Y264_METJA Q57712 METHANOCOCCUS JANNASCHII 2190 -11540559 173117 formate hydrogenlyase:subunit 2 (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:rev252386-251925) A64333 A64333 Methanococcus jannaschii 2190 -11540559 246699 mj0264 carbon monoxide dehydrogenase:iron sulfur (db:genpept-bct1) (de:methanococcus jannaschii section 24 of 150 of the complete genome.) (nt:similar to gb:m90421 sp:p31894 pid:1171263) (le:145) (re:606) (di:complement) U67482 U67482 g1592278 Methanococcus jannaschii 2190 -11540559 5000697878 (de:(mj0264) (pn:formate hydrogenlyase, subunit 2) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0264 MJ0264 Methanococcus jannaschii 2190 10060247

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924226	19825	41981	912	303

Description

6500736702 carbon monoxide dehydrogenase:iron sulfur subunit coof-1:coof2:formate hydrogenlyase:subunit 2 (gtcfc:1.8:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0265 MJ0265 Methanococcus jannaschii 2190 -11540560 173118 formate hydrogenlyase:subunit 2 (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:rev252934-252428) B64333 B64333 Methanococcus jannaschii 2190 -11540560 246700 mju67482 (le:252428) (re:252934) (di:direct) (de:or:methanococcus jannaschii pn:formate hydrogenlyase, subunit 2 gn:mj0265 le:648 re:1154 di:complement nt:similar to p16428 percent identity: 40.7;) U67482 U67482 g1590993 Methanococcus jannaschii 2190 -11540560 5000697879 (de:(mj0265) (pn:formate hydrogenlyase, subunit 2) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0265 MJ0265 Methanococcus jannaschii 2190 10091506

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924244	19826	41982	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924251	19827	41983	969	322

Description

6500736703 carbon monoxide dehydrogenase:hydrogenase subunit cooh:cooh:formate hydrogenlyase:subunit 5 (gtcfc:1.8:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0515 MJ0515 Methanococcus jannaschii 2190 -11540561 173120 formate hydrogenlyase:subunit 5 (cl:nadh dehydrogenase (ubiquinone) 49k protein) (db:pir2.dat) (mp:rev458767-457625) C64364 C64364 Methanococcus jannaschii 2190 -11540561 246949 mj0515 carbon monoxide dehydrogenase:hydrogenase (db:genpept-bct1) (de:methanococcus jannaschii section 43 of 150 of the complete genome.) (nt:similar to gp:1498746 percent identity: 34.64;) (le:6209) (re:7351) (di:complement) U67501 U67501 g1591218 Methanococcus jannaschii 2190 -11540561 5000697880 (de:(mj0515) (pn:formate hydrogenlyase, subunit 5) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0515 MJ0515 Methanococcus jannaschii 2190 10091508

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924256	19828	41984	1389	462

Description

6500736704 carbon monoxide dehydrogenase:hydrogenase subunit cool:cool:formate hydrogenlyase:subunit 7 (gtcfc:1.8:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0516 MJ0516 Methanococcus jannaschii 2190 -11540562 173122 formate hydrogenlyase:subunit 7 (db:pir2.dat) (mp:rev459221-458760) D64364 D64364 Methanococcus jannaschii 2190 -11540562 246950 mju67501 (le:458760) (re:459221) (di:direct) (de:or:methanococcus jannaschii pn:formate hydrogenlyase, subunit 7 gn:mj0516 le:7344 re:7805 di:complement nt:similar to p16433 percent identity: 48.1;) U67501 U67501 g1591219 Methanococcus jannaschii 2190 -11540562 5000697881 (de:(mj0516) (pn:formate hydrogenlyase, subunit 7) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0516 MJ0516 Methanococcus jannaschii 2190 10091510

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924264	19829	41985	279	92

Description

6500736705 carbon monoxide dehydrogenase:catalytic subunit:coos:carbon monoxide dehydrogenase:beta subunit (gtcfc:1.8:2.2) (ec:1.2.99.2) (keggfc:2.2) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ0728 MJ0728 Methanococcus jannaschii 2190 -11540563 173000 carbon-monoxide dehydrogenase:beta chain (cl:carbon-monoxide dehydrogenase beta chain) (ec:1.2.99.2) (db:pir2.dat) (mp:rev662463-660577) H64390 H64390 Methanococcus jannaschii 2190 -11540563 247162 mju67519 (le:660577) (re:662463) (di:direct) (de:or:methanococcus jannaschii pn:carbon monoxide dehydrogenase, beta subunit gn:mj0728 le:6701 re:8587 di:complement nt:similar to p31896 percent identity: 36.0;) U67519 U67519 g1591444 Methanococcus jannaschii 2190 10091440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924284	19830	41986	543	180

Description

6500736706 carbon monoxide dehydrogenase:hydrogenase anchor subunit coom:nadh dehydrogenase i:subunit n (gtcfc:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.10) (db:gtc-methanococcus jannaschii) MJ1309 MJ1309 Methanococcus jannaschii 2190 -11540564 173993 conserved hypothetical protein mj1309 (cl:methanococcus jannaschii conserved hypothetical protein mj1309) (db:pir2.dat) (mp:rev1255903-1254458) D64463 D64463 Methanococcus jannaschii 2190 -11540564 247742 mj1309 carbon monoxide dehydrogenase:hydrogenase (db:genpept-bct1) (de:methanococcus jannaschii section 113 of 150 of the complete genome.) (nt:similar to gp:1515466 percent identity: 31.71;) (le:5695) (re:7140) (di:complement) U67571 U67571 g1591948 Methanococcus jannaschii 2190 -11540564 5000699449 (de:(mj1309) (pn:hypothetical protein mj1309) (gtcfc:13.7) (ec:) (keggfc:11.2) (db:gtc-methanococcus jannaschii)) MJ1309 MJ1309 Methanococcus jannaschii 2190 10092126

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924288	19831	41987	2502	833

Description

5000698448 bcpc phosphonopyruvate decarboxylase:hypothetical protein (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ0010 MJ0010 Methanococcus jannaschii 2190 -11540565 118721 mj0010 (de:hypothetical protein mj0010) (db:swissprot) Y010_METJA Q60326 METHANOCOCCUS JANNASCHII 2190 -11540565 174417 probable phosphonopyruvate decarboxylase (cl:phosphonopyruvate decarboxylase) (ec:4.1.1.-) (db:pir2.dat) (mp:for11581-12867) B64301 B64301 Methanococcus jannaschii 2190 -11540565 246444 mj0010 bcpc phosphonopyruvate decarboxylase (db:genpept-bct1) (de:methanococcus jannaschii section 2 of 150 of the complete genome.) (nt:similar to gb:d37809 pid:520857 sp:q54271 percent) (le:1566) (re:2852) (di:direct) U67460 U67460 g1590821 Methanococcus jannaschii 2190 -11540565 6500736707 bcpc phosphonopyruvate decarboxylase:hypothetical protein (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ0010 MJ0010 Methanococcus jannaschii 2190 -11540565

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924299	19832	41988	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924301	19833	41989	474	157

Description

5000698449 fom2 phosphonopyruvate decarboxylase:fom2:hypothetical protein (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ0256 MJ0256 Methanococcus jannaschii 2190 -11540566 500684999 mj0256 (de:hypothetical protein mj0256) (db:swissprot) Y256_METJA Q57704 METHANOCOCCUS JANNASCHII 2190 -11540566 174416 probable phosphonopyruvate decarboxylase:fom2 (cl:methanococcus jannaschii phosphonopyruvate decarboxylase fom2) (ec:4.1.1.-) (db:pir2.dat) (mp:for242038-242604) A64332 A64332 Methanococcus jannaschii 2190 -11540566 6500736708 fom2 phosphonopyruvate decarboxylase:fom2:hypothetical protein (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ0256 MJ0256 Methanococcus jannaschii 2190 -11540566 246691 mju67481 (le:242038) (re:242604) (di:direct) (de:or:methanococcus jannaschii pn:fom2 phosphonopyruvate decarboxylase gn:mj0256 le:365 re:931 di:direct nt:similar to d38561_9 percent identity: 33.8;) U67481 U67481 g1590986 Methanococcus jannaschii 2190 -11540566

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924305	19834	41990	480	159

Description

5000698452 wilms tumor suppressor homolog:50s ribosomal protein l10e (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ0543 MJ0543 Methanococcus jannaschii 2190 -11540567 4000709635 mj0543 (de:50s ribosomal protein l10e) (db:swissprot) RL10_METJA Q57963 METHANOCOCCUS JANNASCHII 2190 -11540567 174618 wilms tumor suppressor homolog (cl:ribosomal protein l10.e) (db:pir2.dat) (mp:rev481784-481260) G64367 G64367 Methanococcus jannaschii 2190 -11540567 246977 mj0543 ubiquinol-cytochrome c reductase complex (db:genpept-bct1) (de:methanococcus jannaschii section 45 of 150 of the complete genome.) (nt:similar to gb:z15157 sp:q08770 pid:17584 pid:17682) (le:9415) (re:9939) (di:complement) U67503 U67503 g1591247 Methanococcus jannaschii 2190 -11540567 6500736709 wilms tumor suppressor homolog:50s ribosomal protein l10e (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ0543 MJ0543 Methanococcus jannaschii 2190 -11540567

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924311	19835	41991	402	133

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924331	19836	41992	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924344	19837	41993	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924347	19838	41994	726	241

Description

6500736710 sure:mj0559 sure stationary-phase survival protein sure:survival protein sure homolog (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ0559 MJ0559 Methanococcus jannaschii 2190 -11540568 4000709772 sure:mj0559 (de:survival protein sure homolog) (db:swissprot) SURE_METJA Q57979 METHANOCOCCUS JANNASCHII 2190 -11540568 174558 sure survival protein homolog (cl:stationary-phase survival protein sure) (db:pir2.dat) (mp:for494046-494876) G64369 G64369 Methanococcus jannaschii 2190 -11540568 246993 mj0559 sure stationary-phase survival protein sure (db:genpept-bct1) (de:methanococcus jannaschii section 47 of 150 of the complete genome.) (nt:similar to percent identity: 34.43; identified by) (le:1570) (re:2400) (di:direct) U67505 U67505 g1591265 Methanococcus jannaschii 2190 -11540568 5000698453 (de:(mj0559) (pn:sure survival protein) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:14.6) (db:gtc-methanococcus jannaschii)) MJ0559 MJ0559 Methanococcus jannaschii 2190 10092482

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924364	19839	41995	633	210

Description

6500736711 galactoside acetyltransferase:laca:acetyltransferase (gtcfc:1.8) (ec:2.3.1.18) (keggfc:14.1) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ1064 MJ1064 Methanococcus jannaschii 2190 -11540569 7500895896 mj1064 (de:hypothetical protein mj1064) (db:swissprot) YA64_METJA Q58464 METHANOCOCCUS JANNASCHII 2190 -11540569 172935 acetyltransferase (cl:galactoside acetyltransferase) (db:pir2.dat) (mp:rev1005909-1005265) G64432 G64432 Methanococcus jannaschii 2190 -11540569 7500895898 mj1064 galactoside acetyltransferase laca (db:genpept-bct1) (de:methanococcus jannaschii section 91 of 150 of the complete genome.) (nt:similar to gb:j01636 sp:p07464 gb:x51872 pid:551814) (le:8936) (re:9580) (di:complement) U67549 U67549 g1591716 Methanococcus jannaschii 2190 -11540569 247497 mju67549 (le:1005265) (re:1005909) (di:direct) (de:or:methanococcus jannaschii pn:acetyltransferase gn:mj1064 le:8936 re:9580 di:complement nt:similar to p07464 percent identity: 46.9;) U67549 U67549 g1591716 Methanococcus jannaschii 2190 -11540569 5000698459 (de:(mj1064) (pn:acetyltransferase) (gtcfc:13.7) (ec:2.3.1.18) (keggfc:11.1) (tigrfc:14.6) (db:gtc-methanococcus jannaschii)) MJ1064 MJ1064 Methanococcus jannaschii 2190 10091403

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924367	19840	41996	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924373	19841	41997	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924374	19842	41998	1509	502

Description

5000699148 gerc2 protein:hypothetical protein (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ1252 MJ1252 Methanococcus jannaschii 2190 -11540570 4000708430 mj1252 (de:hypothetical protein mj1252) (db:swissprot) YC52_METJA Q58648 METHANOCOCCUS JANNASCHII 2190 -11540570 172983 bioc protein homolog (cl:conserved hypothetical protein mj1123:bioc homology) (db:pir2.dat) (mp:rev1194506-1193751) B64456 B64456 Methanococcus jannaschii 2190 -11540570 247684 mj1252 gerc2 protein (db:genpept-bct1) (de:methanococcus jannaschii section 107 of 150 of the complete genome.) (nt:similar to gb:l14679 sp:p49016 pid:410740 percent) (le:7836) (re:8591) (di:complement) U67565 U67565 g1591885 Methanococcus jannaschii 2190 -11540570 6500736712 gerc2 protein:hypothetical protein (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ1252 MJ1252 Methanococcus jannaschii 2190 -11540570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924389	19843	41999	723	240

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924393	19844	42000	2196	731

Description

5000698461 phosphonopyruvate decarboxylase:bcpc:hypothetical protein (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ1612 MJ1612 Methanococcus jannaschii 2190 -11540571 1500686311 mj1612 (de:hypothetical protein mj1612) (db:swissprot) YG12_METJA Q59007 METHANOCOCCUS JANNASCHII 2190 -11540571 174415 probable phosphonopyruvate decarboxylase (cl:phosphonopyruvate decarboxylase) (ec:4.1.1.-) (db:pir2.dat) (mp:for1587809-1589044) C64501 C64501 Methanococcus jannaschii 2190 -11540571 248045 mj1612 phosphonopyruvate decarboxylase bcpc (db:genpept-bct1) (de:methanococcus jannaschii section 143 of 150 of the complete genome.) (nt:similar to gb:d37809 pid:520857 sp:q54271 percent) (le:6204) (re:7439) (di:direct) U67601 U67601 g1592213 Methanococcus jannaschii 2190 -11540571 6500736713 phosphonopyruvate decarboxylase:bcpc:hypothetical protein (gtcfc:1.8) (keggfc:14.2) (tigrfc:14.5) (db:gtc-methanococcus jannaschii) MJ1612 MJ1612 Methanococcus jannaschii 2190 -11540571

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924394	19845	42001	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924396	19846	42002	519	172

Description

6500736714 formate dehydrogenase:beta subunit:putative formate dehydrogenase beta chain (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0005 MJ0005 Methanococcus jannaschii 2190 -11540572 118168 mj0005 (ec:1.2.1.2) (de:putative formate dehydrogenase beta chain,) (db:swissprot) FDHB_METJA Q60316 METHANOCOCCUS JANNASCHII 2190 -11540572 173115 formate dehydrogenase:beta chain (cl:formate dehydrogenase chain b) (ec:1.2.1.2) (db:pir2.dat) (mp:rev7250-6111) E64300 E64300 Methanococcus jannaschii 2190 -11540572 246439 mj0005 formate dehydrogenase:beta subunit (db:genpept-bct1) (de:methanococcus jannaschii section 1 of 150 of the complete genome.) (nt:similar to sp:p06130 pid:149709 percent identity:) (le:6111) (re:7250) (di:complement) U67459 U67459 g1590818 Methanococcus jannaschii 2190 -11540572 5000697841 (de:(mj0005) (pn:putative formate dehydrogenase beta chain:formate dehydrogenase, beta subunit) (gtcfc:1.9:2.2) (ec:1.2.1.2) (fdhb_metja) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0005 MJ0005 Methanococcus jannaschii 2190 10060239

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924397	19847	42003	885	294

Description

6500736715 formate dehydrogenase:alpha subunit:putative formate dehydrogenase alpha chain (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0006 MJ0006 Methanococcus jannaschii 2190 -11540573 119996 mj0006 (ec:1.2.1.2) (de:putative formate dehydrogenase alpha chain,) (db:swissprot) FDHA_METJA Q60314 METHANOCOCCUS JANNASCHII 2190 -11540573 173113 formate dehydrogenase:alpha chain (ec:1.2.1.2) (db:pir2.dat) (mp:rev8474-7338) F64300 F64300 Methanococcus jannaschii 2190 -11540573 246440 mj0006 formate dehydrogenase:alpha subunit (db:genpept-bct1) (de:methanococcus jannaschii section 1 of 150 of the complete genome.) (nt:similar to gb:j02581 sp:p06131 pid:149708 percent) (le:7338) (re:8474) (di:complement) U67459 U67459 g1498763 Methanococcus jannaschii 2190 -11540573 5000697842 (de:(mj0006) (pn:putative formate dehydrogenase alpha chain:formate dehydrogenase, alpha subunit) (gtcfc:1.9:2.2) (ec:1.2.1.2) (fdha_metja) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0006 MJ0006 Methanococcus jannaschii 2190 10062790

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924404	19848	42004	327	108

Description

6500736716 formate dehydrogenase:iron-sulfur subunit (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0155 MJ0155 Methanococcus jannaschii 2190 -11540574 5500685203 mj0155 (de:putative ferredoxin mj0155) (db:swissprot) FER8_METJA Q57619 METHANOCOCCUS JANNASCHII 2190 -11540574 173116 probable formate dehydrogenase:iron-sulfur protein (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (ec:1.2.1.2) (db:pir2.dat) (mp:for152594-153049) D64319 D64319 Methanococcus jannaschii 2190 -11540574 246590 mj0155 formate dehydrogenase:iron-sulfur subunit (db:genpept-bct1) (de:methanococcus jannaschii section 14 of 150 of the complete genome.) (nt:similar to sp:p27273 pid:48508 percent identity:) (le:9066) (re:9521) (di:direct) U67472 U67472 g1498926 Methanococcus jannaschii 2190 -11540574 5000697843 (de:(mj0155) (pn:formate dehydrogenase, iron-sulfur subunit) (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0155 MJ0155 Methanococcus jannaschii 2190 10091505

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924420	19849	42005	747	248

Description

6500736717 hydrogenase expression/formation protein:hypa:putative hydrogenase expression/formation protein (gtcfc:1.9:2.2:10.7) (ec:1.18.99.1) (keggfc:1.9:2.2) (tigrfc:12.3) (db:gtc-methanococcus jannaschii) MJ0214 MJ0214 Methanococcus jannaschii 2190 -11540575 500684963 mj0214 (de:putative hydrogenase expression/formation protein mj0214) (db:swissprot) Y214_METJA Q57667 METHANOCOCCUS JANNASCHII 2190 -11540575 173189 hydrogenase accessory protein (cl:hydrogenase accessory protein) (db:pir2.dat) (mp:for204676-205050) G64326 G64326 Methanococcus jannaschii 2190 -11540575 246649 mj0214 hydrogenase expression/formation protein hypa (db:genpept-bct1) (de:methanococcus jannaschii section 19 of 150 of the complete genome.) (nt:similar to gb:l23970 sp:p31879 gb:x63650 pid:39241) (le:3702) (re:4076) (di:direct) U67477 U67477 g1590952 Methanococcus jannaschii 2190 -11540575 5000697844 (de:(mj0214) (pn:hydrogenase accessory protein) (gtcfc:1.9:2.2) (ec:1.18.99.1) (keggfc:1.9:2.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii)) MJ0214 MJ0214 Methanococcus jannaschii 2190 10060963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924422	19850	42006	2670	889

Description

6500736718 formate dehydrogenase:fdhd:nitrate assimilation protein:narq (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0295 MJ0295 Methanococcus jannaschii 2190 -11540576 500685017 mj0295 (de:hypothetical protein mj0295) (db:swissprot) Y295_METJA Q57743 METHANOCOCCUS JANNASCHII 2190 -11540576 173112 formate dehydrogenase fdhd (ec:1.2.-.-) (db:pir2.dat) (mp:rev279737-279054) H64336 H64336 Methanococcus jannaschii 2190 -11540576 246730 mj0295 formate dehydrogenase fdhd (db:genpept-bct1) (de:methanococcus jannaschii section 26 of 150 of the complete genome.) (nt:similar to sp:p28181 pid:48510 percent identity:) (le:7890) (re:8573) (di:complement) U67484 U67484 g1591017 Methanococcus jannaschii 2190 -11540576 5000697845 (de:(mj0295) (pn:formate dehydrogenase:fdhd) (gn:fdhd) (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0295 MJ0295 Methanococcus jannaschii 2190 10061244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924437	19851	42007	342	113

Description

6500736719 hydrogenase expression regulatory protein:hypf:hydrogenase accessory protein (gtcfc:1.9:2.2:10.7) (ec:1.18.99.1) (keggfc:1.9:2.2) (tigrfc:12.3) (db:gtc-methanococcus jannaschii) MJ0713 MJ0713 Methanococcus jannaschii 2190 -11540577 7500895474 mj0713 (de:putative hydrogenase expression/formation protein mj0713) (db:swissprot) Y713_METJA Q58123 METHANOCOCCUS JANNASCHII 2190 -11540577 173188 hydrogenase accessory protein (cl:probabe transcription regulator hypf) (db:pir2.dat) (mp:rev648382-646082) A64389 A64389 Methanococcus jannaschii 2190 -11540577 7500895476 mj0713 hydrogenase expression regulatory protein (db:genpept-bct1) (de:methanococcus jannaschii section 60 of 150 of the complete genome.) (nt:similar to pid:882605 gb:u00096 pid:2367152 percent) (le:2824) (re:5124) (di:complement) U67518 U67518 g1591430 Methanococcus jannaschii 2190 -11540577 247147 mju67518 (le:646082) (re:648382) (di:direct) (de:or:methanococcus jannaschii pn:hydrogenase accessory protein gn:mj0713 le:4074 re:6374 di:complement nt:similar to jn0648 percent identity: 34.1;) U67518 U67518 g1591430 Methanococcus jannaschii 2190 -11540577 5000697846 (de:(mj0713) (pn:hydrogenase accessory protein) (gtcfc:1.9:2.2) (ec:1.18.99.1) (keggfc:1.9:2.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii)) MJ0713 MJ0713 Methanococcus jannaschii 2190 10091550

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924440	19852	42008	807	268

Description

GTC ORF with score 209 to: (sr:fission yeast strain=bap1) (db:genpept-pln2) (de:schizosaccharomyces pombe brefeldin a resistance protein (hba1) andunknown orf genes, complete cds.) (nt:orf of unknown function; method: conceptual) (le:3468) (re:5405) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924441	19853	42009	525	174

Description

GTC ORF with score 116 to: (sr:fission yeast strain=bap1) (db:genpept-pln2) (de:schizosaccharomyces pombe brefeldin a resistance protein (hba1) andunknown orf genes, complete cds.) (nt:orf of unknown function; method: conceptual) (le:3468) (re:5405) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924450	19854	42010	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924452	19855	42011	435	144

Description

6500736720 formate hydrogenlyase:subunit 5 (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ1027 MJ1027 Methanococcus jannaschii 2190 -11540578 173119 formate hydrogenlyase:subunit 5 (cl:nadh dehydrogenase (ubiquinone) 49k protein) (db:pir2.dat) (mp:for958362-959495) B64428 B64428 Methanococcus jannaschii 2190 -11540578 247460 mj1027 formate hydrogenlyase:subunit 5 (db:genpept-bct1) (de:methanococcus jannaschii section 87 of 150 of the complete genome.) (nt:similar to sp:p16431 gb:x17506 pid:41684 pid:882614) (le:6537) (re:7670) (di:direct) U67545 U67545 g1499869 Methanococcus jannaschii 2190 -11540578 5000697894 (de:(mj1027) (pn:formate hydrogenlyase, subunit 5) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1027 MJ1027 Methanococcus jannaschii 2190 10091507

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924453	19856	42012	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924456	19857	42013	282	93

Description

6500736721 rbcl:ribulose bisphosphate carboxylase:large subunit (gtcfc:1.9:2.4) (ec:4.1.1.39) (keggfc:1.9:2.3) (tigrfc:5.8) (db:gtc-methanococcus jannaschii) MJ1235 MJ1235 Methanococcus jannaschii 2190 -11540579 174532 ribulose-bisphosphate carboxylase:large subunit (cl:ribulose-bisphosphate carboxylase large chain) (ec:4.1.1.39) (db:pir2.dat) (mp:rev1179982-1178687) B64454 B64454 Methanococcus jannaschii 2190 -11540579 247668 mju67564 (le:1178687) (re:1179982) (di:direct) (de:or:methanococcus jannaschii pn:ribulose bisphosphate carboxylase, large gn:mj1235 le:3394 re:4689 di:complement nt:similar to p00880 percent identity: 40.7;) U67564 U67564 g1591867 Methanococcus jannaschii 2190 -11540579 5000697847 (de:(mj1235) (pn:ribulose bisphosphate carboxylase, large subunit) (gtcfc:1.9:2.4) (ec:4.1.1.39) (keggfc:1.9:2.3) (tigrfc:5.8) (db:gtc-methanococcus jannaschii)) MJ1235 MJ1235 Methanococcus jannaschii 2190 10092470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924480	19858	42014	735	244

Description

6500736722 formate dehydrogenase:alpha subunit (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ1353 MJ1353 Methanococcus jannaschii 2190 -11540580 173114 formate dehydrogenase:alpha chain (ec:1.2.1.2) (db:pir2.dat) (mp:rev1303623-1302016) H64468 H64468 Methanococcus jannaschii 2190 -11540580 247786 mju67575 (le:1302016) (re:1303623) (di:direct) (de:or:methanococcus jannaschii pn:formate dehydrogenase, alpha subunit gn:mj1353 le:4705 re:6312 di:complement nt:similar to p06131 percent identity: 54.3;) U67575 U67575 g1591996 Methanococcus jannaschii 2190 -11540580 5000697848 (de:(mj1353) (pn:formate dehydrogenase, alpha subunit) (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1353 MJ1353 Methanococcus jannaschii 2190 10091504

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924495	19859	42015	1674	557

Description

6500736723 formate hydrogenlyase:subunit 7 (gtcfc:1.9:2.2) (ec:1.2.1.2) (keggfc:1.9:2.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ1363 MJ1363 Methanococcus jannaschii 2190 -11540581 173121 formate hydrogenlyase:subunit 7 (db:pir2.dat) (mp:rev1312797-1312342) B64470 B64470 Methanococcus jannaschii 2190 -11540581 247796 mj1363 formate hydrogenlyase:subunit 7 (db:genpept-bct1) (de:methanococcus jannaschii section 118 of 150 of the complete genome.) (nt:similar to sp:p16433 gb:x17506 pid:41686 pid:882612) (le:3881) (re:4336) (di:complement) U67576 U67576 g1592007 Methanococcus jannaschii 2190 -11540581 5000697899 (de:(mj1363) (pn:formate hydrogenlyase, subunit 7) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1363 MJ1363 Methanococcus jannaschii 2190 10091509

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924525	19860	42016	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924536	19861	42017	1440	479

Description

6500736724 atpb:mj0216 h+-transporting atp synthase:subunit b:atp synthase beta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii) MJ0216 MJ0216 Methanococcus jannaschii 2190 -11540582 117574 atpb:mj0216 (ec:3.6.1.34) (de:atp synthase beta chain,) (db:swissprot) ATPB_METJA Q57669 METHANOCOCCUS JANNASCHII 2190 -11540582 173160 h+-transporting atp synthase:b chain (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir2.dat) (mp:rev207140-205743) A64327 A64327 Methanococcus jannaschii 2190 -11540582 246651 mj0216 h+-transporting atp synthase:subunit b atpb (db:genpept-bct1) (de:methanococcus jannaschii section 19 of 150 of the complete genome.) (nt:similar to gb:j04836 sp:p22663 pid:149821 percent) (le:4769) (re:6166) (di:complement) U67477 U67477 g1590954 Methanococcus jannaschii 2190 -11540582 5000697862 (de:(mj0216) (pn:atp synthase beta chain:atp synthase, subunit b) (gn:atpb) (gtcfc:2.1) (ec:3.6.1.34) (atpb_metja) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii)) MJ0216 MJ0216 Methanococcus jannaschii 2190 10059425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924552	19862	42018	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924562	19863	42019	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924566	19864	42020	549	182

Description

6500736725 atpa:mj0217 h+-transporting atp synthase:subunit a:atp synthase alpha chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii) MJ0217 MJ0217 Methanococcus jannaschii 2190 -11540583 117573 atpa:mj0217 (ec:3.6.1.34) (de:atp synthase alpha chain,) (db:swissprot) ATPA_METJA Q57670 METHANOCOCCUS JANNASCHII 2190 -11540583 173161 h+-transporting atp synthase:subunit a (cl:vacuolar h+-transporting atpase 69k chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir2.dat) (mp:rev208971-207187) B64327 B64327 Methanococcus jannaschii 2190 -11540583 246652 mj0217 h+-transporting atp synthase:subunit a atpa (db:genpept-bct1) (de:methanococcus jannaschii section 19 of 150 of the complete genome.) (nt:similar to gb:j04836 sp:p22662 pid:149820 percent) (le:6213) (re:7997) (di:complement) U67477 U67477 g1590955 Methanococcus jannaschii 2190 -11540583 5000697863 (de:(mj0217) (pn:atp synthase alpha chain:atp synthase, subunit a) (gn:atpa) (gtcfc:2.1) (ec:3.6.1.34) (atpa_metja) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii)) MJ0217 MJ0217 Methanococcus jannaschii 2190 10059423

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924567	19865	42021	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924568	19866	42022	375	124

Description

6500736726 atpf:mj0218 h+-transporting atp synthase:subunit f:atp synthase:subunit f (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii) MJ0218 MJ0218 Methanococcus jannaschii 2190 -11540584 500684784 atpf:mj0218 (ec:3.6.1.34) (de:atp synthase, subunit f,) (db:swissprot) ATPF_METJA Q57671 METHANOCOCCUS JANNASCHII 2190 -11540584 173165 h+-transporting atp synthase:subunit f (cl:h+-transporting atp synthase subunit f) (ec:3.6.1.34) (db:pir2.dat) (mp:rev209307-209011) C64327 C64327 Methanococcus jannaschii 2190 -11540584 246653 mj0218 h+-transporting atp synthase:subunit f atpf (db:genpept-bct1) (de:methanococcus jannaschii section 19 of 150 of the complete genome.) (nt:similar to pid:1199637 sp:q60185 percent identity:) (le:8037) (re:8333) (di:complement) U67477 U67477 g1498994 Methanococcus jannaschii 2190 -11540584 5000697864 (de:(mj0218) (pn:atp synthase, subunit f) (gtcfc:2.1) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii)) MJ0218 MJ0218 Methanococcus jannaschii 2190 10059435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924579	19867	42023	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924585	19868	42024	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924592	19869	42025	660	219

Description

6500736727 atpc:mj0219 h+-transporting atp synthase:subunit c:atp synthase:subunit c (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii) MJ0219 MJ0219 Methanococcus jannaschii 2190 -11540585 500684777 atpc:mj0219 (ec:3.6.1.34) (de:atp synthase, subunit c,) (db:swissprot) ATPC_METJA Q57672 METHANOCOCCUS JANNASCHII 2190 -11540585 173162 h+-transporting atp synthase:subunit c (cl:h+ transporting atp synthase c subunit) (ec:3.6.1.34) (db:pir2.dat) (mp:rev210517-209318) D64327 D64327 Methanococcus jannaschii 2190 -11540585 246654 mj0219 h+-transporting atp synthase:subunit c atpc (db:genpept-bct1) (de:methanococcus jannaschii section 19 of 150 of the complete genome.) (nt:similar to pid:1199636 sp:q60184 percent identity:) (le:8344) (re:9543) (di:complement) U67477 U67477 g1590956 Methanococcus jannaschii 2190 -11540585 5000697865 (de:(mj0219) (pn:atp synthase, subunit c) (gtcfc:2.1) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii)) MJ0219 MJ0219 Methanococcus jannaschii 2190 10059428

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924610	19870	42026	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924635	19871	42027	540	179

Description

6500736728 atpe:mj0220 h+-transporting atp synthase:subunit e:atp synthase:subunit e (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii) MJ0220 MJ0220 Methanococcus jannaschii 2190 -11540586 500684781 atpe:mj0220 (ec:3.6.1.34) (de:atp synthase, subunit e,) (db:swissprot) ATPE_METJA Q57673 METHANOCOCCUS JANNASCHII 2190 -11540586 173164 h+-transporting atp synthase:subunit e (cl:atp synthase subunit e) (ec:3.6.1.34) (db:pir2.dat) (mp:rev211241-210621) E64327 E64327 Methanococcus jannaschii 2190 -11540586 246655 mj0220 h+-transporting atp synthase:subunit e atpe (db:genpept-bct1) (de:methanococcus jannaschii section 19 of 150 of the complete genome.) (nt:similar to pid:1199635 sp:q60183 percent identity:) (le:9647) (re:10267) (di:complement) U67477 U67477 g1590957 Methanococcus jannaschii 2190 -11540586 5000697866 (de:(mj0220) (pn:atp synthase, subunit e) (gtcfc:2.1) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii)) MJ0220 MJ0220 Methanococcus jannaschii 2190 10059432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924640	19872	42028	435	144

Description

6500736729 h+-transporting atp synthase:subunit k:atpk:probable atpase proteolipid chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii) MJ0221 MJ0221 Methanococcus jannaschii 2190 -11540587 500684787 mj0221 (ec:3.6.1.34) (de:probable atpase proteolipid chain,) (db:swissprot) ATPL_METJA Q57674 METHANOCOCCUS JANNASCHII 2190 -11540587 173167 h+-transporting atp synthase:subunit k (cl:na+-atpase complex k chain) (ec:3.6.1.34) (db:pir2.dat) (mp:rev211960-211298) F64327 F64327 Methanococcus jannaschii 2190 -11540587 246656 mj0221 h+-transporting atp synthase:subunit k atpk (db:genpept-bct1) (de:methanococcus jannaschii section 20 of 150 of the complete genome.) (nt:similar to gb:d16334 gb:x76913 sp:p43457 pid:416405) (le:54) (re:716) (di:complement) U67478 U67478 g1590959 Methanococcus jannaschii 2190 -11540587 5000697867 (de:(mj0221) (pn:atp synthase, subunit k) (gtcfc:2.1) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii)) MJ0221 MJ0221 Methanococcus jannaschii 2190 10059438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924644	19873	42029	423	140

Description

6500736730 h+-transporting atp synthase:subunit i:atpi:probalbe atp synthase subunit i (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii) MJ0222 MJ0222 Methanococcus jannaschii 2190 -11540588 500684788 mj0222 (ec:3.6.1.34) (de:probalbe atp synthase subunit i,) (db:swissprot) ATPI_METJA Q57675 METHANOCOCCUS JANNASCHII 2190 -11540588 173166 h+-transporting atp synthase:subunit i (ec:3.6.1.34) (db:pir2.dat) (mp:rev214151-212064) G64327 G64327 Methanococcus jannaschii 2190 -11540588 246657 mj0222 h+-transporting atp synthase:subunit i atpi (db:genpept-bct1) (de:methanococcus jannaschii section 20 of 150 of the complete genome.) (nt:similar to gb:d17462 gb:x76913 sp:p43439 pid:472918) (le:820) (re:2907) (di:complement) U67478 U67478 g1590960 Methanococcus jannaschii 2190 -11540588 5000697868 (de:(mj0222) (pn:atp synthase, subunit i) (gtcfc:2.1) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii)) MJ0222 MJ0222 Methanococcus jannaschii 2190 10059468

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924646	19874	42030	294	97

Description

6500736731 nadh-ubiquinone oxidoreductase:subunit 1 (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.2) (db:gtc-methanococcus jannaschii) MJ0520 MJ0520 Methanococcus jannaschii 2190 -11540589 174374 nadh dehydrogenase ubiquinone::nadh-ubiquinone oxidoreductase:subunit 1 (ec:1.6.5.3) (db:pir2.dat) (mp:rev461355-460468) H64364 H64364 Methanococcus jannaschii 2190 -11540589 246954 mj0520 nadh-ubiquinone oxidoreductase:subunit 1 (db:genpept-bct1) (de:methanococcus jannaschii section 43 of 150 of the complete genome.) (nt:similar to sp:p12772 percent identity: 28.08;) (le:9052) (re:9939) (di:complement) U67501 U67501 g1591222 Methanococcus jannaschii 2190 -11540589 5000697869 (de:(mj0520) (pn:nadh-ubiquinone oxidoreductase, subunit 1) (gtcfc:2.1:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:6.2) (db:gtc-methanococcus jannaschii)) MJ0520 MJ0520 Methanococcus jannaschii 2190 10092409

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924650	19875	42031	1125	374

Description

6500736732 atpd:mj0615 h+-transporting atp synthase:subunit d:atp synthase:subunit d (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii) MJ0615 MJ0615 Methanococcus jannaschii 2190 -11540590 4000707604 atpd:mj0615 (ec:3.6.1.34) (de:atp synthase, subunit d,) (db:swissprot) ATPD_METJA Q58032 METHANOCOCCUS JANNASCHII 2190 -11540590 173163 h+-transporting atp synthase:chain d (cl:h+-transporting atpase chain d) (ec:3.6.1.34) (db:pir2.dat) (mp:rev546347-545697) G64376 G64376 Methanococcus jannaschii 2190 -11540590 247049 mj0615 h+-transporting atp synthase:subunit d atpd (db:genpept-bct1) (de:methanococcus jannaschii section 52 of 150 of the complete genome.) (nt:similar to pid:1199640 sp:q60188 percent identity:) (le:148) (re:798) (di:complement) U67510 U67510 g1592298 Methanococcus jannaschii 2190 -11540590 5000697870 (de:(mj0615) (pn:atp synthase, subunit d) (gtcfc:2.1) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-methanococcus jannaschii)) MJ0615 MJ0615 Methanococcus jannaschii 2190 10091535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924656	19876	42032	810	269

Description

6500736733 nadh dehydrogenase:subunit 1 (gtcfc:9.12) (ec:1.6.5.3) (keggfc:2.1:9.13) (tigrfc:15.1) (db:gtc-methanococcus jannaschii) MJ1362 MJ1362 Methanococcus jannaschii 2190 -11540591 174375 nadh dehydrogenase:subunit 1 (cl:methanococcus jannaschii nadh dehydrogenase (ubiquinone) chain 1) (ec:1.6.-.-) (db:pir2.dat) (mp:rev1312273-1311305) A64470 A64470 Methanococcus jannaschii 2190 -11540591 247795 mj1362 nadh ubiquinone oxidoreductase:subunit 1 (db:genpept-bct1) (de:methanococcus jannaschii section 118 of 150 of the complete genome.) (nt:similar to sp:p03887 percent identity: 24.02;) (le:2844) (re:3812) (di:complement) U67576 U67576 g1592006 Methanococcus jannaschii 2190 -11540591 5000697933 (de:(mj1362) (pn:nadh dehydrogenase, subunit 1) (gtcfc:2.8) (ec:) (keggfc:11.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ1362 MJ1362 Methanococcus jannaschii 2190 10092410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924666	19877	42033	339	112

Description

6500736734 adk:mj0479 adenylate kinase:atp-amp transphosphorylase (gtcfc:2.1:4.1) (ec:2.7.4.3) (keggfc:4.1) (tigrfc:6.1) (db:gtc-methanococcus jannaschii) MJ0479 MJ0479 Methanococcus jannaschii 2190 -11540592 172943 adenylate kinase (cl:methanococcus adenylate kinase) (ec:2.7.4.3) (db:pir2.dat) (mp:for421829-422416) G64359 G64359 Methanococcus jannaschii 2190 -11540592 246913 mj0479 adenylate kinase adk (db:genpept-bct1) (de:methanococcus jannaschii section 40 of 150 of the complete genome.) (nt:similar to pid:1086550 pid:1591182 percent) (le:1641) (re:2228) (di:direct) U67498 U67498 g1591182 Methanococcus jannaschii 2190 -11540592 5000697955 (de:(mj0479) (pn:atp-amp transphosphorylase:adenylate kinase) (gn:adk) (gtcfc:4.1) (ec:2.7.4.3) (kad_metja) (keggfc:4.1) (tigrfc:6.1) (db:gtc-methanococcus jannaschii)) MJ0479 MJ0479 Methanococcus jannaschii 2190 10091408

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924671	19878	42034	423	140

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924672	19879	42035	615	204

Description

6500736735 nadh oxidase:nox:putative nadh oxidase:noxase (gtcfc:2.1) (ec:1.6.-.-) (keggfc:14.1) (tigrfc:6.2) (db:gtc-methanococcus jannaschii) MJ0649 MJ0649 Methanococcus jannaschii 2190 -11540593 4000709573 mj0649 (ec:1.6.99.3) (de:putative nadh oxidase, (noxase)) (db:swissprot) NAOX_METJA Q58065 METHANOCOCCUS JANNASCHII 2190 -11540593 174376 nadh oxidase (cl:nadh peroxidase) (db:pir2.dat) (mp:for576056-577447) A64381 A64381 Methanococcus jannaschii 2190 -11540593 247083 mj0649 nadh oxidase nox (db:genpept-bct1) (de:methanococcus jannaschii section 54 of 150 of the complete genome.) (nt:similar to pid:642030 percent identity: 30.89;) (le:6126) (re:7517) (di:direct) U67512 U67512 g1591361 Methanococcus jannaschii 2190 -11540593 5000699461 (de:(mj0649) (pn:nadh oxidase) (gtcfc:13.7) (ec:1.6.-.-) (keggfc:11.1) (tigrfc:6.2) (db:gtc-methanococcus jannaschii)) MJ0649 MJ0649 Methanococcus jannaschii 2190 10092411

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924677	19880	42036	474	157

Description

6500736736 glya:mj1597 serine hydroxymethyltransferase:serine methylase:shmt (gtcfc:2.2:5.3:5.9:6.5:9.3:9.6) (ec:2.1.2.1) (keggfc:2.2:5.3:5.9:6.5:9.3:9.8) (tigrfc:1.6) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:l-amino acid metab... MJ1597 MJ1597 Methanococcus jannaschii 2190 -11540594 121394 glya:mj1597 (ec:2.1.2.1) (de:(shmt)) (db:swissprot) GLYA_METJA Q58992 METHANOCOCCUS JANNASCHII 2190 -11540594 173150 glycine hydroxymethyltransferase (cl:glycine hydroxymethyltransferase) (ec:2.1.2.1) (db:pir2.dat) (mp:for1568607-1569896) D64499 D64499 Methanococcus jannaschii 2190 -11540594 248030 mj1597 serine hydroxymethyltransferase glya (db:genpept-bct1) (de:methanococcus jannaschii section 141 of 150 of the complete genome.) (nt:similar to pid:1103705 sp:p50436 gb:ae000666) (le:7907) (re:9196) (di:direct) U67599 U67599 g1592207 Methanococcus jannaschii 2190 -11540594 5000697871 (de:(mj1597) (pn:serine hydroxymethyltransferase:serine methylase:shmt:glycine hydroxymethyltransferase) (gn:glya) (gtcfc:2.2:5.3:5.9:6.5:9.3:9.8) (ec:2.1.2.1) (glya_metja) (keggfc:2.2:5.3:5.9:6.5:9.3:9.8) (tigrfc:1.5) (db:gtc-m) MJ1597 MJ1597 Methanococcus jannaschii 2190 10064742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924690	19881	42037	390	129

Description

5000697829 2-hydroxyglutaryl-coa dehydratase:subunit beta:hgdb:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ0007 MJ0007 Methanococcus jannaschii 2190 -11540595 118718 mj0007 (de:hypothetical protein mj0007) (db:swissprot) Y007_METJA Q60318 METHANOCOCCUS JANNASCHII 2190 -11540595 172908 2-hydroxyglutaryl-coa dehydratase:subunit beta (db:pir2.dat) (mp:for8884-10005) G64300 G64300 Methanococcus jannaschii 2190 -11540595 246441 mj0007 2-hydroxyglutaryl-coa dehydratase:subunit beta (db:genpept-bct1) (de:methanococcus jannaschii section 1 of 150 of the complete genome.) (nt:similar to gb:x14252 sp:p11570 pid:38802 percent) (le:8884) (re:10005) (di:direct) U67459 U67459 g1592253 Methanococcus jannaschii 2190 -11540595 6500736737 2-hydroxyglutaryl-coa dehydratase:subunit beta:hgdb:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ0007 MJ0007 Methanococcus jannaschii 2190 -11540595

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924698	19882	42038	1710	569

Description

5000698543 2-ketoglutarate ferredoxin oxidoreductase:subunit delta:kord:putative ferredoxin (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ0146 MJ0146 Methanococcus jannaschii 2190 -11540596 118167 mj0146 (de:putative ferredoxin mj0146) (db:swissprot) FER3_METJA Q57610 METHANOCOCCUS JANNASCHII 2190 -11540596 173366 hypothetical protein mj0146 (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:rev143409-143200) C64318 C64318 Methanococcus jannaschii 2190 -11540596 246581 mj0146 2-ketoglutarate ferredoxin oxidoreductase (db:genpept-bct1) (de:methanococcus jannaschii section 13 of 150 of the complete genome.) (nt:similar to gb:m63654 sp:p23481 pid:147018 gb:u00096) (le:9204) (re:9413) (di:complement) U67471 U67471 g1498915 Methanococcus jannaschii 2190 -11540596 6500736738 2-ketoglutarate ferredoxin oxidoreductase:subunit delta:kord:putative ferredoxin (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ0146 MJ0146 Methanococcus jannaschii 2190 -11540596

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924707	19883	42039	279	92

Description

5000697830 pyruvate formate-lyase activating enzyme:actb:m (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ0804 MJ0804 Methanococcus jannaschii 2190 -11540597 173729 hypothetical protein mj0804 (cl:hypothetical protein mj0804) (db:pir2.dat) (mp:for727532-728392) D64400 D64400 Methanococcus jannaschii 2190 -11540597 5500686409 mj0804 (de:hypothetical protein mj0804) (db:swissprot) Y804_METJA Q58214 METHANOCOCCUS JANNASCHII 2190 -11540597 6500736739 pyruvate formate-lyase activating enzyme:actb:m (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ0804 MJ0804 Methanococcus jannaschii 2190 -11540597 247238 mju67525 (le:727532) (re:728392) (di:direct) (de:or:methanococcus jannaschii pn:m. jannaschii predicted coding region mj0804 gn:mj0804 le:1268 re:2128 di:direct nt:identified by genemark; putative) U67525 U67525 g1499627 Methanococcus jannaschii 2190 -11540597

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924708	19884	42040	618	205

Description

6500736740 pyruvate-formate-lyase-activating enzyme:actc:pyruvate formate-lyase activating enzyme related protein (gtcfc:2.2) (ec:1.97.1.4) (keggfc:14.1) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ0808 MJ0808 Methanococcus jannaschii 2190 -11540598 5500686413 mj0808 (de:hypothetical protein mj0808) (db:swissprot) Y808_METJA Q58218 METHANOCOCCUS JANNASCHII 2190 -11540598 173732 hypothetical protein mj0808 (cl:conserved hypothetical protein mj0808) (db:pir2.dat) (mp:for730808-731809) H64400 H64400 Methanococcus jannaschii 2190 -11540598 247242 mj0808 pyruvate-formate-lyase-activating enzyme act (db:genpept-bct1) (de:methanococcus jannaschii section 67 of 150 of the complete genome.) (nt:similar to pid:1072362 sp:q46267 percent identity:) (le:4544) (re:5545) (di:direct) U67525 U67525 g1499631 Methanococcus jannaschii 2190 -11540598 5000697831 (de:(mj0808) (pn:pyruvate-formate-lyase-ivating enzyme:pyruvate-formate-lyase-activating enzyme:act) (gn:act) (gtcfc:1.4:13.7) (ec:) (keggfc:11.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii)) MJ0808 MJ0808 Methanococcus jannaschii 2190 10091887

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924729	19885	42041	594	197

Description

5000699112 putative aldehyde ferredoxin oxidoreductase:aor:m (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ1185 MJ1185 Methanococcus jannaschii 2190 -11540599 173929 hypothetical protein mj1185 (db:pir2.dat) (mp:rev1125034-1123166) H64447 H64447 Methanococcus jannaschii 2190 -11540599 247618 mj1185 putative aldehyde ferredoxin oxidoreductase (db:genpept-bct1) (de:methanococcus jannaschii section 101 of 150 of the complete genome.) (nt:similar to pid:736274 percent identity: 26.51;) (le:11729) (re:13597) (di:complement) U67559 U67559 g1591812 Methanococcus jannaschii 2190 -11540599 6500736741 putative aldehyde ferredoxin oxidoreductase:aor:m (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ1185 MJ1185 Methanococcus jannaschii 2190 -11540599

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924740	19886	42042	366	121

Description

6500736742 acta:pyruvate formate-lyase activating enzyme (gtcfc:2.2) (ec:1.97.1.4) (keggfc:14.1) (tigrfc:6.6) (db:gtc-methanococcus jannaschii) MJ1227 MJ1227 Methanococcus jannaschii 2190 -11540600 174457 pyruvate formate-lyase activating enzyme homolog (cl:pyruvate formate-lyase activating enzyme) (db:pir2.dat) (mp:for1170387-1171109) B64453 B64453 Methanococcus jannaschii 2190 -11540600 247660 mj1227 pyruvate formate-lyase activating enzyme act (db:genpept-bct1) (de:methanococcus jannaschii section 105 of 150 of the complete genome.) (nt:similar to gb:l42023 sp:p43751 pid:1003258) (le:8189) (re:8911) (di:direct) U67563 U67563 g1591858 Methanococcus jannaschii 2190 -11540600 5000697931 (de:(mj1227) (pn:pyruvate formate-lyase activating enzyme) (gtcfc:2.8) (ec:1.97.1.4) (keggfc:11.1) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ1227 MJ1227 Methanococcus jannaschii 2190 10092454

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924748	19887	42043	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924753	19888	42044	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924758	19889	42045	597	198

Description

6500736743 frha:mj0029 coenzyme f420-reducing hydrogenase:alpha subunit:coenzyme f420 hydrogenase alpha subunit:8-hydroxy-5-deazaflavin-reducing hydrogenase alpha subunit:frh (gtcfc:2.2:9.6) (ec:1.12.99.1) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0029 MJ0029 Methanococcus jannaschii 2190 -11540601 5000698129 (de:(mj0029) (pn:coenzyme f420 hydrogenase alpha subunit:8-hydroxy-5- deazaflavin-reducing hydrogenase alpha subunit:frh:coenzyme f420-reducing hydrogenase, alpha subunit) (gn:frha) (gtcfc:9.6) (ec:1.12.99.1) (frha_metja) (keggfc) MJ0029 MJ0029 Methanococcus jannaschii 2190 10316865

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924759	19890	42046	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924761	19891	42047	1104	367

Description

6500736744 frhd:mj0030 coenzyme f420-reducing hydrogenase:delta subunit:frcd:coenzyme f420 hydrogenase delta subunit:putative coenzyme f420 hydrogenase processing subunit (gtcfc:2.2:9.6) (ec:1.12.99.1) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0030 MJ0030 Methanococcus jannaschii 2190 -11540602 118561 frhd:mj0030 (de:hydrogenase processing subunit)) (db:swissprot) FRHD_METJA Q60339 METHANOCOCCUS JANNASCHII 2190 -11540602 173032 coenzyme f420 hydrogenase alpha chain:coenzyme f420-reducing hydrogenase:alpha subunit (cl:coenzyme f420-reducing hydrogenase delta chain) (db:pir2.dat) (mp:for31255-31806) F64303 F64303 Methanococcus jannaschii 2190 -11540602 246464 mj0030 coenzyme f420-reducing hydrogenase:delta (db:genpept-bct1) (de:methanococcus jannaschii section 3 of 150 of the complete genome.) (nt:similar to gb:x61202 pid:44706 percent identity:) (le:8699) (re:9250) (di:direct) U67461 U67461 g1590832 Methanococcus jannaschii 2190 -11540602 5000698130 (de:(mj0030) (pn:coenzyme f420 hydrogenase delta subunit:putative coenzyme f420 hydrogenase processing subunit:coenzyme f420-reducing hydrogenase, alpha subunit) (gn:frhd) (gtcfc:9.6) (ec:1.12.99.1) (frhd_metja) (keggfc:9.7) (ti) MJ0030 MJ0030 Methanococcus jannaschii 2190 10060951

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924772	19892	42048	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924786	19893	42049	729	242

Description

6500736745 frhg:mj0031 coenzyme f420-reducing hydrogenase:gamma subunit:coenzyme f420 hydrogenase gamma subunit:8-hydroxy-5-deazaflavin-reducing hydrogenase gamma subunit:frh (gtcfc:2.2:9.6) (ec:1.12.99.1) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0031 MJ0031 Methanococcus jannaschii 2190 -11540603 118170 frhg:mj0031 (ec:1.12.99.1) (de:deazaflavin-reducing hydrogenase gamma subunit) (frh)) (db:swissprot) FRHG_METJA Q60340 METHANOCOCCUS JANNASCHII 2190 -11540603 173035 coenzyme f420 hydrogenase gamma chain homolog:coenzyme f420-reducing hydrogenase:gamma subunit (db:pir2.dat) (mp:for31799-32491) G64303 G64303 Methanococcus jannaschii 2190 -11540603 246465 mj0031 coenzyme f420-reducing hydrogenase:gamma (db:genpept-bct1) (de:methanococcus jannaschii section 3 of 150 of the complete genome.) (nt:similar to gb:x61202 gb:m31474 pid:44707 percent) (le:9243) (re:9935) (di:direct) U67461 U67461 g1590833 Methanococcus jannaschii 2190 -11540603 5000698131 (de:(mj0031) (pn:coenzyme f420 hydrogenase gamma subunit:8-hydroxy-5- deazaflavin-reducing hydrogenase gamma subunit:frh:coenzyme f420-reducing hydrogenase, gamma subunit) (gn:frhg) (gtcfc:9.6) (ec:1.12.99.1) (frhg_metja) (keggfc) MJ0031 MJ0031 Methanococcus jannaschii 2190 10060241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924787	19894	42050	630	209

Description

GTC ORF with score 597 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid zk637, complete sequence.) (nt:predicted using genefinder; arsa homologue; cdna) (le:11124:11606:12073:12411) (re:11557:11864:12282:12536) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924790	19895	42051	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924792	19896	42052	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924811	19897	42053	477	158

Description

6500736746 frhb:mj0032 coenzyme f420-reducing hydrogenase:beta subunit:coenzyme f420 hydrogenase beta subunit:8-hydroxy-5-deazaflavin-reducing hydrogenase beta subunit:frh (gtcfc:2.2:9.6) (ec:1.12.99.1) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0032 MJ0032 Methanococcus jannaschii 2190 -11540604 118169 frhb:mj0032 (ec:1.12.99.1) (de:deazaflavin-reducing hydrogenase beta subunit) (frh)) (db:swissprot) FRHB_METJA Q60341 METHANOCOCCUS JANNASCHII 2190 -11540604 173030 coenzyme f420 hydrogenase:delta chain homolog:coenzyme f420-reducing hydrogenase:delta subunit (cl:coenzyme f420 hydrogenase beta chain) (ec:1.12.99.1) (db:pir2.dat) (mp:for32511-33374) H64303 H64303 Methanococcus jannaschii 2190 -11540604 246466 mj0032 coenzyme f420-reducing hydrogenase:beta subunit (db:genpept-bct1) (de:methanococcus jannaschii section 3 of 150 of the complete genome.) (nt:similar to gb:x61202 pid:44708 percent identity:) (le:9955) (re:10818) (di:direct) U67461 U67461 g1590834 Methanococcus jannaschii 2190 -11540604 5000698132 (de:(mj0032) (pn:coenzyme f420 hydrogenase beta subunit:8-hydroxy-5-deazaflavin- reducing hydrogenase beta subunit:frh:coenzyme f420-reducing hydrogenase, delta subunit) (gn:frhb) (gtcfc:9.6) (ec:1.12.99.1) (frhb_metja) (keggfc:9) MJ0032 MJ0032 Methanococcus jannaschii 2190 10060240

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924813	19898	42054	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924814	19899	42055	585	194

Description

6500736747 mcrb:mj0081 methyl coenzyme m reductase ii:subunit beta:mrtb:methyl-coenzyme m reductase beta subunit (gtcfc:2.2:9.6) (ec:1.8.-.-) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0081 MJ0081 Methanococcus jannaschii 2190 -11540605 174324 methyl coenzyme m reductase:ii beta chain (ec:1.8.-.-) (db:pir2.dat) (mp:for74658-76013) A64310 A64310 Methanococcus jannaschii 2190 -11540605 119962 mcrb:mj0081 (ec:1.8.-.-) (de:methyl-coenzyme m reductase beta subunit,) (db:swissprot) MCRB_METJA Q60390 METHANOCOCCUS JANNASCHII 2190 -11540605 246515 mju67465 (le:74658) (re:76013) (di:direct) (de:or:methanococcus jannaschii pn:methyl coenzyme m reductase ii, beta subunit gn:mj0081 le:5522 re:6877 di:direct nt:similar to s43899 percent identity: 79.7;) U67465 U67465 g1590864 Methanococcus jannaschii 2190 -11540605 5000697872 (de:(mj0081) (pn:methyl-coenzyme m reductase beta subunit:methyl coenzyme m reductase ii, beta subunit) (gn:mcrb) (gtcfc:2.2) (ec:1.8.-.-) (mcrb_metja) (keggfc:11.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0081 MJ0081 Methanococcus jannaschii 2190 10062738

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924816	19900	42056	402	133

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924851	19901	42057	3039	1012

Description

6500736748 mcrg:mj0082 methyl coenzyme m reductase ii:subunit gamma:mtrg:methyl-coenzyme m reductase gamma subunit (gtcfc:2.2:9.6) (ec:1.8.-.-) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0082 MJ0082 Methanococcus jannaschii 2190 -11540606 119963 mcrg:mj0082 (ec:1.8.-.-) (de:methyl-coenzyme m reductase gamma subunit,) (db:swissprot) MCRG_METJA Q60387 METHANOCOCCUS JANNASCHII 2190 -11540606 174325 methyl coenzyme m reductase ii gamma chain homolog (cl:methyl coenzyme m reductase gamma chain) (db:pir2.dat) (mp:for76026-76826) B64310 B64310 Methanococcus jannaschii 2190 -11540606 246516 mj0082 methyl coenzyme m reductase ii:subunit gamma (db:genpept-bct1) (de:methanococcus jannaschii section 7 of 150 of the complete genome.) (nt:similar to gb:x70765 pid:488817 percent identity:) (le:6890) (re:7690) (di:direct) U67465 U67465 g1498845 Methanococcus jannaschii 2190 -11540606 5000697873 (de:(mj0082) (pn:methyl-coenzyme m reductase gamma subunit:methyl coenzyme m reductase ii, gamma subunit) (gn:mcrg) (gtcfc:2.2) (ec:1.8.-.-) (mcrg_metja) (keggfc:11.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0082 MJ0082 Methanococcus jannaschii 2190 10062739

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924862	19902	42058	1020	339

Description

6500736749 mcra:mj0083 methyl coenzyme m reductase ii:subunit alpha:mtra:methyl-coenzyme m reductase alpha subunit (gtcfc:2.2:9.6) (ec:1.8.-.-) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0083 MJ0083 Methanococcus jannaschii 2190 -11540607 119961 mcra:mj0083 (ec:1.8.-.-) (de:methyl-coenzyme m reductase alpha subunit,) (db:swissprot) MCRA_METJA Q60391 METHANOCOCCUS JANNASCHII 2190 -11540607 174327 methyl coenzyme m reductase:ii alpha chain (cl:methyl coenzyme m reductase alpha chain) (ec:1.8.-.-) (db:pir2.dat) (mp:for76826-78484) C64310 C64310 Methanococcus jannaschii 2190 -11540607 246517 mj0083 methyl coenzyme m reductase ii:subunit alpha (db:genpept-bct1) (de:methanococcus jannaschii section 7 of 150 of the complete genome.) (nt:similar to gb:x70765 pid:488818 percent identity:) (le:7690) (re:9348) (di:direct) U67465 U67465 g1590865 Methanococcus jannaschii 2190 -11540607 5000697874 (de:(mj0083) (pn:methyl-coenzyme m reductase alpha subunit:methyl coenzyme m reductase ii, alpha subunit) (gn:mcra) (gtcfc:2.2) (ec:1.8.-.-) (mcra_metja) (keggfc:11.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0083 MJ0083 Methanococcus jannaschii 2190 10062737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924869	19903	42059	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924903	19904	42060	1515	504

Description

5000697875 methyl coenzyme m reductase ii:operon protein c:mtrc:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0094 MJ0094 Methanococcus jannaschii 2190 -11540608 118778 mj0094 (de:hypothetical protein mj0094) (db:swissprot) Y094_METJA Q57559 METHANOCOCCUS JANNASCHII 2190 -11540608 173335 hypothetical protein mj0094 (db:pir2.dat) (mp:rev89493-88561) F64311 F64311 Methanococcus jannaschii 2190 -11540608 246528 mj0094 methyl coenzyme m reductase ii:operon protein c (db:genpept-bct1) (de:methanococcus jannaschii section 8 of 150 of the complete genome.) (nt:similar to gb:m16893 sp:p07960 pid:150057 percent) (le:9024) (re:9956) (di:complement) U67466 U67466 g1590873 Methanococcus jannaschii 2190 -11540608 6500736750 methyl coenzyme m reductase ii:operon protein c:mtrc:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0094 MJ0094 Methanococcus jannaschii 2190 -11540608

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924912	19905	42061	1770	589

Description

6500736751 mcrd:mj0118 methyl coenzyme m reductase ii:operon protein d:mtrd:methyl-coenzyme m reductase operon protein d (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0118 MJ0118 Methanococcus jannaschii 2190 -11540609 119964 mcrd:mj0118 (de:methyl-coenzyme m reductase operon protein d) (db:swissprot) MCRD_METJA Q57582 METHANOCOCCUS JANNASCHII 2190 -11540609 174326 methyl coenzyme m reductase ii operon protein d homolog (cl:methyl coenzyme m reductase d) (db:pir2.dat) (mp:for115194-115697) F64314 F64314 Methanococcus jannaschii 2190 -11540609 246552 mj0118 methyl coenzyme m reductase ii:operon protein d (db:genpept-bct1) (de:methanococcus jannaschii section 11 of 150 of the complete genome.) (nt:similar to gb:x70765 pid:488816 percent identity:) (le:3564) (re:4067) (di:direct) U67469 U67469 g1498885 Methanococcus jannaschii 2190 -11540609 5000697876 (de:(mj0118) (pn:methyl-coenzyme m reductase operon protein d:methyl coenzyme m reductase ii operon, protein d) (gn:mcrd) (gtcfc:2.2) (ec:) (mcrd_metja) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0118 MJ0118 Methanococcus jannaschii 2190 10062740

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924921	19906	42062	879	292

Description

5000697877 coenzyme f420-reducing hydrogenase:delta subunit:frcd:putative hydrogenase maturation protease (gtcfc:2.2) (keggfc:14.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0253 MJ0253 Methanococcus jannaschii 2190 -11540610 500684958 mj0253 (ec:3.-.-.-) (de:putative hydrogenase maturation protease mj0253,) (db:swissprot) Y253_METJA Q57701 METHANOCOCCUS JANNASCHII 2190 -11540610 172924 8-hydroxy-5-deazaflavin-reducing hydrogenase delta subunit homolog (cl:coenzyme f420-reducing hydrogenase delta chain) (db:pir2.dat) (mp:for239495-239959) F64331 F64331 Methanococcus jannaschii 2190 -11540610 246688 mj0253 coenzyme f420-reducing hydrogenase:delta (db:genpept-bct1) (de:methanococcus jannaschii section 22 of 150 of the complete genome.) (nt:similar to gb:x61201 pid:44702 percent identity:) (le:7424) (re:7888) (di:direct) U67480 U67480 g1590983 Methanococcus jannaschii 2190 -11540610 6500736752 coenzyme f420-reducing hydrogenase:delta subunit:frcd:putative hydrogenase maturation protease (gtcfc:2.2) (keggfc:14.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0253 MJ0253 Methanococcus jannaschii 2190 -11540610

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924923	19907	42063	2520	839

Description

6500736753 ftr:mj0318 formylmethanofuran:tetrahydromethanopterin formyltransferase (gtcfc:2.2:9.6) (ec:2.3.1.101) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0318 MJ0318 Methanococcus jannaschii 2190 -11540611 1500686939 ftr:mj0318 (ec:2.3.1.101) (de:(ec 2.3.1.101)) (db:swissprot) FTR_METJA Q57766 METHANOCOCCUS JANNASCHII 2190 -11540611 173131 formylmethanofuran--tetrahydromethanopterin n-formyltransferase (cl:formylmethanofuran--tetrahydromethanopterin n-formyltransferase) (ec:2.3.1.101) (db:pir2.dat) (mp:rev297440-296535) G64339 G64339 Methanococcus jannaschii 2190 -11540611 246753 mj0318 formylmethanofuran:tetrahydromethanopterin (db:genpept-bct1) (de:methanococcus jannaschii section 28 of 150 of the complete genome.) (nt:similar to sp:p21348 pid:1196492 gb:ae000666) (le:5457) (re:6362) (di:complement) U67486 U67486 g1591038 Methanococcus jannaschii 2190 -11540611 5000698133 (de:(mj0318) (pn:formylmethanofuran:tetrahydromethanopterin formyltransferase) (gtcfc:9.6) (ec:2.3.1.101) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0318 MJ0318 Methanococcus jannaschii 2190 10063096

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924927	19908	42064	723	240

Description

5000697882 h2-forming n5:n10-methylene-tetrahydromethanopterin dehydrogenase related protein:hmd (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0715 MJ0715 Methanococcus jannaschii 2190 -11540612 5500685354 mj0715 (de:protein mj0715) (db:swissprot) HMDX_METJA Q58125 METHANOCOCCUS JANNASCHII 2190 -11540612 173169 n5:n10-methylenetetrahydromethanopterin dehydrogenase h2-forming homolog 2 (db:pir2.dat) (mp:for648927-649943) C64389 C64389 Methanococcus jannaschii 2190 -11540612 247149 mj0715 h2-forming (db:genpept-bct1) (de:methanococcus jannaschii section 60 of 150 of the complete genome.) (nt:similar to pid:1149527 sp:q50840 percent identity:) (le:5669) (re:6685) (di:direct) U67518 U67518 g1591432 Methanococcus jannaschii 2190 -11540612 6500736754 h2-forming n5:n10-methylene-tetrahydromethanopterin dehydrogenase related protein:hmd (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0715 MJ0715 Methanococcus jannaschii 2190 -11540612

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924931	19909	42065	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924956	19910	42066	1446	481

Description

5000698135 coenzyme f420-reducing hydrogenase:beta subunit:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0725 MJ0725 Methanococcus jannaschii 2190 -11540613 1500686305 mj0725 (de:hypothetical protein mj0725) (db:swissprot) Y725_METJA Q58135 METHANOCOCCUS JANNASCHII 2190 -11540613 173034 coenzyme f420 hydrogenase beta chain:coenzyme f420-reducing hydrogenase:beta subunit (cl:coenzyme f420 hydrogenase beta chain) (db:pir2.dat) (mp:rev658692-657907) E64390 E64390 Methanococcus jannaschii 2190 -11540613 247159 mj0725 coenzyme f420-reducing hydrogenase:beta (db:genpept-bct1) (de:methanococcus jannaschii section 61 of 150 of the complete genome.) (nt:similar to gb:j02914 sp:p19499 pid:149718) (le:4031) (re:4816) (di:complement) U67519 U67519 g1591441 Methanococcus jannaschii 2190 -11540613 6500736755 coenzyme f420-reducing hydrogenase:beta subunit:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0725 MJ0725 Methanococcus jannaschii 2190 -11540613

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924978	19911	42067	423	140

Description

5000698136 coenzyme f420-reducing hydrogenase:gamma subunit:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0726 MJ0726 Methanococcus jannaschii 2190 -11540614 1500686306 mj0726 (de:hypothetical protein mj0726) (db:swissprot) Y726_METJA Q58136 METHANOCOCCUS JANNASCHII 2190 -11540614 173031 coenzyme f420 hydrogenase:gamma chain:coenzyme f420-reducing hydrogenase:gamma subunit (ec:1.12.99.1) (db:pir2.dat) (mp:rev659511-658861) F64390 F64390 Methanococcus jannaschii 2190 -11540614 247160 mj0726 coenzyme f420-reducing hydrogenase:gamma (db:genpept-bct1) (de:methanococcus jannaschii section 61 of 150 of the complete genome.) (nt:similar to gb:x61201 pid:809730 sp:q00393 percent) (le:4985) (re:5635) (di:complement) U67519 U67519 g1591442 Methanococcus jannaschii 2190 -11540614 6500736756 coenzyme f420-reducing hydrogenase:gamma subunit:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0726 MJ0726 Methanococcus jannaschii 2190 -11540614

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924984	19912	42068	1125	374

Description

5000698137 coenzyme f420-reducing hydrogenase:alpha subunit:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0727 MJ0727 Methanococcus jannaschii 2190 -11540615 1500686307 mj0727 (de:hypothetical protein mj0727) (db:swissprot) Y727_METJA Q58137 METHANOCOCCUS JANNASCHII 2190 -11540615 173033 coenzyme f420 hydrogenase alpha chain homolog:coenzyme f420-reducing hydrogenase:alpha subunit (db:pir2.dat) (mp:rev660531-659635) G64390 G64390 Methanococcus jannaschii 2190 -11540615 247161 mj0727 coenzyme f420-reducing hydrogenase:alpha (db:genpept-bct1) (de:methanococcus jannaschii section 61 of 150 of the complete genome.) (nt:similar to gb:j02914 sp:p19496 pid:551889) (le:5759) (re:6655) (di:complement) U67519 U67519 g1591443 Methanococcus jannaschii 2190 -11540615 6500736757 coenzyme f420-reducing hydrogenase:alpha subunit:hypothetical protein (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0727 MJ0727 Methanococcus jannaschii 2190 -11540615

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924996	19913	42069	693	230

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501924998	19914	42070	492	163

Description

6500736758 heterodisulfide reductase:subunit b1:hdrb1:heterodisulfide reductase:subunit b (gtcfc:2.2) (ec:1.6.4.-) (keggfc:14.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0743 MJ0743 Methanococcus jannaschii 2190 -11540616 173175 heterodisulfide reductase:chain b (ec:1.97.1.-) (db:pir2.dat) (mp:rev670822-669938) G64392 G64392 Methanococcus jannaschii 2190 -11540616 247177 mj0743 heterodisulfide reductase:subunit b1 hdrb1 (db:genpept-bct1) (de:methanococcus jannaschii section 62 of 150 of the complete genome.) (nt:similar to gp:1001685 percent identity: 31.74;) (le:4483) (re:5367) (di:complement) U67520 U67520 g1591456 Methanococcus jannaschii 2190 -11540616 5000697883 (de:(mj0743) (pn:heterodisulfide reductase, subunit b) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0743 MJ0743 Methanococcus jannaschii 2190 10091541

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925002	19915	42071	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925003	19916	42072	798	265

Description

6500736759 heterodisulfide reductase:subunit c1:hdrc1:heterodisulfide reductase:subunit c (gtcfc:2.2) (ec:1.6.4.-) (keggfc:14.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0744 MJ0744 Methanococcus jannaschii 2190 -11540617 173177 heterodisulfide reductase:chain c (ec:1.97.1.-) (db:pir2.dat) (mp:rev671455-670871) H64392 H64392 Methanococcus jannaschii 2190 -11540617 247178 mj0744 heterodisulfide reductase:subunit c hdrc (db:genpept-bct1) (de:methanococcus jannaschii section 62 of 150 of the complete genome.) (nt:similar to gb:177117 pid:1499692 percent identity:) (le:5416) (re:6000) (di:complement) U67520 U67520 g1591457 Methanococcus jannaschii 2190 -11540617 5000697884 (de:(mj0744) (pn:heterodisulfide reductase, subunit c) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0744 MJ0744 Methanococcus jannaschii 2190 10091543

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925006	19917	42073	885	294

Description

6500736760 h2-forming n5:n10-methylene-tetrahydromethanopterin dehydrogenase:hmd (gtcfc:2.2) (ec:1.12.99.-) (keggfc:14.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0784 MJ0784 Methanococcus jannaschii 2190 -11540618 5500685356 hmd:mj0784 (ec:1.12.99.-) (de:(ec 1.12.99.-) (h2-dependent methylene-h4mpt dehydrogenase)) (db:swissprot) HMD_METJA Q58194 METHANOCOCCUS JANNASCHII 2190 -11540618 174337 n5:n10-methylenetetrahydromethanopterin dehydrogenase h2-forming::h2-forming n5:n10-methylene-tetrahydromethanopterin dehydrogenease (ec:1.12.99.-) (db:pir2.dat) (mp:for707018-708094) H64397 H64397 Methanococcus jannaschii 2190 -11540618 247218 mj0784 h2-forming (db:genpept-bct1) (de:methanococcus jannaschii section 65 of 150 of the complete genome.) (nt:similar to pid:1149527 sp:q50840 percent identity:) (le:945) (re:2021) (di:direct) U67523 U67523 g1591484 Methanococcus jannaschii 2190 -11540618 5000697885 (de:(mj0784) (pn:h2-forming n5,n10-methylene-tetrahydromethanopterin dehydrogenase) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0784 MJ0784 Methanococcus jannaschii 2190 10092381

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925027	19918	42074	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925033	19919	42075	540	179

Description

GTC ORF with score 101 to: (sr:baker's yeast s288c) (db:genpept-pln1) (de:ybl03-16=basic motif/leucine zipper domain protein homolog,ybl03-23=multidrug resistance pdr1 protein homolog (saccharomycescerevisiae, s288c, genomic, 10 genes, 12684 nt).) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925043	19920	42076	1506	501

Description

6500736761 methyl coenzyme m reductase i:subunit beta:mcrb:methyl coenzyme m reductase:beta subunit (gtcfc:2.2:9.6) (ec:1.8.-.-) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0842 MJ0842 Methanococcus jannaschii 2190 -11540619 174333 methyl coenzyme m reductase:beta chain (ec:1.8.-.-) (db:pir2.dat) (mp:for768441-769790) B64405 B64405 Methanococcus jannaschii 2190 -11540619 5500685540 mrtb:mj0842 (ec:1.8.-.-) (de:methyl-coenzyme m reductase ii beta subunit,) (db:swissprot) MCRY_METJA Q58252 METHANOCOCCUS JANNASCHII 2190 -11540619 247276 mju67528 (le:768441) (re:769790) (di:direct) (de:or:methanococcus jannaschii pn:methyl coenzyme m reductase, beta subunit gn:mj0842 le:6775 re:8124 di:direct nt:similar to p07956 percent identity: 75.2;) U67528 U67528 g1591528 Methanococcus jannaschii 2190 -11540619 5000697886 (de:(mj0842) (pn:methyl coenzyme m reductase, beta subunit) (gtcfc:2.2) (ec:1.8.-.-) (keggfc:11.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0842 MJ0842 Methanococcus jannaschii 2190 10092378

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925093	19921	42077	255	84

Description

5000697887 methyl coenzyme m reductase i:operon protein d:mcrd:methyl coenzyme m reductase operon:protein d (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0843 MJ0843 Methanococcus jannaschii 2190 -11540620 5500685538 mrtd:mj0843 (de:methyl-coenzyme m reductase operon ii protein d) (db:swissprot) MCRW_METJA Q58253 METHANOCOCCUS JANNASCHII 2190 -11540620 174328 methyl coenzyme m reductase operon protein d homolog (cl:methyl coenzyme m reductase d) (db:pir2.dat) (mp:for769803-770297) C64405 C64405 Methanococcus jannaschii 2190 -11540620 247277 mj0843 methyl coenzyme m reductase i:operon protein d (db:genpept-bct1) (de:methanococcus jannaschii section 70 of 150 of the complete genome.) (nt:similar to gb:m16893 sp:p07957 pid:150056 percent) (le:7000) (re:7494) (di:direct) U67528 U67528 g1591529 Methanococcus jannaschii 2190 -11540620 6500736762 methyl coenzyme m reductase i:operon protein d:mcrd:methyl coenzyme m reductase operon:protein d (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0843 MJ0843 Methanococcus jannaschii 2190 -11540620

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925094	19922	42078	333	111

Description

5000697888 methyl coenzyme m reductase i:operon protein c:mcrc:methyl coenzyme m reductase operon:protein c (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0844 MJ0844 Methanococcus jannaschii 2190 -11540621 5500685537 mrtc:mj0844 (de:methyl-coenzyme m reductase operon ii protein c) (db:swissprot) MCRV_METJA Q58254 METHANOCOCCUS JANNASCHII 2190 -11540621 174329 methyl coenzyme m reductase operon:protein c homolog (cl:mcrd protein) (db:pir2.dat) (mp:for770299-770901) D64405 D64405 Methanococcus jannaschii 2190 -11540621 247278 mj0844 methyl coenzyme m reductase i:operon protein c (db:genpept-bct1) (de:methanococcus jannaschii section 70 of 150 of the complete genome.) (nt:similar to gb:m16893 sp:p07960 pid:150057 percent) (le:7496) (re:8098) (di:direct) U67528 U67528 g1591530 Methanococcus jannaschii 2190 -11540621 6500736763 methyl coenzyme m reductase i:operon protein c:mcrc:methyl coenzyme m reductase operon:protein c (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0844 MJ0844 Methanococcus jannaschii 2190 -11540621

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925095	19923	42079	1272	423

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925133	19924	42080	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925150	19925	42081	999	332

Description

6500736764 methyl coenzyme m reductase i:subunit gamma:mcrg:methyl coenzyme m reductase:gamma subunit (gtcfc:2.2:9.6) (ec:1.8.-.-) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0845 MJ0845 Methanococcus jannaschii 2190 -11540622 5500685541 mrtg:mj0845 (ec:1.8.-.-) (de:methyl-coenzyme m reductase ii gamma subunit,) (db:swissprot) MCRZ_METJA Q58255 METHANOCOCCUS JANNASCHII 2190 -11540622 174334 methyl coenzyme m reductase:gamma subunit homolog (cl:methyl coenzyme m reductase gamma chain) (db:pir2.dat) (mp:for770911-771693) E64405 E64405 Methanococcus jannaschii 2190 -11540622 247279 mj0845 methyl coenzyme m reductase i:subunit gamma (db:genpept-bct1) (de:methanococcus jannaschii section 70 of 150 of the complete genome.) (nt:similar to gb:m16893 sp:p07963 pid:150058 percent) (le:8108) (re:8890) (di:direct) U67528 U67528 g1591531 Methanococcus jannaschii 2190 -11540622 5000697889 (de:(mj0845) (pn:methyl coenzyme m reductase, gamma subunit) (gtcfc:2.2) (ec:1.8.-.-) (keggfc:11.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0845 MJ0845 Methanococcus jannaschii 2190 10069777

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925165	19926	42082	294	97

Description

6500736765 methyl coenzyme m reductase i:subunit alpha:mcra:methyl coenzyme m reductase:alpha subunit (gtcfc:2.2:9.6) (ec:1.8.-.-) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0846 MJ0846 Methanococcus jannaschii 2190 -11540623 174332 methyl coenzyme m reductase:alpha chain (cl:methyl coenzyme m reductase alpha chain) (ec:1.8.-.-) (db:pir2.dat) (mp:for771816-773486) F64405 F64405 Methanococcus jannaschii 2190 -11540623 5500685539 mrta:mj0846 (ec:1.8.-.-) (de:alpha)) (db:swissprot) MCRX_METJA Q58256 METHANOCOCCUS JANNASCHII 2190 -11540623 247280 mju67529 (le:771816) (re:773486) (di:direct) (de:or:methanococcus jannaschii pn:methyl coenzyme m reductase, alpha subunit gn:mj0846 le:87 re:1757 di:direct nt:similar to p11559 percent identity: 85.2;) U67529 U67529 g1592312 Methanococcus jannaschii 2190 -11540623 5000697890 (de:(mj0846) (pn:methyl coenzyme m reductase, alpha subunit) (gtcfc:2.2) (ec:1.8.-.-) (keggfc:11.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0846 MJ0846 Methanococcus jannaschii 2190 10069774

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925166	19927	42083	480	159

Description

6500736766 mtre:mj0847 n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase:subunit e:tetrahydromethanopterin s-methyltransferase 28 kd subunit (gtcfc:2.2:9.6) (ec:2.1.1.86) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0847 MJ0847 Methanococcus jannaschii 2190 -11540624 119972 mtre:mj0847 (ec:2.1.1.86) (de:methyltransferase 28 kd subunit)) (db:swissprot) MTRE_METJA Q58257 METHANOCOCCUS JANNASCHII 2190 -11540624 174369 n5-methyl-tetrahydromethanopterin--coenzyme m methyltransferase homolog (db:pir2.dat) (mp:for773706-774617) G64405 G64405 Methanococcus jannaschii 2190 -11540624 247281 mj0847 n5-methyl-tetrahydromethanopterin:coenzyme m (db:genpept-bct1) (de:methanococcus jannaschii section 71 of 150 of the complete genome.) (nt:similar to gb:x73123 gb:x84218 pid:312120) (le:1977) (re:2888) (di:direct) U67529 U67529 g1591534 Methanococcus jannaschii 2190 -11540624 5000698139 (de:(mj0847) (pn:tetrahydromethanopterin s-methyltransferase 28 kd subunit:n5- methyltetrahydromethanopterin--coenzyme m methyltransferase 28 kd subunit:n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase) (gn:mtre) (gtcfc:9.) MJ0847 MJ0847 Methanococcus jannaschii 2190 10062748

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925180	19928	42084	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925209	19929	42085	5061	1686

Description

6500736767 mtrd:mj0848 n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase:subunit d:tetrahydromethanopterin s-methyltransferase 21 kd subunit:n5-methyltetrahydromethanopterin--coenzyme m methyltransferase 21 kd subunit (gtcfc:2.2:9.6) (ec:2.1.1.86) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0848 MJ0848 Methanococcus jannaschii 2190 -11540625 119970 mtrd:mj0848 (ec:2.1.1.86) (de:methyltransferase 21 kd subunit)) (db:swissprot) MTRD_METJA Q58258 METHANOCOCCUS JANNASCHII 2190 -11540625 174370 n5-methyl-tetrahydromethanopterin--coenzyme m methyltransferase homolog (db:pir2.dat) (mp:for774631-775323) H64405 H64405 Methanococcus jannaschii 2190 -11540625 247282 mj0848 n5-methyl-tetrahydromethanopterin:coenzyme m (db:genpept-bct1) (de:methanococcus jannaschii section 71 of 150 of the complete genome.) (nt:similar to sp:p80183 gb:x73123 pid:312121) (le:2902) (re:3594) (di:direct) U67529 U67529 g1591535 Methanococcus jannaschii 2190 -11540625 5000698140 (de:(mj0848) (pn:tetrahydromethanopterin s-methyltransferase 21 kd subunit:n5- methyltetrahydromethanopterin--coenzyme m methyltransferase 21 kd subunit:n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase) (gn:mtrd) (gtcfc:9.) MJ0848 MJ0848 Methanococcus jannaschii 2190 10062746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925212	19930	42086	1182	393

Description

6500736768 mtrc:mj0849 n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase:subunit c:mrtc:tetrahydromethanopterin s-methyltransferase 24 kd subunit:n5-methyltetrahydromethanopterin--coenzyme m methyltransferase 24 kd subunit (gtcfc:2.2:9.6) (ec:2.1.1.86) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0849 MJ0849 Methanococcus jannaschii 2190 -11540626 119969 mtrc:mj0849 (ec:2.1.1.86) (de:methyltransferase 24 kd subunit)) (db:swissprot) MTRC_METJA Q58259 METHANOCOCCUS JANNASCHII 2190 -11540626 174364 n5-methyl-tetrahydromethanopterin--coenzyme m methyltransferase homolog (cl:methanobacterium thermoautotrophicum tetrahydromethanopterin s-methyltransferase chain c) (db:pir2.dat) (mp:for775353-776150) A64406 A64406 Methanococcus jannaschii 2190 -11540626 247283 mj0849 n5-methyl-tetrahydromethanopterin:coenzyme m (db:genpept-bct1) (de:methanococcus jannaschii section 71 of 150 of the complete genome.) (nt:similar to sp:p80185 gb:x73123 pid:312122) (le:3624) (re:4421) (di:direct) U67529 U67529 g1591536 Methanococcus jannaschii 2190 -11540626 5000698141 (de:(mj0849) (pn:tetrahydromethanopterin s-methyltransferase 24 kd subunit:n5- methyltetrahydromethanopterin--coenzyme m methyltransferase 24 kd subunit:n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase) (gn:mtrc) (gtcfc:9.) MJ0849 MJ0849 Methanococcus jannaschii 2190 10062745

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925213	19931	42087	561	186

Description

6500736769 mtrb:mj0850 n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase:subunit b:mrtb:tetrahydromethanopterin s-methyltransferase 12 (gtcfc:2.2:9.6) (ec:2.1.1.86) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0850 MJ0850 Methanococcus jannaschii 2190 -11540627 119967 mtrb:mj0850 (ec:2.1.1.86) (de:methyltransferase 12.5 kd subunit)) (db:swissprot) MTRB_METJA Q58260 METHANOCOCCUS JANNASCHII 2190 -11540627 174365 n5-methyl-tetrahydromethanopterin--coenzyme m methyltransferase homolog (cl:tetrahydromethanopterin s-methyltransferase chain b) (db:pir2.dat) (mp:for776160-776471) B64406 B64406 Methanococcus jannaschii 2190 -11540627 247284 mj0850 n5-methyl-tetrahydromethanopterin:coenzyme m (db:genpept-bct1) (de:methanococcus jannaschii section 71 of 150 of the complete genome.) (nt:similar to gb:x73123 pid:312123 sp:q59584) (le:4431) (re:4742) (di:direct) U67529 U67529 g1499677 Methanococcus jannaschii 2190 -11540627 5000698142 (de:(mj0850) (pn:tetrahydromethanopterin s-methyltransferase 12:n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase) (gn:mtrb) (gtcfc:9.6) (ec:2.1.1.86) (mtrb_metja) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus ja) MJ0850 MJ0850 Methanococcus jannaschii 2190 10062743

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925217	19932	42088	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925218	19933	42089	417	138

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925220	19934	42090	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925224	19935	42091	600	199

Description

6500736770 mtra:mj0851 n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase:subunit a:tetrahydromethanopterin s-methyltransferase 23 kd subunit:n5-methyltetrahydromethanopterin--coenzyme m methyltransferase 23 kd subunit (gtcfc:2.2:9.6) (ec:2.1.1.86) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0851 MJ0851 Methanococcus jannaschii 2190 -11540628 119966 mtra:mj0851 (ec:2.1.1.86) (de:methyltransferase 23 kd subunit)) (db:swissprot) MTRA_METJA Q58261 METHANOCOCCUS JANNASCHII 2190 -11540628 174366 n5-methyl-tetrahydromethanopterin--coenzyme m methyltransferase homolog (db:pir2.dat) (mp:for776491-777228) C64406 C64406 Methanococcus jannaschii 2190 -11540628 247285 mj0851 n5-methyl-tetrahydromethanopterin:coenzyme m (db:genpept-bct1) (de:methanococcus jannaschii section 71 of 150 of the complete genome.) (nt:similar to gb:ae000666 percent identity: 54.36;) (le:4762) (re:5499) (di:direct) U67529 U67529 g1591537 Methanococcus jannaschii 2190 -11540628 5000698143 (de:(mj0851) (pn:tetrahydromethanopterin s-methyltransferase 23 kd subunit:n5- methyltetrahydromethanopterin--coenzyme m methyltransferase 23 kd subunit:n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase) (gn:mtra) (gtcfc:9.) MJ0851 MJ0851 Methanococcus jannaschii 2190 10062742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925239	19936	42092	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925256	19937	42093	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925272	19938	42094	1410	469

Description

6500736771 mtrf:mj0852 n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase:subunit f:tetrahydromethanopterin s-methyltransferase 12 kd subunit:n5-methyltetrahydromethanopterin--coenzyme m methyltransferase 12 kd subunit (gtcfc:2.2:9.6) (ec:2.1.1.86) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0852 MJ0852 Methanococcus jannaschii 2190 -11540629 119975 mtrf:mj0852 (ec:2.1.1.86) (de:methyltransferase 12 kd subunit)) (db:swissprot) MTRF_METJA Q58262 METHANOCOCCUS JANNASCHII 2190 -11540629 174367 n5-methyl-tetrahydromethanopterin--coenzyme m methyltransferase homolog (cl:tetrahydromethanopterin s-methyltransferase chain f) (db:pir2.dat) (mp:for777246-777452) D64406 D64406 Methanococcus jannaschii 2190 -11540629 247286 mj0852 n5-methyl-tetrahydromethanopterin:coenzyme m (db:genpept-bct1) (de:methanococcus jannaschii section 71 of 150 of the complete genome.) (nt:similar to pid:668977 sp:q50773 gb:ae000666 percent) (le:5517) (re:5723) (di:direct) U67529 U67529 g1499679 Methanococcus jannaschii 2190 -11540629 5000698144 (de:(mj0852) (pn:tetrahydromethanopterin s-methyltransferase 12 kd subunit:n5-methyltetrahydromethanopterin--coenzyme m methyltransferase 12 kd subunit:n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase) (gn:mtrf) (gtcfc:9.) MJ0852 MJ0852 Methanococcus jannaschii 2190 10062751

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925284	19939	42095	642	213

Description

6500736772 mtrg:mj0853 n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase:subunit g:tetrahydromethanopterin s-methyltransferase 13 kd subunit:n5-methyltetrahydromethanopterin--coenzyme m methyltransferase 13 kd subunit (gtcfc:2.2:9.6) (ec:2.1.1.86) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0853 MJ0853 Methanococcus jannaschii 2190 -11540630 119977 mtrg:mj0853 (ec:2.1.1.86) (de:methyltransferase 13 kd subunit)) (db:swissprot) MTRG_METJA Q58263 METHANOCOCCUS JANNASCHII 2190 -11540630 174363 tetrahydromethanopterin s-methyltransferase:chain g (cl:methanococcus jannaschii tetrahydromethanopterin s-methyltransferase chain g) (ec:2.1.1.86) (db:pir2.dat) (mp:for777473-777727) E64406 E64406 Methanococcus jannaschii 2190 -11540630 247287 mj0853 n5-methyl-tetrahydromethanopterin:coenzyme m (db:genpept-bct1) (de:methanococcus jannaschii section 71 of 150 of the complete genome.) (nt:similar to pid:668978 sp:q50774 gb:ae000666 percent) (le:5744) (re:5998) (di:direct) U67529 U67529 g1591538 Methanococcus jannaschii 2190 -11540630 5000698145 (de:(mj0853) (pn:tetrahydromethanopterin s-methyltransferase 13 kd subunit:n5- methyltetrahydromethanopterin--coenzyme m methyltransferase 13 kd subunit:n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase g) (gn:mtrg) (gtcfc:) MJ0853 MJ0853 Methanococcus jannaschii 2190 10062753

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925289	19940	42096	1050	349

Description

6500736773 mtrh:mj0854 n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase:subunit h:tetrahydromethanopterin s-methyltransferase 34 kd subunit:n5-methyltetrahydromethanopterin--coenzyme m methyltransferase 34 kd subunit (gtcfc:2.2:9.6) (ec:2.1.1.86) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0854 MJ0854 Methanococcus jannaschii 2190 -11540631 119979 mtrh:mj0854 (ec:2.1.1.86) (de:methyltransferase 34 kd subunit)) (db:swissprot) MTRH_METJA Q58264 METHANOCOCCUS JANNASCHII 2190 -11540631 174368 n5-methyl-tetrahydromethanopterin--coenzyme m methyltransferase homolog (cl:probable n5-methyl-tetrahydromethanopterin--coenzyme m methyltransferase) (db:pir2.dat) (mp:for777714-778715) F64406 F64406 Methanococcus jannaschii 2190 -11540631 247288 mj0854 n5-methyl-tetrahydromethanopterin:coenzyme m (db:genpept-bct1) (de:methanococcus jannaschii section 71 of 150 of the complete genome.) (nt:similar to sp:p80187 gb:x84219 percent identity:) (le:5985) (re:6986) (di:direct) U67529 U67529 g1591539 Methanococcus jannaschii 2190 -11540631 5000698146 (de:(mj0854) (pn:tetrahydromethanopterin s-methyltransferase 34 kd subunit:n5- methyltetrahydromethanopterin--coenzyme m methyltransferase 34 kd subunit:n5-methyl-tetrahydromethanopterin:coenzyme m methyltransferase) (gn:mtrh) (gtcfc:9.) MJ0854 MJ0854 Methanococcus jannaschii 2190 10062755

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925292	19941	42097	564	187

Description

5000697891 heterodisulfide reductase:subunit b2:hdrb2:heterodisulfide reductase:subunit b (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0863 MJ0863 Methanococcus jannaschii 2190 -11540632 173176 heterodisulfide reductase:chain b (ec:1.97.1.-) (db:pir2.dat) (mp:rev787449-786562) G64407 G64407 Methanococcus jannaschii 2190 -11540632 247297 mj0863 heterodisulfide reductase:subunit b2 hdrb2 (db:genpept-bct1) (de:methanococcus jannaschii section 72 of 150 of the complete genome.) (nt:similar to gp:1001685 percent identity: 32.54;) (le:4637) (re:5524) (di:complement) U67530 U67530 g1591548 Methanococcus jannaschii 2190 -11540632 6500736774 heterodisulfide reductase:subunit b2:hdrb2:heterodisulfide reductase:subunit b (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0863 MJ0863 Methanococcus jannaschii 2190 -11540632

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925297	19942	42098	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925300	19943	42099	681	226

Description

5000697892 heterodisulfide reductase:subunit c2:hdrc2:heterodisulfide reductase:subunit c (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0864 MJ0864 Methanococcus jannaschii 2190 -11540633 173178 heterodisulfide reductase:chain c (ec:1.97.1.-) (db:pir2.dat) (mp:rev788080-787520) H64407 H64407 Methanococcus jannaschii 2190 -11540633 247298 mj0864 heterodisulfide reductase:subunit c2 hdrc2 (db:genpept-bct1) (de:methanococcus jannaschii section 72 of 150 of the complete genome.) (nt:similar to gb:l77117 pid:1591457 percent identity:) (le:5595) (re:6155) (di:complement) U67530 U67530 g1499692 Methanococcus jannaschii 2190 -11540633 6500736775 heterodisulfide reductase:subunit c2:hdrc2:heterodisulfide reductase:subunit c (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ0864 MJ0864 Methanococcus jannaschii 2190 -11540633

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925301	19944	42100	993	330

Description

6500736776 coenzyme f420-reducing hydrogenase:beta subunit:frhb:coenzyme f420-reducing hydrogenase:beta subunit homolog (gtcfc:2.2:9.6) (ec:1.12.99.1) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ0870 MJ0870 Methanococcus jannaschii 2190 -11540634 1500686309 mj0870 (de:hypothetical protein mj0870) (db:swissprot) Y870_METJA Q58280 METHANOCOCCUS JANNASCHII 2190 -11540634 173029 coenzyme f420 hydrogenase:beta chain homolog:coenzyme f420-reducing hydrogenase:beta subunit (ec:1.12.99.1) (db:pir2.dat) (mp:rev794850-792988) F64408 F64408 Methanococcus jannaschii 2190 -11540634 247304 mj0870 coenzyme f420-reducing hydrogenase:beta subunit (db:genpept-bct1) (de:methanococcus jannaschii section 73 of 150 of the complete genome.) (nt:similar to gb:j02914 sp:p19499 pid:149718) (le:1210) (re:3072) (di:complement) U67531 U67531 g1591554 Methanococcus jannaschii 2190 -11540634 5000697893 (de:(mj0870) (pn:coenzyme f420-reducing hydrogenase, beta subunit) (gtcfc:2.2) (ec:1.2.-.-) (keggfc:11.1) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ0870 MJ0870 Methanococcus jannaschii 2190 10061290

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925302	19945	42101	1701	566

Description

6500736777 mtd:mj1035 n5:n10-methylene-tetrahydromethanopterin dehydrogenase:f420-dependent methylenetetrahydromethanopterin dehydrogenase:mtd:coenzyme f420 dependent n5:n10-methylenetetrahydromethanopterin dehydrogenase (gtcfc:2.2:9.6) (ec:1.5.99.9) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1035 MJ1035 Methanococcus jannaschii 2190 -11540635 4000709111 mtd:mj1035 (ec:1.5.99.9) (de:methylenetetrahydromethanopterin dehydrogenase)) (db:swissprot) MTD_METJA Q58441 METHANOCOCCUS JANNASCHII 2190 -11540635 174336 methylenetetrahydromethanopterin dehydrogenase::coenzyme f420-dependent n5:n10-methylene-tetrahydromethanopterin dehydrogenase (cl:methylenetetrahydromethanopterin dehydrogenase) (ec:1.5.99.9) (db:pir2.dat) (mp:rev967171-966338) B64429 B64429 Methanococcus jannaschii 2190 -11540635 247468 mj1035 n5:n10-methylene-tetrahydromethanopterin (db:genpept-bct1) (de:methanococcus jannaschii section 88 of 150 of the complete genome.) (nt:similar to pid:685181 pid:726050 sp:p55300) (le:2440) (re:3273) (di:complement) U67546 U67546 g1591688 Methanococcus jannaschii 2190 -11540635 5000697895 (de:(mj1035) (pn:coenzyme f420-dependent n5,n10-methylene-tetrahydromethanopterin dehydrogenase) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1035 MJ1035 Methanococcus jannaschii 2190 10092380

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925305	19946	42102	774	257

Description

6500736778 formylmethanofuran dehydrogenase:subunit e:tungsten:fwde:tungsten formylmethanofuran dehydrogenase:subunit e (gtcfc:2.2:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1165 MJ1165 Methanococcus jannaschii 2190 -11540636 173128 formylmethanofuran dehydrogenase tungsten:subunit e (cl:methanobacterium thermoautotrophicum formylmethanofuran dehydrogenase (tungsten) chain e) (ec:1.2.99.-) (db:pir2.dat) (mp:for1106289-1106729) D64445 D64445 Methanococcus jannaschii 2190 -11540636 247598 mj1165 formylmethanofuran dehydrogenase:subunit e (db:genpept-bct1) (de:methanococcus jannaschii section 100 of 150 of the complete genome.) (nt:similar to pid:871458 gb:ae000666 pid:1890206) (le:9130) (re:9570) (di:direct) U67558 U67558 g1591791 Methanococcus jannaschii 2190 -11540636 5000698148 (de:(mj1165) (pn:tungsten formylmethanofuran dehydrogenase, subunit e) (gtcfc:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1165 MJ1165 Methanococcus jannaschii 2190 10091516

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925307	19947	42103	1797	598

Description

GTC ORF with score 173 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925326	19948	42104	693	230

Description

6500736779 formylmethanofuran dehydrogenase:subunit f:tungsten:fwdf:tungsten formylmethanofuran dehydrogenase:subunit f (gtcfc:2.2:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1166 MJ1166 Methanococcus jannaschii 2190 -11540637 173129 formylmethanofuran dehydrogenase tungsten:subunit f (cl:formylmethanofuran dehydrogenase (tungsten) chain f) (ec:1.2.99.-) (db:pir2.dat) (mp:for1106732-1107799) E64445 E64445 Methanococcus jannaschii 2190 -11540637 247599 mj1166 formylmethanofuran dehydrogenase:subunit f (db:genpept-bct1) (de:methanococcus jannaschii section 100 of 150 of the complete genome.) (nt:similar to pid:871459 gb:ae000666 pid:1890207) (le:9573) (re:10640) (di:direct) U67558 U67558 g1591792 Methanococcus jannaschii 2190 -11540637 5000698149 (de:(mj1166) (pn:tungsten formylmethanofuran dehydrogenase, subunit f) (gtcfc:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1166 MJ1166 Methanococcus jannaschii 2190 10091517

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925333	19949	42105	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925342	19950	42106	681	226

Description

6500736780 formylmethanofuran dehydrogenase:subunit g:tungsten:fwdg:tungsten formylmethanofuran dehydrogenase:subunit g (gtcfc:2.2:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1167 MJ1167 Methanococcus jannaschii 2190 -11540638 173130 formylmethanofuran dehydrogenase tungsten:subunit g (ec:1.2.99.-) (db:pir2.dat) (mp:for1107847-1108095) F64445 F64445 Methanococcus jannaschii 2190 -11540638 247600 mj1167 formylmethanofuran dehydrogenase:subunit g (db:genpept-bct1) (de:methanococcus jannaschii section 100 of 150 of the complete genome.) (nt:similar to pid:871460 gb:ae000666 pid:1890208) (le:10688) (re:10936) (di:direct) U67558 U67558 g1591793 Methanococcus jannaschii 2190 -11540638 5000698150 (de:(mj1167) (pn:tungsten formylmethanofuran dehydrogenase, subunit g) (gtcfc:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1167 MJ1167 Methanococcus jannaschii 2190 10091518

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925345	19951	42107	1857	618

Description

6500736781 formylmethanofuran dehydrogenase:subunit d:tungsten:fwdd:tungsten formylmethanofuran dehydrogenase:subunit d (gtcfc:2.2:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1168 MJ1168 Methanococcus jannaschii 2190 -11540639 173127 formylmethanofuran dehydrogenase tungsten:subunit d (ec:1.2.99.-) (db:pir2.dat) (mp:for1108113-1108514) G64445 G64445 Methanococcus jannaschii 2190 -11540639 247601 mj1168 formylmethanofuran dehydrogenase:subunit d (db:genpept-bct1) (de:methanococcus jannaschii section 100 of 150 of the complete genome.) (nt:similar to pid:871461 gb:ae000666 pid:1890209) (le:10954) (re:11355) (di:direct) U67558 U67558 g1591794 Methanococcus jannaschii 2190 -11540639 5000698151 (de:(mj1168) (pn:tungsten formylmethanofuran dehydrogenase, subunit d) (gtcfc:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1168 MJ1168 Methanococcus jannaschii 2190 10091515

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925354	19952	42108	432	143

Description

6500736782 formylmethanofuran dehydrogenase:subunit a:tungsten:fwda:tungsten formylmethanofuran dehydrogenase:subunit a (gtcfc:2.2:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1169 MJ1169 Methanococcus jannaschii 2190 -11540640 173124 formylmethanofuran dehydrogenase tungsten:subunit a (cl:formylmethanofuran dehydrogenase (molybdenum) alpha chain) (ec:1.2.99.-) (db:pir2.dat) (mp:for1108541-1110244) H64445 H64445 Methanococcus jannaschii 2190 -11540640 247602 mj1169 formylmethanofuran dehydrogenase:subunit a (db:genpept-bct1) (de:methanococcus jannaschii section 100 of 150 of the complete genome.) (nt:similar to pid:871462 gb:ae000666 pid:1890210) (le:11382) (re:13085) (di:direct) U67558 U67558 g1591795 Methanococcus jannaschii 2190 -11540640 5000698152 (de:(mj1169) (pn:tungsten formylmethanofuran dehydrogenase, subunit a) (gtcfc:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1169 MJ1169 Methanococcus jannaschii 2190 10091512

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925355	19953	42109	225	74

Description

6500736783 formylmethanofuran dehydrogenase:subunit c:tungsten:fwdc:tungsten formylmethanofuran dehydrogenase:subunit c (gtcfc:2.2:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1171 MJ1171 Methanococcus jannaschii 2190 -11540641 173125 formylmethanofuran dehydrogenase tungsten:subunit c (cl:formylmethanofuran dehydrogenase chain c) (ec:1.2.99.-) (db:pir2.dat) (mp:for1110572-1111393) B64446 B64446 Methanococcus jannaschii 2190 -11540641 247604 mj1171 formylmethanofuran dehydrogenase:subunit c (db:genpept-bct1) (de:methanococcus jannaschii section 100 of 150 of the complete genome.) (nt:similar to pid:871463 gb:ae000666 pid:1890211) (le:13413) (re:14234) (di:direct) U67558 U67558 g1591797 Methanococcus jannaschii 2190 -11540641 5000698153 (de:(mj1171) (pn:tungsten formylmethanofuran dehydrogenase, subunit c) (gtcfc:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1171 MJ1171 Methanococcus jannaschii 2190 10091513

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925359	19954	42110	555	184

Description

5000697896 hdra:heterodisulfide reductase:subunit a (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ1190 MJ1190 Methanococcus jannaschii 2190 -11540642 173174 heterodisulfide reductase (ec:1.-.-.-) (db:pir2.dat) (mp:for1129981-1131363) E64448 E64448 Methanococcus jannaschii 2190 -11540642 6500736784 hdra:heterodisulfide reductase:subunit a (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ1190 MJ1190 Methanococcus jannaschii 2190 -11540642 247623 mju67560 (le:1129981) (re:1131363) (di:direct) (de:or:methanococcus jannaschii pn:heterodisulfide reductase, subunit a gn:mj1190 le:4891 re:6273 di:direct nt:similar to s48720 percent identity: 60.1;) U67560 U67560 g1591818 Methanococcus jannaschii 2190 -11540642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925372	19955	42111	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925374	19956	42112	633	210

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925380	19957	42113	480	159

Description

6500736785 formylmethanofuran dehydrogenase:subunit b:tungsten:fwdb:tungsten formylmethanofuran dehydrogenase:subunit b (gtcfc:2.2:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1194 MJ1194 Methanococcus jannaschii 2190 -11540643 173123 formylmethanofuran dehydrogenase tungsten:chain b (cl:formylmethanofuran dehydrogenase (molybdenum) beta chain) (ec:1.2.99.-) (db:pir2.dat) (mp:for1136183-1137106) A64449 A64449 Methanococcus jannaschii 2190 -11540643 247627 mju67561 (le:1136183) (re:1137106) (di:direct) (de:or:methanococcus jannaschii pn:tungsten formylmethanofuran dehydrogenase, gn:mj1194 le:229 re:1152 di:direct nt:similar to x87970_7 percent identity: 71.5;) U67561 U67561 g1591823 Methanococcus jannaschii 2190 -11540643 5000698154 (de:(mj1194) (pn:tungsten formylmethanofuran dehydrogenase,subunit b:tungsten formylmethanofuran dehydrogenase, subunit b) (gtcfc:9.6) (ec:1.2.99.5) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1194 MJ1194 Methanococcus jannaschii 2190 10091511

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925392	19958	42114	582	193

Description

6500736786 atwa:methyl coenzyme m reductase system:component a2 (gtcfc:2.2:9.6) (ec:1.8.-.-) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1242 MJ1242 Methanococcus jannaschii 2190 -11540644 174330 methyl coenzyme m reductase:component a2 (cl:atp-binding cassette homology) (ec:1.8.-.-) (db:pir2.dat) (mp:rev1187641-1186022) A64455 A64455 Methanococcus jannaschii 2190 -11540644 247675 mj1242 methyl coenzyme m reductase system:component a2 (db:genpept-bct1) (de:methanococcus jannaschii section 107 of 150 of the complete genome.) (nt:similar to gb:l11748 pid:293151 pid:385924) (le:107) (re:1726) (di:complement) U67565 U67565 g1592327 Methanococcus jannaschii 2190 -11540644 5000697897 (de:(mj1242) (pn:methyl coenzyme m reductase system, component a2) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1242 MJ1242 Methanococcus jannaschii 2190 10092376

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925396	19959	42115	546	181

Description

6500736787 h:2-dependent methylenetetrahydromethanopterin dehydrogenase related protein (gtcfc:2.2:9.6) (ec:1.5.99.9) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1338 MJ1338 Methanococcus jannaschii 2190 -11540645 5500685355 mj1338 (de:protein mj1338) (db:swissprot) HMDY_METJA Q58734 METHANOCOCCUS JANNASCHII 2190 -11540645 173159 n5:n10-methylenetetrahydromethanopterin dehydrogenase h2-forming homolog 1 (db:pir2.dat) (mp:for1286298-1287359) A64467 A64467 Methanococcus jannaschii 2190 -11540645 247771 mj1338 h 2 -dependent methylenetetrahydromethanopterin (db:genpept-bct1) (de:methanococcus jannaschii section 116 of 150 of the complete genome.) (nt:similar to sp:p32440 gb:u19363 gb:u19364 gb:x59547) (le:917) (re:1978) (di:direct) U67574 U67574 g1591980 Methanococcus jannaschii 2190 -11540645 5000697898 (de:(mj1338) (pn:h:2-dependent methylenetetrahydromethanopterin dehydrogenase related protein) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1338 MJ1338 Methanococcus jannaschii 2190 10091534

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925397	19960	42116	369	122

Description

6500736788 coenzyme f420-reducing hydrogenase:beta subunit (gtcfc:2.2:9.6) (ec:1.12.99.1) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1349 MJ1349 Methanococcus jannaschii 2190 -11540646 7000687508 mj1349 (de:hypothetical protein mj1349) (db:swissprot) YD49_METJA Q58744 METHANOCOCCUS JANNASCHII 2190 -11540646 173028 coenzyme f420 hydrogenase:beta chain homolog:coenzyme f420-reducing hydrogenase:beta subunit (ec:1.12.99.1) (db:pir2.dat) (mp:rev1297220-1296138) D64468 D64468 Methanococcus jannaschii 2190 -11540646 247782 mj1349 coenzyme f420-reducing hydrogenase:beta (db:genpept-bct1) (de:methanococcus jannaschii section 116 of 150 of the complete genome.) (nt:similar to gb:x61201 pid:809731 sp:q00391 percent) (le:10757) (re:11839) (di:complement) U67574 U67574 g1591991 Methanococcus jannaschii 2190 -11540646 5000698155 (de:(mj1349) (pn:coenzyme f420-reducing hydrogenase, betasubunit:coenzyme f420-reducing hydrogenase, beta subunit) (gtcfc:9.6) (ec:1.12.99.1) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1349 MJ1349 Methanococcus jannaschii 2190 10091460

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925398	19961	42117	297	99

Description

5000699453 molybdenum formylmethanofuran dehydrogenase subunit:fmdc:m (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ1350 MJ1350 Methanococcus jannaschii 2190 -11540647 174019 conserved hypothetical protein mj1350 (cl:methanococcus jannaschii conserved hypothetical protein mj1350) (db:pir2.dat) (mp:rev1298238-1297453) E64468 E64468 Methanococcus jannaschii 2190 -11540647 247783 mj1350 formylmethanofuran dehydrogenase:subunt c (db:genpept-bct1) (de:methanococcus jannaschii section 117 of 150 of the complete genome.) (nt:similar to gb:ae000782 percent identity: 46.59;) (le:142) (re:927) (di:complement) U67575 U67575 g1591993 Methanococcus jannaschii 2190 -11540647 6500736789 molybdenum formylmethanofuran dehydrogenase subunit:fmdc:m (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) MJ1350 MJ1350 Methanococcus jannaschii 2190 -11540647

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925399	19962	42118	732	243

Description

6500736790 n5:n10-methylene-tetrahydromethanopterin reductase:mer:n5:n10-methylene tetrahydromethanopterin reductase (gtcfc:2.2:9.6) (ec:1.5.99.9) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1534 MJ1534 Methanococcus jannaschii 2190 -11540648 174362 n5:n10-methylenetetrahydromethanopterin dehydrogenase coenzyme f420-dependent (ec:1.-.-.-) (db:pir2.dat) (mp:for1511780-1512808) E64491 E64491 Methanococcus jannaschii 2190 -11540648 247967 mju67594 (le:1511780) (re:1512808) (di:direct) (de:or:methanococcus jannaschii pn:n5,n10-methylene tetrahydromethanopterin gn:mj1534 le:4787 re:5815 di:direct nt:similar to x86477_1 percent identity: 66.1;) U67594 U67594 g1592165 Methanococcus jannaschii 2190 -11540648 5000697900 (de:(mj1534) (pn:n5,n10-methylene tetrahydromethanopterin reductase) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1534 MJ1534 Methanococcus jannaschii 2190 10092406

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925413	19963	42119	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925431	19964	42120	258	85

Description

6500736791 mch:n5:n10-methenyl-tetrahydromethanopterin cyclohydrolase (gtcfc:2.2:9.6) (ec:3.5.4.27) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1636 MJ1636 Methanococcus jannaschii 2190 -11540649 174321 methenyltetrahydromethanopterin cyclohydrolase::n5:n10-methenyl-tetrahydromethanopterin cyclohydrolase (ec:3.5.4.27) (db:pir2.dat) (mp:for1617242-1618213) B64504 B64504 Methanococcus jannaschii 2190 -11540649 248068 mj1636 n5:n10-methenyl-tetrahydromethanopterin (db:genpept-bct1) (de:methanococcus jannaschii section 146 of 150 of the complete genome.) (nt:similar to pid:1103709 sp:p51616 gb:ae000666) (le:2312) (re:3283) (di:direct) U67604 U67604 g1592341 Methanococcus jannaschii 2190 -11540649 5000698156 (de:(mj1636) (pn:n5,n10-methenyl-tetrahydromethanopterin cyclohydrolase) (gtcfc:9.6) (ec:3.5.4.27) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1636 MJ1636 Methanococcus jannaschii 2190 10092374

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925438	19965	42121	339	112

Description

6500736792 methyl coenzyme m reductase system:component a2-like:methyl coenzyme m reductase system:component a2 (gtcfc:2.2:9.6) (ec:1.8.-.-) (keggfc:9.7) (tigrfc:6.13) (db:gtc-methanococcus jannaschii) (gtcfc:energy metabolism-methane metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) MJ1662 MJ1662 Methanococcus jannaschii 2190 -11540650 174331 methyl coenzyme m reductase system:component a2 homolog (cl:atp-binding cassette homology) (db:pir2.dat) (mp:rev1645810-1644134) D64507 D64507 Methanococcus jannaschii 2190 -11540650 248094 mju67606 (le:1644134) (re:1645810) (di:direct) (de:or:methanococcus jannaschii pn:methyl coenzyme m reductase system, component gn:mj1662 le:7172 re:8848 di:complement nt:similar to l11748_1 percent identity: 37.1;) U67606 U67606 g1592242 Methanococcus jannaschii 2190 -11540650 5000697901 (de:(mj1662) (pn:methyl coenzyme m reductase system, component a2) (gtcfc:2.2) (ec:) (keggfc:11.2) (tigrfc:6.13) (db:gtc-methanococcus jannaschii)) MJ1662 MJ1662 Methanococcus jannaschii 2190 10092377

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925439	19966	42122	408	135

Description

6500736793 aspartate aminotransferase:aspb1:probable aspartate aminotransferase:transaminase a:aspat (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (ec:2.6.1.1) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (tigrfc:1.3) (db:gtc-methanococcus jannaschii) MJ0001 MJ0001 Methanococcus jannaschii 2190 -11540651 117444 mj0001 (ec:2.6.1.1) (de:(aspat)) (db:swissprot) AAT1_METJA Q60317 METHANOCOCCUS JANNASCHII 2190 -11540651 172974 aspartate transaminase::aspartate aminotransferase (cl:aspartate transaminase) (ec:2.6.1.1) (db:pir2.dat) (mp:rev3343-2216) A64300 A64300 Methanococcus jannaschii 2190 -11540651 246435 mj0001 aspartate aminotransferase aspb1 (db:genpept-bct1) (de:methanococcus jannaschii section 1 of 150 of the complete genome.) (nt:similar to pid:1146246 sp:p53001 gb:al009126) (le:2216) (re:3343) (di:complement) U67459 U67459 g1592252 Methanococcus jannaschii 2190 -11540651 5000697902 (de:(mj0001) (pn:probable aspartate aminotransferase:transaminase a:aspat:aspartate aminotransferase) (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (ec:2.6.1.1) (aat_metja) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (tigrfc:1.2) (db:gtc-methanococ) MJ0001 MJ0001 Methanococcus jannaschii 2190 10059245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925440	19967	42123	636	211

Description

6500736794 aspb2:aspartate aminotransferase (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (ec:2.6.1.1) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (tigrfc:1.3) (db:gtc-methanococcus jannaschii) MJ0684 MJ0684 Methanococcus jannaschii 2190 -11540652 172975 aspartate transaminase::aspartate aminotransferase (cl:aspartate transaminase) (ec:2.6.1.1) (db:pir2.dat) (mp:rev612861-611728) D64385 D64385 Methanococcus jannaschii 2190 -11540652 5500684835 mj0684 (ec:2.6.1.1) (de:(aspat)) (db:swissprot) AAT2_METJA Q58097 METHANOCOCCUS JANNASCHII 2190 -11540652 247118 mju67515 (le:611728) (re:612861) (di:direct) (de:or:methanococcus jannaschii pn:aspartate aminotransferase gn:mj0684 le:9748 re:10881 di:complement nt:similar to p14909 percent identity: 37.7;) U67515 U67515 g1591399 Methanococcus jannaschii 2190 -11540652 5000697903 (de:(mj0684) (pn:aspartate aminotransferase) (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (ec:2.6.1.1) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (tigrfc:1.2) (db:gtc-methanococcus jannaschii)) MJ0684 MJ0684 Methanococcus jannaschii 2190 10091422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925444	19968	42124	1023	340

Description

GTC ORF with score 267 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0540.) (nt:similar to saccharomyces cerevisiae bcs1 protein,) (le:<1) (re:1261) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925490	19969	42125	3003	1000

Description

6500736795 putative aminotransferase:aspartate aminotransferase (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5:14.3) (ec:2.6.1.1) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (tigrfc:5.1) (db:gtc-methanococcus jannaschii) MJ1391 MJ1391 Methanococcus jannaschii 2190 -11540653 5500686515 mj1391 (ec:2.6.1.-) (de:putative aminotransferase mt1391,) (db:swissprot) YD91_METJA Q58786 METHANOCOCCUS JANNASCHII 2190 -11540653 173042 d-alanine transaminase::aspartate aminotransferase:d-aspartate transaminase (cl:aspartate transaminase) (ec:2.6.1.21) (db:pir2.dat) (mp:rev1339783-1338527) F64473 F64473 Methanococcus jannaschii 2190 -11540653 247824 mj1391 putative aminotransferase (db:genpept-bct1) (de:methanococcus jannaschii section 121 of 150 of the complete genome.) (nt:similar to gb:x73124 sp:p39643 pid:414009) (le:119) (re:1375) (di:complement) U67579 U67579 g1592038 Methanococcus jannaschii 2190 -11540653 5000697904 (de:(mj1391) (pn:aspartate aminotransferase) (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (ec:2.6.1.1) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (tigrfc:1.2) (db:gtc-methanococcus jannaschii)) MJ1391 MJ1391 Methanococcus jannaschii 2190 10091464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925497	19970	42126	453	150

Description

6500736796 putative aminotransferase:alanine aminotransferase 2 (gtcfc:2.4:5.1:5.2:14.3) (ec:2.6.1.2) (keggfc:2.3:5.1:5.2) (tigrfc:5.1) (db:gtc-methanococcus jannaschii) MJ1479 MJ1479 Methanococcus jannaschii 2190 -11540654 172948 alanine transaminase::alanine aminotransferase 2 (ec:2.6.1.2) (db:pir2.dat) (mp:for1449710-1451008) F64484 F64484 Methanococcus jannaschii 2190 -11540654 247912 mj1479 putative aminotransferase (db:genpept-bct1) (de:methanococcus jannaschii section 131 of 150 of the complete genome.) (nt:similar to gp:1573250 percent identity: 31.82;) (le:153) (re:1451) (di:direct) U67589 U67589 g2826418 Methanococcus jannaschii 2190 -11540654 7000696910 mj1479 putative aminotransferase (db:genpept-bct1) (de:methanococcus jannaschii section 131 of 150 of the complete genome.) (nt:similar to gp:1573250 percent identity: 31.82;) (le:153) (re:1451) (di:direct) U67589 L77117 g2826418 Methanococcus jannaschii 2190 -11540654 5000697905 (de:(mj1479) (pn:alanine aminotransferase 2) (gtcfc:2.4:5.1:5.2) (ec:2.6.1.2) (keggfc:2.3:5.1:5.2) (tigrfc:6.7) (db:gtc-methanococcus jannaschii)) MJ1479 MJ1479 Methanococcus jannaschii 2190 10091412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925518	19971	42127	321	106

Description

6500736797 probable l-asparaginase:l-asparagine amidohydrolase:ansa (gtcfc:5.16:5.2) (ec:3.5.1.1) (keggfc:2.5:5.2:6.5) (tigrfc:1.3) (db:gtc-methanococcus jannaschii) MJ0020 MJ0020 Methanococcus jannaschii 2190 -11540655 117512 mj0020 (ec:3.5.1.1) (de:probable l-asparaginase, (l-asparagine amidohydrolase)) (db:swissprot) ASPG_METJA Q60331 METHANOCOCCUS JANNASCHII 2190 -11540655 174305 l-asparaginase i (db:pir2.dat) (mp:rev22401-21148) D64302 D64302 Methanococcus jannaschii 2190 -11540655 246454 mj0020 asparaginase ansa (db:genpept-bct1) (de:methanococcus jannaschii section 2 of 150 of the complete genome.) (nt:similar to gb:m63264 sp:p26900 pid:142517) (le:11133) (re:12386) (di:complement) U67460 U67460 g1592255 Methanococcus jannaschii 2190 -11540655 5000697906 (de:(mj0020) (pn:probable l-asparaginase:l-asparagine amidohydrolase:l-asparaginase i) (gtcfc:2.6:5.2:6.5) (ec:3.5.1.1) (aspg_metja) (keggfc:2.5:5.2:6.5) (tigrfc:1.2) (db:gtc-methanococcus jannaschii)) MJ0020 MJ0020 Methanococcus jannaschii 2190 10059346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925524	19972	42128	339	112

Description

6500736798 nitrogenase reductase-related protein:nifh2:nitrogenase reductase related protein (gtcfc:2.6:5.16) (ec:1.18.6.1) (keggfc:2.5) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ0685 MJ0685 Methanococcus jannaschii 2190 -11540656 5500686341 mj0685 (de:hypothetical atp-binding protein mj0685) (db:swissprot) Y685_METJA Q58098 METHANOCOCCUS JANNASCHII 2190 -11540656 174386 nitrogenase reductase-related protein homolog (cl:conserved hypothetical protein mj0823) (db:pir2.dat) (mp:for612909-613670) E64385 E64385 Methanococcus jannaschii 2190 -11540656 247119 mj0685 nitrogenase reductase nifh2 (db:genpept-bct1) (de:methanococcus jannaschii section 57 of 150 of the complete genome.) (nt:similar to sp:p22548 gb:m21537 sp:p00456 sp:p09552) (le:10929) (re:11690) (di:direct) U67515 U67515 g1591400 Methanococcus jannaschii 2190 -11540656 5000697907 (de:(mj0685) (pn:nitrogenase reductase related protein) (gtcfc:2.6) (ec:1.18.6.1) (keggfc:2.5) (tigrfc:5.7) (db:gtc-methanococcus jannaschii)) MJ0685 MJ0685 Methanococcus jannaschii 2190 10092417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925526	19973	42129	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925539	19974	42130	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925547	19975	42131	624	207

Description

6500736799 codh nickel-insertion accessory protein cooc:cooc:nifh / mind related protein (gtcfc:2.6:10.7) (ec:1.18.6.1) (keggfc:2.5) (tigrfc:12.3) (db:gtc-methanococcus jannaschii) MJ0823 MJ0823 Methanococcus jannaschii 2190 -11540657 118853 mj0823 (de:hypothetical atp-binding protein mj0823) (db:swissprot) Y823_METJA Q58233 METHANOCOCCUS JANNASCHII 2190 -11540657 173743 hypothetical protein mj0823 (cl:conserved hypothetical protein mj0823) (db:pir2.dat) (mp:for744832-745605) G64402 G64402 Methanococcus jannaschii 2190 -11540657 247257 mj0823 codh nickel-insertion accessory protein cooc (db:genpept-bct1) (de:methanococcus jannaschii section 68 of 150 of the complete genome.) (nt:similar to gp:1498749 percent identity: 45.65;) (le:3041) (re:3814) (di:direct) U67526 U67526 g1499647 Methanococcus jannaschii 2190 -11540657 5000697855 (de:(mj0823) (pn:hypothetical protein mj0823:nitrogenase reductase) (gtcfc:1.9:13.7) (ec:) (y823_metja) (keggfc:11.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii)) MJ0823 MJ0823 Methanococcus jannaschii 2190 10061287

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925565	19976	42132	1650	549

Description

GTC ORF with score 239 to: (fn:hydrolysis of isoprimeverose) (db:genpept-bct2) (de:lactobacillus pentosus isoprimeverose cation-symporter xylp (xylp)and alpha-xylosidase xylq (xylq) genes, complete cds.) (le:1843) (re:4131) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925566	19977	42133	951	316

Description

GTC ORF with score 180 to: (or:Homo sapiens) (sr:homo sapiens male myeloblast cell_line kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0088 gene, partial cds.) (nt:the ha1225 gene product is related to human) (le:<1) (re:2833) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925578	19978	42134	753	250

Description

6500736800 nifh:mj0879 nitrogenase iron protein:nitrogenase component ii:nitrogenase reductase (gtcfc:2.6:5.16) (ec:1.18.6.1) (keggfc:2.5) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ0879 MJ0879 Methanococcus jannaschii 2190 -11540658 500685174 nifh:mj0879 (ec:1.18.6.1) (de:(nitrogenase reductase)) (db:swissprot) NIFH_METJA Q58289 METHANOCOCCUS JANNASCHII 2190 -11540658 174385 nitrogenase:iron protein (cl:nitrogenase iron protein) (ec:1.18.6.1) (db:pir2.dat) (mp:for804543-805382) G64409 G64409 Methanococcus jannaschii 2190 -11540658 247313 mj0879 nitrogenase iron protein nifh (db:genpept-bct1) (de:methanococcus jannaschii section 74 of 150 of the complete genome.) (nt:similar to sp:p06119 gb:x03777 pid:44733 percent) (le:1540) (re:2379) (di:direct) U67532 U67532 g1592313 Methanococcus jannaschii 2190 -11540658 5000697908 (de:(mj0879) (pn:nitrogenase iron protein:nitrogenase component ii:nitrogenase reductase) (gn:nifh) (gtcfc:2.6) (ec:1.18.6.1) (nifh_metja) (keggfc:2.5) (tigrfc:5.7) (db:gtc-methanococcus jannaschii)) MJ0879 MJ0879 Methanococcus jannaschii 2190 10063669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925588	19979	42135	576	191

Description

6500736801 asnb:asparagine synthetase (gtcfc:2.6:5.2) (ec:6.3.5.4) (keggfc:2.5:5.2) (tigrfc:1.3) (db:gtc-methanococcus jannaschii) MJ1056 MJ1056 Methanococcus jannaschii 2190 -11540659 172969 asparagine synthase (ec:6.3.-.-) (db:pir2.dat) (mp:for995672-996196) G64431 G64431 Methanococcus jannaschii 2190 -11540659 247489 mju67548 (le:995672) (re:996196) (di:direct) (de:or:methanococcus jannaschii pn:asparagine synthetase gn:mj1056 le:9454 re:9978 di:direct nt:similar to p42113 percent identity: 31.5;) U67548 U67548 g1591708 Methanococcus jannaschii 2190 -11540659 5000697909 (de:(mj1056) (pn:asparagine synthetase) (gtcfc:2.6:5.2) (ec:6.3.5.4) (keggfc:2.5:5.2) (tigrfc:1.2) (db:gtc-methanococcus jannaschii)) MJ1056 MJ1056 Methanococcus jannaschii 2190 10091417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925592	19980	42136	2331	776

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925593	19981	42137	1356	451

Description

6500736802 asparagine synthetase:asnb:putative asparagine synthetase:glutamine-hydrolyzing (gtcfc:2.6:5.2) (ec:6.3.5.4) (keggfc:2.5:5.2) (tigrfc:1.3) (db:gtc-methanococcus jannaschii) MJ1116 MJ1116 Methanococcus jannaschii 2190 -11540660 172970 asparagine synthetase (ec:6.3.-.-) (db:pir2.dat) (mp:rev1058315-1056681) C64439 C64439 Methanococcus jannaschii 2190 -11540660 247549 mj1116 asparagine synthetase asnb (db:genpept-bct1) (de:methanococcus jannaschii section 96 of 150 of the complete genome.) (nt:similar to gb:j05554 sp:p22106 pid:145393 gb:u00096) (le:6372) (re:8006) (di:complement) U67554 U67554 g1591755 Methanococcus jannaschii 2190 -11540660 5000697910 (de:(mj1116) (pn:putative asparagine synthetase:glutamine-hydrolyzing:asparagine synthetase) (gtcfc:2.6:5.2) (ec:6.3.5.4) (asnh_metja) (keggfc:2.5:5.2) (tigrfc:1.2) (db:gtc-methanococcus jannaschii)) MJ1116 MJ1116 Methanococcus jannaschii 2190 10091418

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925596	19982	42138	636	211

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925599	19983	42139	1245	414

Description

6500736803 glna:mj1346 glutamine synthetase:glutamate--ammonia ligase:gs (gtcfc:2.6:5.1:11.4) (ec:6.3.1.2) (keggfc:2.5:5.1:7.3) (tigrfc:1.4) (db:gtc-methanococcus jannaschii) MJ1346 MJ1346 Methanococcus jannaschii 2190 -11540661 118323 glna:mj1346 (ec:6.3.1.2) (de:glutamine synthetase, (glutamate--ammonia ligase) (gs)) (db:swissprot) GLNA_METJA Q60182 METHANOCOCCUS JANNASCHII 2190 -11540661 173143 glutamate--ammonia ligase::glutamine synthetase (cl:glutamate--ammonia ligase) (ec:6.3.1.2) (db:pir2.dat) (mp:for1292934-1294298) A64468 A64468 Methanococcus jannaschii 2190 -11540661 247779 mj1346 glutamine synthetase glna (db:genpept-bct1) (de:methanococcus jannaschii section 116 of 150 of the complete genome.) (nt:similar to sp:p21154 gb:x53509 pid:44712 percent) (le:7553) (re:8917) (di:direct) U67574 U67574 g1591988 Methanococcus jannaschii 2190 -11540661 5000697911 (de:(mj1346) (pn:glutamate--ammonia ligase:gs:glutamine synthetase) (gn:glna) (gtcfc:2.6:5.1:7.2) (ec:6.3.1.2) (glna_metja) (keggfc:2.5:5.1:7.3) (tigrfc:1.3) (db:gtc-methanococcus jannaschii)) MJ1346 MJ1346 Methanococcus jannaschii 2190 10060457

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925630	19984	42140	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925637	19985	42141	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925644	19986	42142	462	154

Description

6500736804 gltb:glutamate synthase:nadph:subunit alpha (gtcfc:2.6:5.1) (ec:1.4.1.13) (keggfc:2.5:5.1) (tigrfc:1.4) (db:gtc-methanococcus jannaschii) MJ1351 MJ1351 Methanococcus jannaschii 2190 -11540662 173142 glutamate synthase nadph:subunit alpha (cl:glutamate synthase (nadph) alpha chain) (ec:1.4.1.13) (db:pir2.dat) (mp:rev1299885-1298353) F64468 F64468 Methanococcus jannaschii 2190 -11540662 247784 mj1351 glutamate synthase gltb (db:genpept-bct1) (de:methanococcus jannaschii section 117 of 150 of the complete genome.) (nt:similar to gb:m18747 sp:p09831 gb:l20253 gb:m33743) (le:1042) (re:2574) (di:complement) U67575 U67575 g1591994 Methanococcus jannaschii 2190 -11540662 5000697912 (de:(mj1351) (pn:glutamate synthase:nadph, subunit alpha) (gtcfc:2.6:5.1) (ec:1.4.1.13) (keggfc:2.5:5.1) (tigrfc:1.3) (db:gtc-methanococcus jannaschii)) MJ1351 MJ1351 Methanococcus jannaschii 2190 10091526

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925652	19987	42143	201	66

Description

5000697913 nade:nh:3-dependent nad+ synthetase (gtcfc:2.6:5.1:9.4) (keggfc:2.5:5.1:9.4) (tigrfc:2.10) (db:gtc-methanococcus jannaschii) MJ1352 MJ1352 Methanococcus jannaschii 2190 -11540663 174378 nh 3 -dependent nad+ synthetase (cl:ammonia-dependent nad+ synthetase) (db:pir2.dat) (mp:rev1301976-1301197) G64468 G64468 Methanococcus jannaschii 2190 -11540663 247785 mj1352 nh 3 -dependent nad+ synthetase nade (db:genpept-bct1) (de:methanococcus jannaschii section 117 of 150 of the complete genome.) (nt:similar to gb:l43967 sp:p47623 pid:1046094 percent) (le:3886) (re:4665) (di:complement) U67575 U67575 g1591995 Methanococcus jannaschii 2190 -11540663 6500736805 nade:nh:3-dependent nad+ synthetase (gtcfc:2.6:5.1:9.4) (keggfc:2.5:5.1:9.4) (tigrfc:2.10) (db:gtc-methanococcus jannaschii) MJ1352 MJ1352 Methanococcus jannaschii 2190 -11540663

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925653	19988	42144	1041	346

Description

5000697849 urease accessory protein:ureg:hypothetical protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ0120 MJ0120 Methanococcus jannaschii 2190 -11540664 118794 mj0120 (de:hypothetical protein mj0120) (db:swissprot) Y120_METJA Q57584 METHANOCOCCUS JANNASCHII 2190 -11540664 173349 hypothetical protein mj0120 (db:pir2.dat) (mp:rev117070-116369) H64314 H64314 Methanococcus jannaschii 2190 -11540664 246554 mj0120 urease accessory protein ureg (db:genpept-bct1) (de:methanococcus jannaschii section 11 of 150 of the complete genome.) (nt:similar to gb:l24101 sp:p42871 pid:431755 percent) (le:4739) (re:5440) (di:complement) U67469 U67469 g1498887 Methanococcus jannaschii 2190 -11540664 6500736806 urease accessory protein:ureg:hypothetical protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ0120 MJ0120 Methanococcus jannaschii 2190 -11540664

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925654	19989	42145	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925664	19990	42146	519	172

Description

5000697852 nitrite reductase:nira isolog:hypothetical protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ0551 MJ0551 Methanococcus jannaschii 2190 -11540665 4000708339 mj0551 (de:hypothetical protein mj0551) (db:swissprot) Y551_METJA Q57971 METHANOCOCCUS JANNASCHII 2190 -11540665 173585 hypothetical protein mj0551 (db:pir2.dat) (mp:rev487932-487105) G64368 G64368 Methanococcus jannaschii 2190 -11540665 246985 mj0551 nitrite reductase nira isolog (db:genpept-bct1) (de:methanococcus jannaschii section 46 of 150 of the complete genome.) (nt:similar to pid:1113082 percent identity: 32.84;) (le:5280) (re:6107) (di:complement) U67504 U67504 g1591256 Methanococcus jannaschii 2190 -11540665 6500736807 nitrite reductase:nira isolog:hypothetical protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ0551 MJ0551 Methanococcus jannaschii 2190 -11540665

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925684	19991	42147	1698	565

Description

5000697857 nodulation protein:nodulation factor production protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ1051 MJ1051 Methanococcus jannaschii 2190 -11540666 7500895872 mj1051 (de:hypothetical protein mj1051) (db:swissprot) YA51_METJA Q58451 METHANOCOCCUS JANNASCHII 2190 -11540666 174388 nodulation factor production protein homolog (db:pir2.dat) (mp:rev989490-987949) B64431 B64431 Methanococcus jannaschii 2190 -11540666 7500895874 mj1051 nodulation protein (db:genpept-bct1) (de:methanococcus jannaschii section 90 of 150 of the complete genome.) (nt:similar to pid:1653353 percent ident: 30.90;) (le:1731) (re:3272) (di:complement) U67548 U67548 g1591704 Methanococcus jannaschii 2190 -11540666 6500736808 nodulation protein:nodulation factor production protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ1051 MJ1051 Methanococcus jannaschii 2190 -11540666 247484 mju67548 (le:987949) (re:989490) (di:direct) (de:or:methanococcus jannaschii pn:nodulation factor production protein gn:mj1051 le:1731 re:3272 di:complement nt:similar to c49300 percent identity: 32.3;) U67548 U67548 g1591704 Methanococcus jannaschii 2190 -11540666

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925685	19992	42148	255	84

Description

5000697858 nodulation protein:nodulation factor production protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ1058 MJ1058 Methanococcus jannaschii 2190 -11540667 7500895891 mj1058 (de:hypothetical protein mj1058) (db:swissprot) YA58_METJA Q58458 METHANOCOCCUS JANNASCHII 2190 -11540667 174387 nodulation factor production protein homolog (db:pir2.dat) (mp:for997396-999225) A64432 A64432 Methanococcus jannaschii 2190 -11540667 7500895893 mj1058 nodulation protein (db:genpept-bct1) (de:methanococcus jannaschii section 91 of 150 of the complete genome.) (nt:similar to pid:1653353 percent ident: 35.19;) (le:1067) (re:2896) (di:direct) U67549 U67549 g1591711 Methanococcus jannaschii 2190 -11540667 6500736809 nodulation protein:nodulation factor production protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ1058 MJ1058 Methanococcus jannaschii 2190 -11540667 247491 mju67549 (le:997396) (re:999225) (di:direct) (de:or:methanococcus jannaschii pn:nodulation factor production protein gn:mj1058 le:1067 re:2896 di:direct nt:similar to c49300 percent identity: 34.5;) U67549 U67549 g1591711 Methanococcus jannaschii 2190 -11540667

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925717	19993	42149	405	134

Description

5000697859 urease accesory protein:ureh:m (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ1092 MJ1092 Methanococcus jannaschii 2190 -11540668 7500895938 mj1092 (de:hypothetical protein mj1092) (db:swissprot) YA92_METJA Q58492 METHANOCOCCUS JANNASCHII 2190 -11540668 173876 hypothetical protein mj1092 (db:pir2.dat) (mp:for1030104-1030748) C64436 C64436 Methanococcus jannaschii 2190 -11540668 7500895940 mj1092 urease accesory protein ureh (db:genpept-bct1) (de:methanococcus jannaschii section 93 of 150 of the complete genome.) (nt:similar to sp:q07404 pid:216367 percent ident:) (le:9532) (re:10176) (di:direct) U67551 U67551 g1591736 Methanococcus jannaschii 2190 -11540668 6500736810 urease accesory protein:ureh:m (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ1092 MJ1092 Methanococcus jannaschii 2190 -11540668 247525 mju67551 (le:1030104) (re:1030748) (di:direct) (de:or:methanococcus jannaschii pn:m. jannaschii predicted coding region mj1092 gn:mj1092 le:9532 re:10176 di:direct nt:identified by genemark; putative) U67551 U67551 g1591736 Methanococcus jannaschii 2190 -11540668

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925729	19994	42150	618	205

Description

5000697860 nifb:nifb protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ1093 MJ1093 Methanococcus jannaschii 2190 -11540669 174380 nifb homolog (db:pir2.dat) (mp:for1030880-1031782) D64436 D64436 Methanococcus jannaschii 2190 -11540669 247526 mj1093 nifb protein nifb (db:genpept-bct1) (de:methanococcus jannaschii section 94 of 150 of the complete genome.) (nt:similar to sp:p20627 pid:142035 percent identity:) (le:91) (re:993) (di:direct) U67552 U67552 g1591738 Methanococcus jannaschii 2190 -11540669 6500736811 nifb:nifb protein (gtcfc:2.6:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-methanococcus jannaschii) MJ1093 MJ1093 Methanococcus jannaschii 2190 -11540669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925735	19995	42151	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925762	19996	42152	2967	988

Description

5000699463 4fe-4s iron-sulfur protein:hypothetical protein (gtcfc:2.7) (keggfc:14.2) (tigrfc:6.3) (db:gtc-methanococcus jannaschii) MJ0208 MJ0208 Methanococcus jannaschii 2190 -11540670 500684888 mj0208 (de:hypothetical protein mj0208) (db:swissprot) Y208_METJA Q57661 METHANOCOCCUS JANNASCHII 2190 -11540670 173392 hypothetical protein mj0208 (cl:hypothetical protein mj0208) (db:pir2.dat) (mp:rev200166-199426) A64326 A64326 Methanococcus jannaschii 2190 -11540670 246643 mj0208 4fe-4s iron-sulfur protein (db:genpept-bct1) (de:methanococcus jannaschii section 18 of 150 of the complete genome.) (nt:similar to gb:d14422 sp:p30132 pid:216575) (le:8234) (re:8974) (di:complement) U67476 U67476 g1498983 Methanococcus jannaschii 2190 -11540670 6500736812 4fe-4s iron-sulfur protein:hypothetical protein (gtcfc:2.7) (keggfc:14.2) (tigrfc:6.3) (db:gtc-methanococcus jannaschii) MJ0208 MJ0208 Methanococcus jannaschii 2190 -11540670

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925763	19997	42153	1155	384

Description

GTC ORF with score 211 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c24a8.) (nt:weak similarity to drosophila homeotic gene) (le:4301:4627:6018) (re:4582:5964:6092) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925767	19998	42154	426	141

Description

5000697914 ferredoxin:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0061 MJ0061 Methanococcus jannaschii 2190 -11540671 118165 mj0061 (de:putative ferredoxin mj0061) (db:swissprot) FER1_METJA Q60368 METHANOCOCCUS JANNASCHII 2190 -11540671 173094 ferredoxin (db:pir2.dat) (mp:for60363-60605) E64307 E64307 Methanococcus jannaschii 2190 -11540671 246495 mj0061 ferredoxin (db:genpept-bct1) (de:methanococcus jannaschii section 6 of 150 of the complete genome.) (nt:similar to sp:p21305 percent identity: 42.86;) (le:1517) (re:1759) (di:direct) U67464 U67464 g1498823 Methanococcus jannaschii 2190 -11540671 6500736813 ferredoxin:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0061 MJ0061 Methanococcus jannaschii 2190 -11540671

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925768	19999	42155	693	230

Description

GTC ORF with score 179 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c04g6.) (nt:coded for by c. elegans cdna yk32d5.3; coded for by) (le:2522:2781:3279) (re:2622:2904:3419) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925771	20000	42156	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925773	20001	42157	1356	451

Description

5000697915 ferredoxin ii:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0099 MJ0099 Methanococcus jannaschii 2190 -11540672 118166 mj0099 (de:putative ferredoxin mj0099) (db:swissprot) FER2_METJA Q57563 METHANOCOCCUS JANNASCHII 2190 -11540672 173093 ferredoxin (cl:conserved hypothetical protein slr2059) (db:pir2.dat) (mp:rev93297-92902) C64312 C64312 Methanococcus jannaschii 2190 -11540672 246533 mj0099 ferredoxin ii (db:genpept-bct1) (de:methanococcus jannaschii section 9 of 150 of the complete genome.) (nt:similar to sp:p00211 percent identity: 40.00;) (le:3398) (re:3793) (di:complement) U67467 U67467 g1590877 Methanococcus jannaschii 2190 -11540672 6500736814 ferredoxin ii:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0099 MJ0099 Methanococcus jannaschii 2190 -11540672

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925780	20002	42158	651	216

Description

5000697916 ferredoxin:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0199 MJ0199 Methanococcus jannaschii 2190 -11540673 173095 ferredoxin 2 4fe-4s) (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:for192376-192573) H64324 H64324 Methanococcus jannaschii 2190 -11540673 246634 mj0199 ferredoxin (db:genpept-bct1) (de:methanococcus jannaschii section 18 of 150 of the complete genome.) (nt:similar to sp:p21305 percent identity: 74.58;) (le:1184) (re:1381) (di:direct) U67476 U67476 g1590944 Methanococcus jannaschii 2190 -11540673 6500736815 ferredoxin:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0199 MJ0199 Methanococcus jannaschii 2190 -11540673

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925782	20003	42159	498	165

Description

5000697917 ferredoxin ii:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0251 MJ0251 Methanococcus jannaschii 2190 -11540674 500684884 mj0251 (de:putative ferredoxin mj0251) (db:swissprot) FER5_METJA Q57699 METHANOCOCCUS JANNASCHII 2190 -11540674 173410 hypothetical protein mj0251 (db:pir2.dat) (mp:rev238728-238285) D64331 D64331 Methanococcus jannaschii 2190 -11540674 246686 mj0251 ferredoxin ii (db:genpept-bct1) (de:methanococcus jannaschii section 22 of 150 of the complete genome.) (nt:similar to sp:p00211 percent identity: 37.04;) (le:6214) (re:6657) (di:complement) U67480 U67480 g1499030 Methanococcus jannaschii 2190 -11540674 6500736816 ferredoxin ii:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0251 MJ0251 Methanococcus jannaschii 2190 -11540674

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925785	20004	42160	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925794	20005	42161	306	101

Description

5000697918 mvhb:polyferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0514 MJ0514 Methanococcus jannaschii 2190 -11540675 174430 polyferredoxin 1 (cl:methanococcus jannaschii polyferredoxin 1) (db:pir2.dat) (mp:rev455889-455137) B64364 B64364 Methanococcus jannaschii 2190 -11540675 246948 mj0514 polyferredoxin mvhb (db:genpept-bct1) (de:methanococcus jannaschii section 43 of 150 of the complete genome.) (nt:similar to gb:j04540 pid:149734 gb:ae000666 percent) (le:3721) (re:4473) (di:complement) U67501 U67501 g1591217 Methanococcus jannaschii 2190 -11540675 6500736817 mvhb:polyferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0514 MJ0514 Methanococcus jannaschii 2190 -11540675

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925800	20006	42162	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925818	20007	42163	297	98

Description

5000697919 ferredoxin:ferredoxin 2 (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0533 MJ0533 Methanococcus jannaschii 2190 -11540676 173097 ferredoxin 2 4fe-4s homolog) (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:rev468955-468785) E64366 E64366 Methanococcus jannaschii 2190 -11540676 246967 mj0533 ferredoxin (db:genpept-bct1) (de:methanococcus jannaschii section 44 of 150 of the complete genome.) (nt:similar to gb:m83188 sp:q01700 pid:149824 percent) (le:7359) (re:7529) (di:complement) U67502 U67502 g1591236 Methanococcus jannaschii 2190 -11540676 6500736818 ferredoxin:ferredoxin 2 (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0533 MJ0533 Methanococcus jannaschii 2190 -11540676

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925838	20008	42164	240	79

Description

5000698451 flavoprotein:fpra:hypothetical protein (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0534 MJ0534 Methanococcus jannaschii 2190 -11540677 173111 flavoprotein (cl:methanobacterium flavoprotein a) (db:pir2.dat) (mp:for469119-470294) F64366 F64366 Methanococcus jannaschii 2190 -11540677 4000708328 mj0534 (de:hypothetical protein mj0534) (db:swissprot) Y534_METJA Q57954 METHANOCOCCUS JANNASCHII 2190 -11540677 6500736819 flavoprotein:fpra:hypothetical protein (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0534 MJ0534 Methanococcus jannaschii 2190 -11540677 246968 mju67502 (le:469119) (re:470294) (di:direct) (de:or:methanococcus jannaschii pn:flavoprotein gn:mj0534 le:7693 re:8868 di:direct nt:similar to u17835_1 percent identity: 34.1;) U67502 U67502 g1591237 Methanococcus jannaschii 2190 -11540677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925858	20009	42165	1572	523

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925862	20010	42166	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925865	20011	42167	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925866	20012	42168	504	167

Description

5000697920 ferredoxin:hypothetical protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0578 MJ0578 Methanococcus jannaschii 2190 -11540678 4000707937 mj0578 (de:hypothetical protein mj0578) (db:swissprot) Y578_METJA Q57998 METHANOCOCCUS JANNASCHII 2190 -11540678 173091 ferredoxin (db:pir2.dat) (mp:rev514290-513460) B64372 B64372 Methanococcus jannaschii 2190 -11540678 247012 mj0578 iron-sulfer cluster binding protein (db:genpept-bct1) (de:methanococcus jannaschii section 48 of 150 of the complete genome.) (nt:similar to sp:p80168 percent identity: 49.02;) (le:8689) (re:9519) (di:complement) U67506 U67506 g1591285 Methanococcus jannaschii 2190 -11540678 6500736820 ferredoxin:hypothetical protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0578 MJ0578 Methanococcus jannaschii 2190 -11540678

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925867	20013	42169	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925868	20014	42170	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925871	20015	42171	423	140

Description

5000697921 ferredoxin:ferredoxin 2 (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0624 MJ0624 Methanococcus jannaschii 2190 -11540679 4000707925 mj0624 (de:putative ferredoxin mj0624) (db:swissprot) FER6_METJA Q58041 METHANOCOCCUS JANNASCHII 2190 -11540679 173096 ferredoxin 2 4fe-4s) (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:for553382-553558) H64377 H64377 Methanococcus jannaschii 2190 -11540679 247058 mj0624 ferredoxin (db:genpept-bct1) (de:methanococcus jannaschii section 52 of 150 of the complete genome.) (nt:similar to percent identity: 48.00; identified by) (le:7833) (re:8009) (di:direct) U67510 U67510 g1591335 Methanococcus jannaschii 2190 -11540679 6500736821 ferredoxin:ferredoxin 2 (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0624 MJ0624 Methanococcus jannaschii 2190 -11540679

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925887	20016	42172	1035	344

Description

5000697922 ferredoxin:fdxa:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0722 MJ0722 Methanococcus jannaschii 2190 -11540680 1500686051 mj0722 (de:putative ferredoxin mj0722) (db:swissprot) FER7_METJA Q58132 METHANOCOCCUS JANNASCHII 2190 -11540680 173092 ferredoxin 2 4fe-4s) (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:rev656555-656322) B64390 B64390 Methanococcus jannaschii 2190 -11540680 247156 mj0722 ferredoxin fdxa (db:genpept-bct1) (de:methanococcus jannaschii section 61 of 150 of the complete genome.) (nt:similar to pid:726054 gb:ae000666 percent identity:) (le:2446) (re:2679) (di:complement) U67519 U67519 g1591439 Methanococcus jannaschii 2190 -11540680 6500736822 ferredoxin:fdxa:putative ferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0722 MJ0722 Methanococcus jannaschii 2190 -11540680

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925888	20017	42173	498	166

Description

5000699428 iron-sulfur flavoprotein:isf:m (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0731 MJ0731 Methanococcus jannaschii 2190 -11540681 173677 conserved hypothetical protein mj0731 (cl:methanococcus jannaschii conserved hypothetical protein mj1083) (db:pir2.dat) (mp:rev664215-663619) C64391 C64391 Methanococcus jannaschii 2190 -11540681 247165 mj0731 iron-sulfur flavoprotein isf (db:genpept-bct1) (de:methanococcus jannaschii section 61 of 150 of the complete genome.) (nt:similar to pid:1236698 percent identity: 41.98;) (le:9743) (re:10339) (di:complement) U67519 U67519 g1499548 Methanococcus jannaschii 2190 -11540681 6500736823 iron-sulfur flavoprotein:isf:m (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0731 MJ0731 Methanococcus jannaschii 2190 -11540681

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925891	20018	42174	240	79

Description

5000697923 flavoprotein:fpra:hypothetical protein (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0732 MJ0732 Methanococcus jannaschii 2190 -11540682 4000708405 mj0732 (de:hypothetical protein mj0732) (db:swissprot) Y732_METJA Q58142 METHANOCOCCUS JANNASCHII 2190 -11540682 173109 flavoprotein (cl:methanobacterium flavoprotein a) (db:pir2.dat) (mp:rev665441-664260) D64391 D64391 Methanococcus jannaschii 2190 -11540682 247166 mj0732 flavoprotein fpra (db:genpept-bct1) (de:methanococcus jannaschii section 61 of 150 of the complete genome.) (nt:similar to pid:687617 percent identity: 40.62;) (le:10384) (re:11565) (di:complement) U67519 U67519 g1591446 Methanococcus jannaschii 2190 -11540682 6500736824 flavoprotein:fpra:hypothetical protein (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0732 MJ0732 Methanococcus jannaschii 2190 -11540682

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925892	20019	42175	1716	571

Description

GTC ORF with score 272 to: (or:Gallus gallus) (sr:chicken (lambda nm1149-gizzard and okayama-berg plasmid-oviduc) (db:genpept-vrt) (de:chicken smooth muscle caldesmon mrna, complete cds.) (nt:smooth muscle caldesmon) (le:235) (re:2505) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925903	20020	42176	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925915	20021	42177	294	97

Description

5000698455 rubrerythrin:rr:putative rubrerythrin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0734 MJ0734 Methanococcus jannaschii 2190 -11540683 4000709702 mj0734 (de:putative rubrerythrin) (db:swissprot) RUBY_METJA Q58144 METHANOCOCCUS JANNASCHII 2190 -11540683 174535 rubrerythrin (cl:rubrerythrin:rubredoxin homology) (db:pir2.dat) (mp:rev666535-665921) F64391 F64391 Methanococcus jannaschii 2190 -11540683 247168 mj0734 rubrerythrin rr (db:genpept-bct1) (de:methanococcus jannaschii section 62 of 150 of the complete genome.) (nt:similar to pid:1200049 sp:p51591 percent identity:) (le:466) (re:1080) (di:complement) U67520 U67520 g1591449 Methanococcus jannaschii 2190 -11540683 6500736825 rubrerythrin:rr:putative rubrerythrin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0734 MJ0734 Methanococcus jannaschii 2190 -11540683

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925924	20022	42178	375	124

Description

5000697924 rubredoxin 1:rd1:rubredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0735 MJ0735 Methanococcus jannaschii 2190 -11540684 174534 rubredoxin (cl:rubredoxin:rubredoxin homology) (db:pir2.dat) (mp:rev666817-666575) G64391 G64391 Methanococcus jannaschii 2190 -11540684 247169 mj0735 rubredoxin 1 rd1 (db:genpept-bct1) (de:methanococcus jannaschii section 62 of 150 of the complete genome.) (nt:similar to sp:p19500 percent identity: 59.62;) (le:1120) (re:1362) (di:complement) U67520 U67520 g1591450 Methanococcus jannaschii 2190 -11540684 6500736826 rubredoxin 1:rd1:rubredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0735 MJ0735 Methanococcus jannaschii 2190 -11540684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925928	20023	42179	1197	398

Description

5000698869 rubredoxin-like non-heme iron protein:hypothetical protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0737 MJ0737 Methanococcus jannaschii 2190 -11540685 4000708406 mj0737 (de:hypothetical protein mj0737) (db:swissprot) Y737_METJA Q58147 METHANOCOCCUS JANNASCHII 2190 -11540685 173679 hypothetical protein mj0737 (cl:rubredoxin homology) (db:pir2.dat) (mp:rev667836-667651) A64392 A64392 Methanococcus jannaschii 2190 -11540685 247171 mj0737 rubredoxin-like non-heme iron protein (db:genpept-bct1) (de:methanococcus jannaschii section 62 of 150 of the complete genome.) (nt:similar to sp:p19500 percent identity: 32.56;) (le:2196) (re:2381) (di:complement) U67520 U67520 g1499555 Methanococcus jannaschii 2190 -11540685 6500736827 rubredoxin-like non-heme iron protein:hypothetical protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0737 MJ0737 Methanococcus jannaschii 2190 -11540685

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925931	20024	42180	195	64

Description

5000697925 rubredoxin 2:rd2:rubredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0740 MJ0740 Methanococcus jannaschii 2190 -11540686 174533 rubredoxin (cl:rubredoxin:rubredoxin homology) (db:pir2.dat) (mp:rev668868-668701) D64392 D64392 Methanococcus jannaschii 2190 -11540686 247174 mj0740 rubredoxin 2 rd2 (db:genpept-bct1) (de:methanococcus jannaschii section 62 of 150 of the complete genome.) (nt:similar to sp:p19500 percent identity: 61.54;) (le:3246) (re:3413) (di:complement) U67520 U67520 g1591453 Methanococcus jannaschii 2190 -11540686 6500736828 rubredoxin 2:rd2:rubredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0740 MJ0740 Methanococcus jannaschii 2190 -11540686

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925933	20025	42181	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925939	20026	42182	360	119

Description

5000698456 flavoprotein:fpaa:hypothetical protein (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0748 MJ0748 Methanococcus jannaschii 2190 -11540687 4000708407 mj0748 (de:hypothetical protein mj0748) (db:swissprot) Y748_METJA Q58158 METHANOCOCCUS JANNASCHII 2190 -11540687 173110 flavoprotein (cl:methanobacterium flavoprotein a) (db:pir2.dat) (mp:rev674937-673687) D64393 D64393 Methanococcus jannaschii 2190 -11540687 247182 mj0748 flavoprotein fpaa (db:genpept-bct1) (de:methanococcus jannaschii section 62 of 150 of the complete genome.) (nt:similar to pid:710356 gb:ae000666 percent identity:) (le:8232) (re:9482) (di:complement) U67520 U67520 g1591461 Methanococcus jannaschii 2190 -11540687 6500736829 flavoprotein:fpaa:hypothetical protein (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0748 MJ0748 Methanococcus jannaschii 2190 -11540687

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925949	20027	42183	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925956	20028	42184	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925959	20029	42185	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501925965	20030	42186	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926005	20031	42187	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926018	20032	42188	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926022	20033	42189	1308	435

Description

5000698876 ferredoxin-type protein:naph:m (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0750 MJ0750 Methanococcus jannaschii 2190 -11540688 173686 hypothetical protein mj0750 (db:pir2.dat) (mp:rev676712-675996) F64393 F64393 Methanococcus jannaschii 2190 -11540688 247184 mj0750 ferredoxin-type protein naph (db:genpept-bct1) (de:methanococcus jannaschii section 63 of 150 of the complete genome.) (nt:similar to sp:p33934 pid:405929 gb:u00096) (le:78) (re:794) (di:complement) U67521 U67521 g1592304 Methanococcus jannaschii 2190 -11540688 6500736830 ferredoxin-type protein:naph:m (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0750 MJ0750 Methanococcus jannaschii 2190 -11540688

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926023	20034	42190	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926047	20035	42191	1032	343

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926059	20036	42192	195	64

Description

GTC ORF with score 91 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t18h9.) (nt:coded for by c. elegans cdna yk68a8.5) (le:25268:25502:25795:26180) (re:25334:25749:26001:26566) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926061	20037	42193	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926086	20038	42194	2352	783

Description

5000697927 mvhb:polyferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0934 MJ0934 Methanococcus jannaschii 2190 -11540689 174431 polyferredoxin (db:pir2.dat) (mp:for864216-864845) F64416 F64416 Methanococcus jannaschii 2190 -11540689 247368 mj0934 polyferredoxin mvhb (db:genpept-bct1) (de:methanococcus jannaschii section 79 of 150 of the complete genome.) (nt:similar to gb:m34016 pid:149806 percent identity:) (le:803) (re:1432) (di:direct) U67537 U67537 g1499769 Methanococcus jannaschii 2190 -11540689 6500736831 mvhb:polyferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ0934 MJ0934 Methanococcus jannaschii 2190 -11540689

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926090	20039	42195	1101	366

Description

5000699441 iron-sulfur flavoprotein:isf:m (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1083 MJ1083 Methanococcus jannaschii 2190 -11540690 173873 conserved hypothetical protein mj1083 (cl:methanococcus jannaschii conserved hypothetical protein mj1083) (db:pir2.dat) (mp:for1022091-1022672) B64435 B64435 Methanococcus jannaschii 2190 -11540690 247516 mj1083 iron-sulfur flavoprotein isf (db:genpept-bct1) (de:methanococcus jannaschii section 93 of 150 of the complete genome.) (nt:similar to pid:1236698 percent identity: 46.84;) (le:1519) (re:2100) (di:direct) U67551 U67551 g1499931 Methanococcus jannaschii 2190 -11540690 6500736832 iron-sulfur flavoprotein:isf:m (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1083 MJ1083 Methanococcus jannaschii 2190 -11540690

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926102	20040	42196	369	122

Description

5000697928 vhug:methylviologen-reducing hydrogenase:gamma chain (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1191 MJ1191 Methanococcus jannaschii 2190 -11540691 174339 methylviologen-reducing hydrogenase gamma chain homolog (db:pir2.dat) (mp:for1132115-1132981) F64448 F64448 Methanococcus jannaschii 2190 -11540691 247624 mj1191 methylviologen-reducing hydrogenase:gamma chain (db:genpept-bct1) (de:methanococcus jannaschii section 102 of 150 of the complete genome.) (nt:similar to gb:x61204 pid:44798 pid:1747407 percent) (le:7025) (re:7891) (di:direct) U67560 U67560 g1591819 Methanococcus jannaschii 2190 -11540691 6500736833 vhug:methylviologen-reducing hydrogenase:gamma chain (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1191 MJ1191 Methanococcus jannaschii 2190 -11540691

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926111	20041	42197	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926131	20042	42198	729	242

Description

5000697929 vhua:methylviologen-reducing hydrogenase:alpha chain (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1192 MJ1192 Methanococcus jannaschii 2190 -11540692 174338 methylviologen-reducing hydrogenase alpha chain homolog (cl:methyl viologen-reducing hydrogenase alpha chain) (db:pir2.dat) (mp:for1133015-1134271) G64448 G64448 Methanococcus jannaschii 2190 -11540692 247625 mj1192 methylviologen-reducing hydrogenase:alpha chain (db:genpept-bct1) (de:methanococcus jannaschii section 102 of 150 of the complete genome.) (nt:similar to gb:x61204 pid:44799 pid:1747408 percent) (le:7925) (re:9181) (di:direct) U67560 U67560 g1591820 Methanococcus jannaschii 2190 -11540692 6500736834 vhua:methylviologen-reducing hydrogenase:alpha chain (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1192 MJ1192 Methanococcus jannaschii 2190 -11540692

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926132	20043	42199	1170	389

Description

5000697930 mvhb:polyferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1193 MJ1193 Methanococcus jannaschii 2190 -11540693 174433 polyferredoxin (cl:polyferredoxin 6x2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) (mp:for1134591-1135775) H64448 H64448 Methanococcus jannaschii 2190 -11540693 247626 mj1193 polyferredoxin mvhb (db:genpept-bct1) (de:methanococcus jannaschii section 102 of 150 of the complete genome.) (nt:similar to gb:m34016 pid:149806 percent identity:) (le:9501) (re:10685) (di:direct) U67560 U67560 g1591821 Methanococcus jannaschii 2190 -11540693 6500736835 mvhb:polyferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1193 MJ1193 Methanococcus jannaschii 2190 -11540693

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926150	20044	42200	183	60

Description

5000697932 mvhb:polyferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1303 MJ1303 Methanococcus jannaschii 2190 -11540694 174432 polyferredoxin 2 (cl:methanococcus jannaschii polyferredoxin 2) (db:pir2.dat) (mp:rev1252164-1250659) F64462 F64462 Methanococcus jannaschii 2190 -11540694 247736 mj1303 polyferredoxin mvhb (db:genpept-bct1) (de:methanococcus jannaschii section 113 of 150 of the complete genome.) (nt:similar to gb:j04540 pid:149734 gb:ae000666 percent) (le:1896) (re:3401) (di:complement) U67571 U67571 g1591942 Methanococcus jannaschii 2190 -11540694 6500736836 mvhb:polyferredoxin (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1303 MJ1303 Methanococcus jannaschii 2190 -11540694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926157	20045	42201	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926163	20046	42202	321	106

Description

6500736837 cytochrome-c3 hydrogenase:gamma chain (gtcfc:2.8) (ec:1.12.2.1) (keggfc:14.1) (tigrfc:6.5) (db:gtc-methanococcus jannaschii) MJ1446 MJ1446 Methanococcus jannaschii 2190 -11540695 173041 cytochrome-c3 hydrogenase gamma chain homolog (db:pir2.dat) (mp:for1414947-1415720) E64480 E64480 Methanococcus jannaschii 2190 -11540695 247879 mj1446 cytochrome-c3 hydrogenase:gamma chain (db:genpept-bct1) (de:methanococcus jannaschii section 127 of 150 of the complete genome.) (nt:similar to pid:563906 percent identity: 40.09;) (le:7748) (re:8521) (di:direct) U67585 U67585 g1592091 Methanococcus jannaschii 2190 -11540695 5000697934 (de:(mj1446) (pn:cytochrome-c3 hydrogenase, gamma chain) (gtcfc:2.8) (ec:1.12.2.1) (keggfc:11.1) (tigrfc:6.5) (db:gtc-methanococcus jannaschii)) MJ1446 MJ1446 Methanococcus jannaschii 2190 10091463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926195	20047	42203	660	219

Description

6500736838 putative beta-ketoacyl acyl-carrier-protein synthase:fabh:acyl carrier protein synthase (gtcfc:3.1:3.2) (ec:2.3.1.41) (keggfc:3.1) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ1546 MJ1546 Methanococcus jannaschii 2190 -11540696 172939 acyl carrier protein synthase (db:pir2.dat) (mp:for1524608-1525645) A64493 A64493 Methanococcus jannaschii 2190 -11540696 247979 mj1546 putative beta-ketoacyl acyl-carrier-protein (db:genpept-bct1) (de:methanococcus jannaschii section 137 of 150 of the complete genome.) (nt:similar to pid:1197357 percent identity: 64.20;) (le:7949) (re:8986) (di:direct) U67595 U67595 g1592177 Methanococcus jannaschii 2190 -11540696 5000697945 (de:(mj1546) (pn:acyl carrier protein synthase) (gtcfc:3.8:8.2:8.3) (ec:) (keggfc:11.2) (tigrfc:7.1) (db:gtc-methanococcus jannaschii)) MJ1546 MJ1546 Methanococcus jannaschii 2190 10091405

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926209	20048	42204	1377	458

Description

6500736839 3-hydroxy-3-methylglutaryl coenzyme a reductase:3-hydroxy-3-methylglutaryl-coenzyme a reductase:hmg-coa reductase (gtcfc:3.1:3.2:3.4) (ec:1.1.1.34) (keggfc:3.4) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ0705 MJ0705 Methanococcus jannaschii 2190 -11540697 5500685351 hmga:mj0705 (ec:1.1.1.34) (de:reductase)) (db:swissprot) HMDH_METJA Q58116 METHANOCOCCUS JANNASCHII 2190 -11540697 172916 3-hydroxy-3-methylglutaryl coenzyme a reductase (cl:methanococcus jannaschii hydroxymethylglutaryl-coa reductase (nadph)) (ec:1.1.1.-) (db:pir2.dat) (mp:for632222-633439) A64388 A64388 Methanococcus jannaschii 2190 -11540697 247139 mj0705 3-hydroxy-3-methylglutaryl coenzyme a reductase (db:genpept-bct1) (de:methanococcus jannaschii section 59 of 150 of the complete genome.) (nt:similar to gb:m83531 pid:149027 sp:q59468 percent) (le:1649) (re:2866) (di:direct) U67517 U67517 g1591421 Methanococcus jannaschii 2190 -11540697 5000697942 (de:(mj0705) (pn:3-hydroxy-3-methylglutaryl coenzyme a reductase) (gtcfc:3.8:8.2:8.3) (ec:) (keggfc:11.2) (tigrfc:7.1) (db:gtc-methanococcus jannaschii)) MJ0705 MJ0705 Methanococcus jannaschii 2190 10091392

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926230	20049	42205	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926234	20050	42206	1953	650

Description

5000697943 glycerol dehydrogenase:glda:m (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ0712 MJ0712 Methanococcus jannaschii 2190 -11540698 5500686361 mj0712 (de:hypothetical protein mj0712) (db:swissprot) Y712_METJA Q58122 METHANOCOCCUS JANNASCHII 2190 -11540698 173671 hypothetical protein mj0712 (cl:hypothetical protein mj0712) (db:pir2.dat) (mp:rev645969-644962) H64388 H64388 Methanococcus jannaschii 2190 -11540698 247146 mj0712 glycerol dehydrogenase glda (db:genpept-bct1) (de:methanococcus jannaschii section 60 of 150 of the complete genome.) (nt:similar to sp:p32665 gb:u00006 pid:396292 gb:u00096) (le:1704) (re:2711) (di:complement) U67518 U67518 g1591429 Methanococcus jannaschii 2190 -11540698 6500736840 glycerol dehydrogenase:glda:m (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ0712 MJ0712 Methanococcus jannaschii 2190 -11540698

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926261	20051	42207	3018	1005

Description

GTC ORF with score 336 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmids 9781, 8198, 9115,9981, and lambda clones 3955 and 6052.) (nt:yer114c; protein involved in bud formation;) (le:16476) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926267	20052	42208	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926280	20053	42209	1485	494

Description

6500736841 phosphatidylserine decarboxylase proenzyme 2 precursor:psd2:phosphatidylserine decarboxylase (gtcfc:3.1:3.2:5.3:8.1) (ec:4.1.1.65) (keggfc:5.3:8.1) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ0817 MJ0817 Methanococcus jannaschii 2190 -11540699 5500686417 mj0817 (de:hypothetical protein mj0817) (db:swissprot) Y817_METJA Q58227 METHANOCOCCUS JANNASCHII 2190 -11540699 173738 probable phosphatidylserine decarboxylase (cl:methanobacterium thermoautotrophicum phosphatidylserine decarboxylase) (db:pir2.dat) (mp:rev741121-740501) A64402 A64402 Methanococcus jannaschii 2190 -11540699 247251 mj0817 phosphatidylserine decarboxylase proenzyme 2 (db:genpept-bct1) (de:methanococcus jannaschii section 67 of 150 of the complete genome.) (nt:similar to sp:p53037 pid:1323300 pid:841244 percent) (le:14237) (re:14857) (di:complement) U67525 U67525 g1591506 Methanococcus jannaschii 2190 -11540699 5000698923 (de:(mj0817) (pn:hypothetical protein mj0817:hypothetical protein) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (tigrfc:15.1) (db:gtc-methanococcus jannaschii)) MJ0817 MJ0817 Methanococcus jannaschii 2190 10091892

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926283	20054	42210	525	174

Description

6500736842 idsa:mj0860 bifunctional short chain isoprenyl diphosphate synthase:farnesyl pyrophosphate synthetase:fpp synthetase:dimethylallyltransferase / geranyltranstransferase (gtcfc:3.1:3.2:3.4:9.13) (keggfc:3.4:9.11) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ0860 MJ0860 Methanococcus jannaschii 2190 -11540700 500685060 idsa:mj0860 (ec:2.5.1.1:2.5.1.10) (de:(ec 2.5.1.1) / geranyltranstransferase,)) (db:swissprot) IDSA_METJA Q58270 METHANOCOCCUS JANNASCHII 2190 -11540700 172982 bifunctional short chain isoprenyl diphosphate synthase homolog (cl:prenyl transferase a) (db:pir2.dat) (mp:rev783844-782861) D64407 D64407 Methanococcus jannaschii 2190 -11540700 247294 mj0860 bifunctional short chain isoprenyl diphosphate (db:genpept-bct1) (de:methanococcus jannaschii section 72 of 150 of the complete genome.) (nt:similar to pid:913252 sp:q53479 percent identity:) (le:936) (re:1919) (di:complement) U67530 U67530 g1591545 Methanococcus jannaschii 2190 -11540700 5000697935 (de:(mj0860) (pn:farnesyl pyrophosphate synthetase:fpp synthetase:dimethylallyltransferase :bifunctional short chain isoprenyl diphosphate synthase) (gn:idsa) (gtcfc:3.4:9.11) (ec:2.5.1.1) (idsa_metja) (keggfc:3.4:9.11) (tigrfc:) MJ0860 MJ0860 Methanococcus jannaschii 2190 10062507

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926285	20055	42211	549	182

Description

6500736843 mevalonate kinase:mk (gtcfc:3.1:3.2:3.4) (ec:2.7.1.36) (keggfc:3.4) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ1087 MJ1087 Methanococcus jannaschii 2190 -11540701 500685065 mj1087 (ec:2.7.1.36) (de:mevalonate kinase, (mk)) (db:swissprot) KIME_METJA Q58487 METHANOCOCCUS JANNASCHII 2190 -11540701 174318 mevalonate kinase (ec:2.7.1.36) (db:pir2.dat) (mp:for1026197-1027135) F64435 F64435 Methanococcus jannaschii 2190 -11540701 247520 mj1087 mevalonate kinase (db:genpept-bct1) (de:methanococcus jannaschii section 93 of 150 of the complete genome.) (nt:similar to pid:1184118 sp:q50559 gb:ae000666) (le:5625) (re:6563) (di:direct) U67551 U67551 g1591731 Methanococcus jannaschii 2190 -11540701 5000697936 (de:(mj1087) (pn:mevalonate kinase:mk:melvalonate kinase) (gtcfc:3.4) (ec:2.7.1.36) (kime_metja) (keggfc:3.4) (tigrfc:7.1) (db:gtc-methanococcus jannaschii)) MJ1087 MJ1087 Methanococcus jannaschii 2190 10062548

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926297	20056	42212	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926318	20057	42213	441	146

Description

6500736844 pssa:mj1212 cdp-diacylglycerol--serine o-phosphatidyltransferase:phosphatidylserine synthase (gtcfc:3.1:3.2:5.3:8.1) (ec:2.7.8.8) (keggfc:5.3:8.1) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ1212 MJ1212 Methanococcus jannaschii 2190 -11540702 5500685776 pssa:mj1212 (ec:2.7.8.8) (de:(phosphatidylserine synthase)) (db:swissprot) PSS_METJA Q58609 METHANOCOCCUS JANNASCHII 2190 -11540702 173002 cdpdiacylglycerol--serine o-phosphatidyltransferase (cl:bacillus subtilis cdpdiacylglycerol--serine o-phosphatidyltransferase:bacillus subtilis cdpdiacylglycerol--serine o-phosphatidyltransferase homology) (ec:2.7.8.8) (db:pir2.dat) (mp:rev1156179-1155574) C64451 C64451 Methanococcus jannaschii 2190 -11540702 247645 mj1212 cdp-diacylglycerol--serine (db:genpept-bct1) (de:methanococcus jannaschii section 104 of 150 of the complete genome.) (nt:similar to gb:d38022 sp:p39823 pid:1065993) (le:9352) (re:9957) (di:complement) U67562 U67562 g1591841 Methanococcus jannaschii 2190 -11540702 5000698054 (de:(mj1212) (pn:cdp-diacylglycerol--serine o-phosphatidyltransferase) (gtcfc:5.3:8.1) (ec:2.7.8.8) (keggfc:5.3:8.1) (tigrfc:7.1) (db:gtc-methanococcus jannaschii)) MJ1212 MJ1212 Methanococcus jannaschii 2190 10091442

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926319	20058	42214	282	93

Description

6500736845 bpld:mj1504 wbpi:lipopolysaccharide biosynthesis protein (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-methanococcus jannaschii) MJ1504 MJ1504 Methanococcus jannaschii 2190 -11540703 174309 lipopolysaccharide biosynthesis protein bpld homolog (cl:lipopolysaccharide biosynthesis protein bpld) (db:pir2.dat) (mp:rev1476248-1475148) G64487 G64487 Methanococcus jannaschii 2190 -11540703 247937 mj1504 lipopolysaccharide biosynthesis protein wbpi (db:genpept-bct1) (de:methanococcus jannaschii section 133 of 150 of the complete genome.) (nt:similar to gp:1545858 percent identity: 45.33;) (le:2993) (re:4093) (di:complement) U67591 U67591 g1592138 Methanococcus jannaschii 2190 -11540703 5000697944 (de:(mj1504) (pn:lipopolysaccharide biosynthesis protein:bpld) (gn:bpld) (gtcfc:3.8:8.2:8.3) (ec:) (keggfc:11.2) (tigrfc:7.1) (db:gtc-methanococcus jannaschii)) MJ1504 MJ1504 Methanococcus jannaschii 2190 10092364

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926325	20059	42215	1185	394

Description

6500736846 cobalamin biosynthesis precorrin-2 methyltransferase:cbil:precorrin-2 methyltransferase (gtcfc:3.7:5.11:5.14:9.10:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (tigrfc:2.3) (db:gtc-methanococcus jannaschii) MJ0771 MJ0771 Methanococcus jannaschii 2190 -11540704 5500686385 mj0771 (de:hypothetical protein mj0771) (db:swissprot) Y771_METJA Q58181 METHANOCOCCUS JANNASCHII 2190 -11540704 174437 precorrin-2 methyltransferase homolog (db:pir2.dat) (mp:for691742-692434) C64396 C64396 Methanococcus jannaschii 2190 -11540704 247205 mj0771 cobalamin biosynthesis precorrin-2 (db:genpept-bct1) (de:methanococcus jannaschii section 64 of 150 of the complete genome.) (nt:similar to gb:m59301 sp:p21639 pid:151174) (le:5055) (re:5747) (di:direct) U67522 U67522 g1592306 Methanococcus jannaschii 2190 -11540704 5000697937 (de:(mj0771) (pn:precorrin-2 methyltransferase) (gtcfc:3.7:5.11:5.13:5.14:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.13:5.14:9.13) (tigrfc:2.4) (db:gtc-methanococcus jannaschii)) MJ0771 MJ0771 Methanococcus jannaschii 2190 10092444

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926344	20060	42216	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926347	20061	42217	396	131

Description

6500736847 cobalamin biosynthesis precorrin-3 methylase:cbih:precorrin-3 methylase (gtcfc:3.7:5.11:5.14:9.10:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (tigrfc:2.3) (db:gtc-methanococcus jannaschii) MJ0813 MJ0813 Methanococcus jannaschii 2190 -11540705 5500684975 cobj:mj0813 (ec:2.1.1.131) (de:3 methyltransferase) (precorrin-3 methylase)) (db:swissprot) COBJ_METJA Q58223 METHANOCOCCUS JANNASCHII 2190 -11540705 174439 precorrin-3 methylase homolog (cl:probable precorrin-3 methylase) (db:pir2.dat) (mp:rev737562-736813) E64401 E64401 Methanococcus jannaschii 2190 -11540705 247247 mj0813 cobalamin biosynthesis precorrin-3 methylase (db:genpept-bct1) (de:methanococcus jannaschii section 67 of 150 of the complete genome.) (nt:similar to gb:l12006 sp:q05590 pid:154428 percent) (le:10549) (re:11298) (di:complement) U67525 U67525 g1591502 Methanococcus jannaschii 2190 -11540705 5000697938 (de:(mj0813) (pn:precorrin-3 methylase) (gtcfc:3.7:5.11:5.13:5.14:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.13:5.14:9.13) (tigrfc:2.4) (db:gtc-methanococcus jannaschii)) MJ0813 MJ0813 Methanococcus jannaschii 2190 10092446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926348	20062	42218	474	157

Description

6500736848 ksga:dimethyladenosine transferase (gtcfc:3.7:5.11:5.14:9.12:10.9) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (tigrfc:11.3) (db:gtc-methanococcus jannaschii) MJ1029 MJ1029 Methanococcus jannaschii 2190 -11540706 173057 dimethyladenosine transferase (cl:rrna (adenine-n6-)-methyltransferase) (db:pir2.dat) (mp:for961664-962491) D64428 D64428 Methanococcus jannaschii 2190 -11540706 247462 mj1029 dimethyladenosine transferase ksga (db:genpept-bct1) (de:methanococcus jannaschii section 87 of 150 of the complete genome.) (nt:similar to gb:d26185 sp:p37468 pid:467431) (le:9839) (re:10666) (di:direct) U67545 U67545 g1591684 Methanococcus jannaschii 2190 -11540706 5000697939 (de:(mj1029) (pn:dimethyladenosine transferase) (gtcfc:3.7:5.11:5.13:5.14:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.13:5.14:9.13) (tigrfc:10.2) (db:gtc-methanococcus jannaschii)) MJ1029 MJ1029 Methanococcus jannaschii 2190 10091475

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926356	20063	42219	882	293

Description

6500736849 cobalamin biosynthesis precorrin-6y methylase:cbie:precorrin-6y methylase (gtcfc:3.7:5.11:5.14:9.10:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (tigrfc:2.3) (db:gtc-methanococcus jannaschii) MJ1522 MJ1522 Methanococcus jannaschii 2190 -11540707 5000697940 cobl:mj1522 (ec:2.1.1.132) (de:methylase)) (db:swissprot) COBL_METJA Q58917 METHANOCOCCUS JANNASCHII 2190 -11540707 174440 precorrin-6y methylase homolog (cl:precorrin-6y methylase) (db:pir2.dat) (mp:for1500322-1500957) A64490 A64490 Methanococcus jannaschii 2190 -11540707 247955 mj1522 cobalamin biosynthesis precorrin-6y methylase (db:genpept-bct1) (de:methanococcus jannaschii section 135 of 150 of the complete genome.) (nt:similar to gb:l12006 sp:q05629 pid:154424 percent) (le:8365) (re:9000) (di:direct) U67593 U67593 g1592152 Methanococcus jannaschii 2190 -11540707

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926357	20064	42220	705	234

Description

6500736850 cobalamin biosynthesis precorrin-3 methylase:cbif:precorrin-3 methylase (gtcfc:3.7:5.11:5.14:9.10:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (tigrfc:2.3) (db:gtc-methanococcus jannaschii) MJ1578 MJ1578 Methanococcus jannaschii 2190 -11540708 174438 precorrin-3 methylase (cl:precorrin-3 methylase) (db:pir2.dat) (mp:for1554061-1554840) A64497 A64497 Methanococcus jannaschii 2190 -11540708 248011 mj1578 cobalamin biosynthesis precorrin-3 methylase (db:genpept-bct1) (de:methanococcus jannaschii section 140 of 150 of the complete genome.) (nt:similar to gb:l12006 sp:q05630 gb:x52093 pid:154426) (le:3379) (re:4158) (di:direct) U67598 U67598 g1500473 Methanococcus jannaschii 2190 -11540708 5000697941 (de:(mj1578) (pn:precorrin-3 methylase) (gtcfc:3.7:5.11:5.13:5.14:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.13:5.14:9.13) (tigrfc:2.4) (db:gtc-methanococcus jannaschii)) MJ1578 MJ1578 Methanococcus jannaschii 2190 10092445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926380	20065	42221	1056	351

Description

6500736851 rpod:mj0192 dna-directed rna polymerase:subunit d:dna-directed rna polymerase subunit d (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ0192 MJ0192 Methanococcus jannaschii 2190 -11540709 121307 rpod:mj0192 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit d,) (db:swissprot) RPOD_METJA Q57648 METHANOCOCCUS JANNASCHII 2190 -11540709 173073 dna-directed rna polymerase:subunit d (ec:2.7.7.6) (db:pir2.dat) (mp:for188641-189216) A64324 A64324 Methanococcus jannaschii 2190 -11540709 246627 mj0192 dna-directed rna polymerase:subunit d rpod (db:genpept-bct1) (de:methanococcus jannaschii section 17 of 150 of the complete genome.) (nt:similar to gp:1707823 percent identity: 40.83;) (le:7311) (re:7886) (di:direct) U67475 U67475 g1590937 Methanococcus jannaschii 2190 -11540709 5000697947 (de:(mj0192) (pn:dna-directed rna polymerase subunit d:dna-dependent rna polymerase, subunit d) (gn:rpod) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpod_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ0192 MJ0192 Methanococcus jannaschii 2190 10064618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926395	20066	42222	615	204

Description

6500736852 rpon:mj0196 dna-directed rna polymerase:subunit n:dna-directed rna polymerase subunit n (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ0196 MJ0196 Methanococcus jannaschii 2190 -11540710 173080 dna-directed rna polymerase:subunit n (cl:dna-directed rna polymerase ii chain rpb10) (ec:2.7.7.6) (db:pir2.dat) (mp:for190573-190803) E64324 E64324 Methanococcus jannaschii 2190 -11540710 121316 rpon:mj0196 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit n,) (db:swissprot) RPON_METJA Q57649 METHANOCOCCUS JANNASCHII 2190 -11540710 246631 mju67475 (le:190573) (re:190803) (di:direct) (de:or:methanococcus jannaschii pn:dna-dependent rna polymerase, subunit n gn:mj0196 le:9243 re:9473 di:direct nt:similar to p29199 percent identity: 53.7;) U67475 U67475 g1590941 Methanococcus jannaschii 2190 -11540710 5000697948 (de:(mj0196) (pn:dna-directed rna polymerase subunit n:dna-directed rna polymerase, subunit n:rpon) (gn:rpon) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpon_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ0196 MJ0196 Methanococcus jannaschii 2190 10064627

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926411	20067	42223	462	153

Description

6500736853 rpok:mj0197 dna-directed rna polymerase:subunit k:dna-directed rna polymerase subunit k (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ0197 MJ0197 Methanococcus jannaschii 2190 -11540711 121312 rpok:mj0197 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit k,) (db:swissprot) RPOK_METJA Q57650 METHANOCOCCUS JANNASCHII 2190 -11540711 173078 dna-directed rna polymerase:chain k (cl:methanococcus jannaschii dna-directed rna polymerase chain k) (ec:2.7.7.6) (db:pir2.dat) (mp:for190944-191117) F64324 F64324 Methanococcus jannaschii 2190 -11540711 246632 mj0197 dna-directed rna polymerase:subunit k rpok (db:genpept-bct1) (de:methanococcus jannaschii section 17 of 150 of the complete genome.) (nt:similar to gb:x80753 sp:p39463 pid:521086 percent) (le:9614) (re:9787) (di:direct) U67475 U67475 g1498971 Methanococcus jannaschii 2190 -11540711 5000697949 (de:(mj0197) (pn:dna-directed rna polymerase subunit k:dna-dependent rna polymerase, subunit k) (gn:rpok) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpok_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ0197 MJ0197 Methanococcus jannaschii 2190 10064623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926415	20068	42224	1455	484

Description

6500736854 phosphoribosylformylglycinamidine cyclo-ligase:purm:probable phosphoribosylformylglycinamidine cyclo-ligase:airs:phosphoribosyl-aminoimidazole synthetase:air synthase (gtcfc:4.1) (ec:6.3.3.1) (keggfc:4.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ0203 MJ0203 Methanococcus jannaschii 2190 -11540712 500685259 purm:mj0203 (ec:6.3.3.1) (de:(airs) (phosphoribosyl-aminoimidazole synthetase) (air synthase)) (db:swissprot) PUR5_METJA Q57656 METHANOCOCCUS JANNASCHII 2190 -11540712 174425 phosphoribosylformylglycinamidine cyclo-ligase (cl:phosphoribosylformylglycinamidine cyclo-ligase:phosphoribosylformylglycinamidine cyclo-ligase homology) (ec:6.3.3.1) (db:pir2.dat) (mp:for194578-195630) D64325 D64325 Methanococcus jannaschii 2190 -11540712 246638 mj0203 phosphoribosylformylglycinamidine cyclo-ligase (db:genpept-bct1) (de:methanococcus jannaschii section 18 of 150 of the complete genome.) (nt:similar to gb:j02732 sp:p12043 pid:143371) (le:3386) (re:4438) (di:direct) U67476 U67476 g1590946 Methanococcus jannaschii 2190 -11540712 5000697950 (de:(mj0203) (pn:phosphoribosylformylglycinamidine cyclo-ligase) (gtcfc:4.1) (ec:6.3.3.1) (keggfc:4.1) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ0203 MJ0203 Methanococcus jannaschii 2190 10064218

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926423	20069	42225	675	224

Description

GTC ORF with score 372 to: (sr:house mouse) (db:genpept-rod) (de:mus musculus major histocompatibility locus class ii region;fas-binding protein daxx (daxx) gene, partial cds; bing1 (bing1),tapasin (tapasin), ralgds-like factor (rlf), ke2 (ke2), ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926430	20070	42226	2271	756

Description

GTC ORF with score 793 to: (or:Rattus norvegicus) (sr:rattus norvegicus (strain:sprague dawley) adult male live) (db:genpept-rod) (de:rat mrna for canalicular multispecific organic aniontransporter(cmoat), complete cds.) (le:36) (re:4661) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926466	20071	42227	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926475	20072	42228	1806	601

Description

6500736855 amidophosphoribosyltransferase:purf:probable amidophosphoribosyltransferase:glutamine phosphoribosylpyrophosphate amidotransferase:atase (gtcfc:4.1:5.1) (ec:2.4.2.14) (keggfc:4.1:5.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ0204 MJ0204 Methanococcus jannaschii 2190 -11540713 172953 amidophosphoribosyltransferase (cl:amidophosphoribosyltransferase) (ec:2.4.2.14) (db:pir2.dat) (mp:for195730-197145) E64325 E64325 Methanococcus jannaschii 2190 -11540713 246639 mj0204 amidophosphoribosyltransferase purf (db:genpept-bct1) (de:methanococcus jannaschii section 18 of 150 of the complete genome.) (nt:similar to sp:p00497 gb:j02732 pid:143370) (le:4538) (re:5953) (di:direct) U67476 U67476 g1590947 Methanococcus jannaschii 2190 -11540713 5000697951 (de:(mj0204) (pn:amidophosphoribosyltransferase) (gtcfc:4.1:5.1) (ec:2.4.2.14) (keggfc:4.1:5.1) (tigrfc:3.2) (db:gtc-methanococcus jannaschii)) MJ0204 MJ0204 Methanococcus jannaschii 2190 10091414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926487	20073	42229	1827	608

Description

6500736856 rpol:mj0387 dna-directed rna polymerase:subunit l:dna-directed rna polymerase subunit l (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ0387 MJ0387 Methanococcus jannaschii 2190 -11540714 121315 rpol:mj0387 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit l,) (db:swissprot) RPOL_METJA Q57832 METHANOCOCCUS JANNASCHII 2190 -11540714 173079 dna-directed rna polymerase:subunit l (cl:dna-directed rna polymerase chain l) (ec:2.7.7.6) (db:pir2.dat) (mp:rev353145-352846) C64348 C64348 Methanococcus jannaschii 2190 -11540714 246821 mj0387 dna-directed rna polymerase:subunit l rpol (db:genpept-bct1) (de:methanococcus jannaschii section 33 of 150 of the complete genome.) (nt:similar to sp:p46217 percent identity: 35.56;) (le:7305) (re:7604) (di:complement) U67491 U67491 g1499176 Methanococcus jannaschii 2190 -11540714 5000697952 (de:(mj0387) (pn:dna-directed rna polymerase subunit l:dna-directed rna polymerase, subunit l:rpol) (gn:rpol) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpol_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ0387 MJ0387 Methanococcus jannaschii 2190 10064626

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926495	20074	42230	1422	473

Description

6500736857 rpoe2:mj0396 dna-directed rna polymerase:subunit e:dna-directed rna polymerase subunit e (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ0396 MJ0396 Methanococcus jannaschii 2190 -11540715 121322 rpoe2:mj0396 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit e",) (db:swissprot) RPE2_METJA Q57839 METHANOCOCCUS JANNASCHII 2190 -11540715 173075 dna-directed rna polymerase:subunit e (ec:2.7.7.6) (db:pir2.dat) (mp:rev357977-357798) D64349 D64349 Methanococcus jannaschii 2190 -11540715 246830 mj0396 dna-directed rna polymerase:subunit e (db:genpept-bct1) (de:methanococcus jannaschii section 34 of 150 of the complete genome.) (nt:similar to gb:x75411 sp:p39466 pid:415999 percent) (le:2075) (re:2254) (di:complement) U67492 U67492 g1591101 Methanococcus jannaschii 2190 -11540715 5000697953 (de:(mj0396) (pn:dna-directed rna polymerase subunit e:dna-dependent rna polymerase, subunit e"") (gn:rpoe2) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpe2_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ0396 MJ0396 Methanococcus jannaschii 2190 10064633

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926505	20075	42231	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926506	20076	42232	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926507	20077	42233	1572	523

Description

6500736858 rpoe1:mj0397 dna-directed rna polymerase:subunit e:dna-directed rna polymerase subunit e (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ0397 MJ0397 Methanococcus jannaschii 2190 -11540716 121321 rpoe1:mj0397 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit e',) (db:swissprot) RPE1_METJA Q57840 METHANOCOCCUS JANNASCHII 2190 -11540716 173074 dna-directed rna polymerase:subunit e (cl:dna-directed rna polymerase subunit e) (ec:2.7.7.6) (db:pir2.dat) (mp:rev358550-357987) E64349 E64349 Methanococcus jannaschii 2190 -11540716 246831 mj0397 dna-directed rna polymerase:subunit e rpoe1 (db:genpept-bct1) (de:methanococcus jannaschii section 34 of 150 of the complete genome.) (nt:similar to gb:x75411 sp:p39466 pid:415999 percent) (le:2264) (re:2827) (di:complement) U67492 U67492 g1591102 Methanococcus jannaschii 2190 -11540716 5000697954 (de:(mj0397) (pn:dna-directed rna polymerase subunit e":dna-dependent rna polymerase, subunit e") (gn:rpoe1) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpe1_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ0397 MJ0397 Methanococcus jannaschii 2190 10064632

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926516	20078	42234	1695	564

Description

6500736859 pura:mj0561 adenylosuccinate synthetase:imp--aspartate ligase (gtcfc:4.1:5.2) (ec:6.3.4.4) (keggfc:4.1:5.2) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ0561 MJ0561 Methanococcus jannaschii 2190 -11540717 4000709543 pura:mj0561 (ec:6.3.4.4) (de:adenylosuccinate synthetase, (imp--aspartate ligase)) (db:swissprot) PURA_METJA Q57981 METHANOCOCCUS JANNASCHII 2190 -11540717 172945 adenylosuccinate synthase (ec:6.3.4.4) (db:pir2.dat) (mp:for495588-496625) A64370 A64370 Methanococcus jannaschii 2190 -11540717 246995 mj0561 adenylosuccinate synthetase pura (db:genpept-bct1) (de:methanococcus jannaschii section 47 of 150 of the complete genome.) (nt:similar to gp:1419160 percent identity: 66.27;) (le:3112) (re:4149) (di:direct) U67505 U67505 g1591267 Methanococcus jannaschii 2190 -11540717 5000697956 (de:(mj0561) (pn:adenylosuccinate synthetase) (gtcfc:4.1:5.2) (ec:6.3.4.4) (keggfc:4.1:5.2) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ0561 MJ0561 Methanococcus jannaschii 2190 10091410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926529	20079	42235	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926535	20080	42236	717	238

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926547	20081	42237	588	195

Description

6500736860 pure:mj0616 phosphoribosylaminoimidazole carboxylase::phosphoribosylaminoimidazole carboxylase catalytic subunit:air carboxylase:airc (gtcfc:4.1) (ec:4.1.1.21) (keggfc:4.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ0616 MJ0616 Methanococcus jannaschii 2190 -11540718 4000709538 pure:mj0616 (ec:4.1.1.21) (de:(ec 4.1.1.21) (air carboxylase) (airc)) (db:swissprot) PUR6_METJA Q58033 METHANOCOCCUS JANNASCHII 2190 -11540718 174421 phosphoribosylaminoimidazole carboxylase (cl:phosphoribosylaminoimidazole carboxylase catalytic chain:phosphoribosylaminoimidazole carboxylase catalytic chain homology) (ec:4.1.1.21) (db:pir2.dat) (mp:rev546892-546419) H64376 H64376 Methanococcus jannaschii 2190 -11540718 247050 mj0616 phosphoribosylaminoimidazole carboxylase (db:genpept-bct1) (de:methanococcus jannaschii section 52 of 150 of the complete genome.) (nt:similar to sp:p22348 gb:x02586 pid:44542 percent) (le:870) (re:1343) (di:complement) U67510 U67510 g1591327 Methanococcus jannaschii 2190 -11540718 5000697957 (de:(mj0616) (pn:phosphoribosylaminoimidazole carboxylase) (gtcfc:4.1) (ec:4.1.1.21) (keggfc:4.1) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ0616 MJ0616 Methanococcus jannaschii 2190 10092435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926549	20082	42238	732	243

Description

6500736861 conserved hypothetical protein:phosphoribosylformylglycinamidine synthase ii related protein (gtcfc:4.1:14.1) (ec:6.3.5.3) (keggfc:4.1) (tigrfc:15.1) (db:gtc-methanococcus jannaschii) MJ0640 MJ0640 Methanococcus jannaschii 2190 -11540719 4000708387 mj0640 (de:hypothetical protein mj0640) (db:swissprot) Y640_METJA Q58057 METHANOCOCCUS JANNASCHII 2190 -11540719 173235 hypothetical protein homolog mj0640 (cl:conserved hypothetical protein mj0640) (db:pir2.dat) (mp:rev569876-568902) H64379 H64379 Methanococcus jannaschii 2190 -11540719 247074 mj0640 conserved hypothetical protein (db:genpept-bct1) (de:methanococcus jannaschii section 53 of 150 of the complete genome.) (nt:similar to gp:1001832 percent identity: 33.81;) (le:9473) (re:10447) (di:complement) U67511 U67511 g1591351 Methanococcus jannaschii 2190 -11540719 5000698823 (de:(mj0640) (pn:hypothetical protein mj0640:hypothetical protein:d64005_53) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (tigrfc:15.1) (db:gtc-methanococcus jannaschii)) MJ0640 MJ0640 Methanococcus jannaschii 2190 10091574

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926556	20083	42239	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926561	20084	42240	1101	366

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926575	20085	42241	702	233

Description

6500736862 thymidine phosphorylase:deoa:putative thymidine phosphorylase:tdrpase (gtcfc:4.1:4.2:4.4) (ec:2.4.2.4) (keggfc:4.1:4.2) (tigrfc:8.5) (db:gtc-methanococcus jannaschii) MJ0667 MJ0667 Methanococcus jannaschii 2190 -11540720 4000709913 mj0667 (ec:2.4.2.4) (de:putative thymidine phosphorylase, (tdrpase)) (db:swissprot) TYPH_METJA Q58081 METHANOCOCCUS JANNASCHII 2190 -11540720 174568 thymidine phosphorylase (cl:thymidine phosphorylase) (ec:2.4.2.4) (db:pir1.dat) (mp:for592705-594216) C64383 C64383 Methanococcus jannaschii 2190 -11540720 247101 mj0667 thymidine phosphorylase deoa (db:genpept-bct1) (de:methanococcus jannaschii section 56 of 150 of the complete genome.) (nt:similar to gb:l43967 sp:p47297 pid:1045724 percent) (le:1420) (re:2931) (di:direct) U67514 U67514 g1591381 Methanococcus jannaschii 2190 -11540720 5000697958 (de:(mj0667) (pn:thymidine phosphorylase) (gtcfc:4.1:4.2) (ec:2.4.2.4) (keggfc:4.1:4.2) (tigrfc:8.4) (db:gtc-methanococcus jannaschii)) MJ0667 MJ0667 Methanococcus jannaschii 2190 10092489

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926577	20086	42242	522	173

Description

GTC ORF with score 325 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f16g20 (essaiiproject).) (nt:strong similarity to beta-adaptin 1, drosophila) (le:56611:56841:57203) (re:56753:56898:57550) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926578	20087	42243	450	149

Description

6500736863 hypothetical protein:dna polymerase delta small subunit (gtcfc:4.1:4.2:14.1) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:15.1) (db:gtc-methanococcus jannaschii) MJ0702 MJ0702 Methanococcus jannaschii 2190 -11540721 5500686354 mj0702 (de:hypothetical protein mj0702) (db:swissprot) Y702_METJA Q58113 METHANOCOCCUS JANNASCHII 2190 -11540721 173665 probable dna-directed dna polymerase:delta small chain:hypothetical protein mj0702 (cl:dna-directed dna polymerase delta small chain:phosphoesterase core homology) (ec:2.7.7.7) (db:pir1.dat) (mp:for628052-629836) F64387 F64387 Methanococcus jannaschii 2190 -11540721 247136 mj0702 dna polymerase delta small subunit (db:genpept-bct1) (de:methanococcus jannaschii section 58 of 150 of the complete genome.) (nt:similar to gb:ae000666 percent identity: 40.47;) (le:12634) (re:14418) (di:direct) U67516 U67516 g1591417 Methanococcus jannaschii 2190 -11540721 5000698857 (de:(mj0702) (pn:hypothetical protein mj0702:hypothetical protein) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (tigrfc:15.1) (db:gtc-methanococcus jannaschii)) MJ0702 MJ0702 Methanococcus jannaschii 2190 10091825

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926579	20088	42244	900	299

Description

6500736864 nrdd:anaerobic ribonucleoside-triphosphate reductase (gtcfc:4.1:4.2) (ec:1.17.4.2) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-methanococcus jannaschii) (tigrfc:purines, pyrimidines, nucleosides, and nucleotides-2'-deoxyribonucleotide metabolism) MJ0832 MJ0832 Methanococcus jannaschii 2190 -11540722 1500686308 mj0832 (de:hypothetical protein mj0832) (db:swissprot) Y832_METJA Q58242 METHANOCOCCUS JANNASCHII 2190 -11540722 174473 ribonucleoside-triphosphate reductase::anaerobic intein-containing (cl:ribonucleoside-triphosphate reductase) (ec:1.17.4.2) (db:pir2.dat) (mp:for752510-757762) H64403 H64403 Methanococcus jannaschii 2190 -11540722 247266 mj0832 anaerobic ribonucleoside-triphosphate reductase (db:genpept-bct1) (de:methanococcus jannaschii section 69 of 150 of the complete genome.) (nt:similar to sp:p28903 gb:l06097 gb:u06195 gb:z46865) (le:155) (re:5407) (di:direct) U67527 U67527 g1591520 Methanococcus jannaschii 2190 -11540722 5000697959 (de:(mj0832) (pn:anaerobic ribonucleoside-triphosphate reductase) (gtcfc:4.1:4.2) (ec:1.17.4.2) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-methanococcus jannaschii)) MJ0832 MJ0832 Methanococcus jannaschii 2190 10061288

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926580	20089	42245	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926581	20090	42246	435	144

Description

GTC ORF with score 212 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid w01a11.) (nt:coded for by c. elegans cdna cm17d4; similar to) (le:26238:26367:27958:28106) (re:26321:26468:28053:28551) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926583	20091	42247	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926586	20092	42248	666	221

Description

6500736865 dna polymerase b1:putative dna polymerase (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-methanococcus jannaschii) MJ0885 MJ0885 Methanococcus jannaschii 2190 -11540723 173068 dna-directed dna polymerase:family b:intein containing precursor (cl:dna-directed dna polymerase kod) (ec:2.7.7.7) (db:pir2.dat) (mp:rev816304-811400) E64410 E64410 Methanococcus jannaschii 2190 -11540723 1500686011 mj0885 (ec:2.7.7.7) (de:putative dna polymerase,) (db:swissprot) DPOL_METJA Q58295 METHANOCOCCUS JANNASCHII 2190 -11540723 247319 mju67532 (le:811400) (re:816304) (di:direct) (de:or:methanococcus jannaschii pn:dna-dependent dna polymerase family b gn:mj0885 le:8706 re:13610 di:complement nt:similar to d29671_1 percent identity: 46.9;) U67532 U67532 g1591563 Methanococcus jannaschii 2190 -11540723 5000697960 (de:(mj0885) (pn:dna-dependent dna polymerase family b) (gtcfc:4.1:4.2) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-methanococcus jannaschii)) MJ0885 MJ0885 Methanococcus jannaschii 2190 10060066

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926604	20093	42249	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926615	20094	42250	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926639	20095	42251	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926646	20096	42252	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926653	20097	42253	600	199

Description

6500736866 purb:adenylosuccinate lyase (gtcfc:4.1:5.2) (ec:4.3.2.2) (keggfc:4.1:5.2) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ0929 MJ0929 Methanococcus jannaschii 2190 -11540724 7500889071 purb:mj0929 (ec:4.3.2.2) (de:adenylosuccinate lyase, (adenylosuccinase) (asl)) (db:swissprot) PUR8_METJA Q58339 METHANOCOCCUS JANNASCHII 2190 -11540724 172944 adenylosuccinate lyase (cl:fumarate hydratase) (ec:4.3.2.2) (db:pir2.dat) (mp:for858843-860231) A64416 A64416 Methanococcus jannaschii 2190 -11540724 7500889073 mj0929 adenylosuccinate lyase purb (db:genpept-bct1) (de:methanococcus jannaschii section 78 of 150 of the complete genome.) (nt:similar to gb:j02732 sp:p12047 pid:143366) (le:5594) (re:6982) (di:direct) U67536 U67536 g1591600 Methanococcus jannaschii 2190 -11540724 247363 mju67536 (le:858843) (re:860231) (di:direct) (de:or:methanococcus jannaschii pn:adenylosuccinate lyase gn:mj0929 le:5594 re:6982 di:direct nt:similar to p12047 percent identity: 42.5;) U67536 U67536 g1591600 Methanococcus jannaschii 2190 -11540724 5000697961 (de:(mj0929) (pn:adenylosuccinate lyase) (gtcfc:4.1:5.2) (ec:4.3.2.2) (keggfc:4.1:5.2) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ0929 MJ0929 Methanococcus jannaschii 2190 10091409

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926657	20098	42254	1281	426

Description

6500736867 phosphoribosylamine--glycine ligase:purd:glycinamide ribonucleotide synthetase (gtcfc:4.1) (ec:6.3.4.13) (keggfc:4.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ0937 MJ0937 Methanococcus jannaschii 2190 -11540725 7500889037 purd:mj0937 (ec:6.3.4.13) (de:synthetase)) (db:swissprot) PUR2_METJA Q58347 METHANOCOCCUS JANNASCHII 2190 -11540725 126040 phosphoribosylamine--glycine ligase::glycinamide ribonucleotide synthetase (cl:phosphoribosylamine--glycine ligase:phosphoribosylamine--glycine ligase homology) (ec:6.3.4.13) (db:pir1.dat) (mp:for866111-867445) A64417 A64417 Methanococcus jannaschii 2190 -11540725 7500889039 mj0937 phosphoribosylamine--glycine ligase purd (db:genpept-bct1) (de:methanococcus jannaschii section 79 of 150 of the complete genome.) (nt:similar to gb:j02732 sp:p12039 pid:143374) (le:2698) (re:4032) (di:direct) U67537 U67537 g1499772 Methanococcus jannaschii 2190 -11540725 247371 mju67537 (le:866111) (re:867445) (di:direct) (de:or:methanococcus jannaschii pn:glycinamide ribonucleotide synthetase gn:mj0937 le:2698 re:4032 di:direct nt:similar to gb:d32051 percent identity: 37.1;) U67537 U67537 g1499772 Methanococcus jannaschii 2190 -11540725 5000697962 (de:(mj0937) (pn:glycinamide ribonucleotide synthetase) (gtcfc:4.1) (ec:6.3.4.13) (keggfc:4.1) (tigrfc:8.1) (db:gtc-methanococcus jannaschii)) MJ0937 MJ0937 Methanococcus jannaschii 2190 10066522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926658	20099	42255	381	126

Description

6500736868 rpoh:mj1039 dna-directed rna polymerase:subunit h:dna-directed rna polymerase subunit h (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ1039 MJ1039 Methanococcus jannaschii 2190 -11540726 121309 rpoh:mj1039 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit h,) (db:swissprot) RPOH_METJA Q58443 METHANOCOCCUS JANNASCHII 2190 -11540726 173076 dna-directed rna polymerase:subunit h (cl:dna-directed rna polymerase chain h) (ec:2.7.7.6) (db:pir2.dat) (mp:for970764-971000) F64429 F64429 Methanococcus jannaschii 2190 -11540726 247472 mj1039 dna-directed rna polymerase:subunit h rpoh (db:genpept-bct1) (de:methanococcus jannaschii section 88 of 150 of the complete genome.) (nt:similar to gb:x59151 sp:p41559 pid:581387) (le:6866) (re:7102) (di:direct) U67546 U67546 g1591692 Methanococcus jannaschii 2190 -11540726 5000697963 (de:(mj1039) (pn:dna-directed rna polymerase subunit h:dna-dependent rna polymerase, subunit h) (gn:rpoh) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpoh_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ1039 MJ1039 Methanococcus jannaschii 2190 10064620

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926669	20100	42256	285	94

Description

6500736869 rpob2:mj1040 dna-directed rna polymerase:subunit b:dna-directed rna polymerase subunit b (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ1040 MJ1040 Methanococcus jannaschii 2190 -11540727 121320 rpob2:mj1040 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit b",) (db:swissprot) RPB2_METJA Q58444 METHANOCOCCUS JANNASCHII 2190 -11540727 173072 dna-directed rna polymerase:subunit b (cl:dna-directed rna polymerase beta chain) (ec:2.7.7.6) (db:pir2.dat) (mp:for971008-972504) G64429 G64429 Methanococcus jannaschii 2190 -11540727 247473 mj1040 dna-directed rna polymerase:subunit b (db:genpept-bct1) (de:methanococcus jannaschii section 88 of 150 of the complete genome.) (nt:similar to gb:x73293 pid:505290 sp:p41558 percent) (le:7110) (re:8606) (di:direct) U67546 U67546 g1591693 Methanococcus jannaschii 2190 -11540727 5000697964 (de:(mj1040) (pn:dna-directed rna polymerase subunit b:dna-dependent rna polymerase, subunit b"") (gn:rpob2) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpb2_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ1040 MJ1040 Methanococcus jannaschii 2190 10064631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926674	20101	42257	1095	364

Description

6500736870 rpob1:mj1041 dna-directed rna polymerase:subunit b:dna-directed rna polymerase subunit b (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ1041 MJ1041 Methanococcus jannaschii 2190 -11540728 121319 rpob1:mj1041 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit b',) (db:swissprot) RPB1_METJA Q60181 METHANOCOCCUS JANNASCHII 2190 -11540728 173071 dna-directed rna polymerase:subunit b (ec:2.7.7.6) (db:pir2.dat) (mp:for972590-974500) H64429 H64429 Methanococcus jannaschii 2190 -11540728 247474 mj1041 dna-directed rna polymerase:subunit b rpob1 (db:genpept-bct1) (de:methanococcus jannaschii section 88 of 150 of the complete genome.) (nt:similar to gb:x73293 sp:p41557 pid:581388 percent) (le:8692) (re:10602) (di:direct) U67546 U67546 g1591694 Methanococcus jannaschii 2190 -11540728 5000697965 (de:(mj1041) (pn:dna-directed rna polymerase subunit b":dna-dependent rna polymerase, subunit b") (gn:rpob1) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpb1_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ1041 MJ1041 Methanococcus jannaschii 2190 10064630

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926675	20102	42258	384	127

Description

6500736871 rpoa1:mj1042 dna-directed rna polymerase:subunit a:dna-directed rna polymerase subunit a (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ1042 MJ1042 Methanococcus jannaschii 2190 -11540729 173069 dna-directed rna polymerase:subunit a intein-containing (ec:2.7.7.6) (db:pir2.dat) (mp:for974597-978634) A64430 A64430 Methanococcus jannaschii 2190 -11540729 121317 rpoa1:mj1042 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit a',) (db:swissprot) RPA1_METJA Q58445 METHANOCOCCUS JANNASCHII 2190 -11540729 247475 mju67547 (le:974597) (re:978634) (di:direct) (de:or:methanococcus jannaschii pn:dna-dependent rna polymerase, subunit a' gn:mj1042 le:74 re:4111 di:direct nt:similar to p41556 percent identity: 74.2;) U67547 U67547 g1591696 Methanococcus jannaschii 2190 -11540729 5000697966 (de:(mj1042) (pn:dna-directed rna polymerase subunit a":dna-dependent rna polymerase, subunit a") (gn:rpoa1) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpa1_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ1042 MJ1042 Methanococcus jannaschii 2190 10064628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926679	20103	42259	1107	368

Description

6500736872 rpoa2:mj1043 dna-directed rna polymerase:subunit a:dna-directed rna polymerase subunit a (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.1) (db:gtc-methanococcus jannaschii) MJ1043 MJ1043 Methanococcus jannaschii 2190 -11540730 121318 rpoa2:mj1043 (ec:2.7.7.6) (de:dna-directed rna polymerase subunit a",) (db:swissprot) RPA2_METJA Q58446 METHANOCOCCUS JANNASCHII 2190 -11540730 173070 dna-directed rna polymerase:subunit a intein-containing (ec:2.7.7.6) (db:pir2.dat) (mp:for978709-981288) B64430 B64430 Methanococcus jannaschii 2190 -11540730 247476 mj1043 dna-directed rna polymerase:subunit a (db:genpept-bct1) (de:methanococcus jannaschii section 89 of 150 of the complete genome.) (nt:similar to gb:x73293 gb:x15970 pid:44781 pid:505293) (le:4186) (re:6765) (di:direct) U67547 U67547 g1591697 Methanococcus jannaschii 2190 -11540730 5000697967 (de:(mj1043) (pn:dna-directed rna polymerase subunit a:dna-dependent rna polymerase, subunit a"") (gn:rpoa2) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpa2_metja) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-methanococcus jannaschii)) MJ1043 MJ1043 Methanococcus jannaschii 2190 10064629

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926687	20104	42260	1950	649

Description

6500736873 gmp synthase:guaa:gmp synthetase (gtcfc:4.1:5.1) (ec:6.3.5.2) (keggfc:4.1:5.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ1131 MJ1131 Methanococcus jannaschii 2190 -11540731 173153 gmp synthase glutamine-hydrolyzing (ec:6.3.5.2) (db:pir2.dat) (mp:rev1073028-1072096) B64441 B64441 Methanococcus jannaschii 2190 -11540731 247564 mj1131 gmp synthase guaa (db:genpept-bct1) (de:methanococcus jannaschii section 98 of 150 of the complete genome.) (nt:similar to gb:m83691 sp:p29727 pid:143012) (le:68) (re:1000) (di:complement) U67556 U67556 g1592321 Methanococcus jannaschii 2190 -11540731 5000697978 (de:(mj1131) (pn:gmp synthetase) (gtcfc:4.1) (ec:) (keggfc:11.2) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ1131 MJ1131 Methanococcus jannaschii 2190 10091530

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926688	20105	42261	297	98

Description

6500736874 purl:phosphoribosylformylglycinamidine synthase ii (gtcfc:4.1) (ec:6.3.5.3) (keggfc:4.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ1264 MJ1264 Methanococcus jannaschii 2190 -11540732 174427 phosphoribosylformylglycinamidine synthase:component ii:formylglycinamide ribotide amidotransferase:phosphoribosylformylglycinamidine synthetase (cl:phosphoribosylformylglycinamidine synthase component ii) (ec:6.3.5.3) (db:pir1.dat) (mp:rev1209847-1207646) G64457 G64457 Methanococcus jannaschii 2190 -11540732 247697 mj1264 phosphoribosylformylglycinamidine synthase ii (db:genpept-bct1) (de:methanococcus jannaschii section 109 of 150 of the complete genome.) (nt:similar to gb:j02732 sp:p12042 pid:143369) (le:2071) (re:4272) (di:complement) U67567 U67567 g1591899 Methanococcus jannaschii 2190 -11540732 5000697968 (de:(mj1264) (pn:phosphoribosylformylglycinamidine synthase ii) (gtcfc:4.1) (ec:6.3.5.3) (keggfc:4.1) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ1264 MJ1264 Methanococcus jannaschii 2190 10092438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926702	20106	42262	342	113

Description

5000697969 ndk:mj1265 nucleoside diphosphate kinase::nucleoside diphosphate kinase:ndk:ndp kinase (gtcfc:4.1:4.2:4.4) (ec:2.7.4.6) (keggfc:4.1:4.2) (tigrfc:8.2) (db:gtc-methanococcus jannaschii) MJ1265 MJ1265 Methanococcus jannaschii 2190 -11540733 120047 ndk:mj1265 (ec:2.7.4.6) (de:nucleoside diphosphate kinase, (ndk) (ndp kinase)) (db:swissprot) NDK_METJA Q58661 METHANOCOCCUS JANNASCHII 2190 -11540733 174390 nucleoside-diphosphate kinase (cl:nucleoside-diphosphate kinase) (ec:2.7.4.6) (db:pir2.dat) (mp:rev1210346-1209924) H64457 H64457 Methanococcus jannaschii 2190 -11540733 247698 mj1265 nucleoside diphosphate kinase:ndk (db:genpept-bct1) (de:methanococcus jannaschii section 109 of 150 of the complete genome.) (nt:similar to gb:l42023 sp:p43802 pid:1005954) (le:4349) (re:4771) (di:complement) U67567 U67567 g1591900 Methanococcus jannaschii 2190 -11540733 6500736875 ndk nucleoside diphosphate kinase::nucleoside diphosphate kinase:ndk:ndp kinase (gtcfc:4.1:4.2:4.4) (ec:2.7.4.6) (keggfc:4.1:4.2) (tigrfc:8.2) (db:gtc-methanococcus jannaschii) MJ1265 MJ1265 Methanococcus jannaschii 2190 -11540733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926703	20107	42263	1215	404

Description

6500736876 adec:adenine deaminase (gtcfc:4.1:4.4) (ec:3.5.4.2) (keggfc:4.1) (tigrfc:8.5) (db:gtc-methanococcus jannaschii) MJ1459 MJ1459 Methanococcus jannaschii 2190 -11540734 5000697970 mj1459 (ec:3.5.4.2) (de:probable adenine deaminase, (adenase) (adenine aminase)) (db:swissprot) ADEC_METJA Q58854 METHANOCOCCUS JANNASCHII 2190 -11540734 172940 adenine deaminase (cl:adenine deaminase adec) (ec:3.5.4.2) (db:pir2.dat) (mp:for1428283-1429953) B64482 B64482 Methanococcus jannaschii 2190 -11540734 247892 mj1459 adenine deaminase adec (db:genpept-bct1) (de:methanococcus jannaschii section 128 of 150 of the complete genome.) (nt:similar to gb:d37799 sp:p39761 gb:x83795 pid:633167) (le:7465) (re:9135) (di:direct) U67586 U67586 g1592101 Methanococcus jannaschii 2190 -11540734

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926707	20108	42264	234	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926722	20109	42265	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926734	20110	42266	597	198

Description

6500736877 gmp synthase:guaa:gmp synthetase (gtcfc:4.1:5.1) (ec:6.3.5.2) (keggfc:4.1:5.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ1575 MJ1575 Methanococcus jannaschii 2190 -11540735 173154 gmp synthetase (cl:glutamine amidotransferase:trpg homology) (ec:6.3.-.-) (db:pir2.dat) (mp:for1550952-1551518) F64496 F64496 Methanococcus jannaschii 2190 -11540735 248008 mj1575 gmp synthase guaa (db:genpept-bct1) (de:methanococcus jannaschii section 140 of 150 of the complete genome.) (nt:similar to gb:l25883 sp:p49056 pid:495734) (le:270) (re:836) (di:direct) U67598 U67598 g1592335 Methanococcus jannaschii 2190 -11540735 5000697981 (de:(mj1575) (pn:gmp synthetase) (gtcfc:4.1) (ec:) (keggfc:11.2) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ1575 MJ1575 Methanococcus jannaschii 2190 10091531

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501926742	20111	42267	1713	570

Description

6500736878 purc:phosphoribosylaminoimidazolesuccinocarboxamide synthase (gtcfc:4.1) (ec:6.3.2.6) (keggfc:4.1) (tigrfc:8.3) (db:gtc-methanococcus jannaschii) MJ1592 MJ1592 Methanococcus jannaschii 2190 -11540736 174422 phosphoribosylaminoimidazolesuccinocarboxamide synthase (cl:phosphoribosylaminoimidazolesuccinocarboxamide synthase) (ec:6.3.2.6) (db:pir2.dat) (mp:for1564604-1565332) G64498 G64498 Methanococcus jannaschii 2190 -11540736 248025 mj1592 phosphoribosylaminoimidazolesuccinocarboxamide (db:genpept-bct1) (de:methanococcus jannaschii section 141 of 150 of the complete genome.) (nt:similar to gb:j02732 sp:p12046 pid:143367) (le:3904) (re:4632) (di:direct) U67599 U67599 g1592203 Methanococcus jannaschii 2190 -11540736 5000697971 (de:(mj1592) (pn:phosphoribosylaminoimidazolesuccinocarboxamide synthase) (gtcfc:4.1) (ec:6.3.2.6) (keggfc:4.1) (tigrfc:8.2) (db:gtc-methanococcus jannaschii)) MJ1592 MJ1592 Methanococcus jannaschii 2190 10092436